The Midstates Consortium for Math and Science presents

Undergraduate Research Symposium

Biological Sciences and Psychology

November 10 & 11, 2023
Washington University in St. Louis

Beloit College - Carthage College - Colorado College - Grinnell College
Gustavus Adolphus College - Hope College - Knox College
Lawrence University - Macalester College
St. Olaf College - University of Chicago
Washington University in St. Louis

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Midstates Consortium for Math and Science Undergraduate Research Symposium
Biological Sciences and Psychology
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November 10 & 11, 2023

Program Schedule
Friday, November 10

All times are Central Time Zone

1:00 – 5:00 pm	**Registration**	**The DoubleTree Hotel Lobby**
5:30 pm	**Welcome** Dr. Anthony Smith and Dr. Ed Hansen	**Eric P. Newman Educational Center (EPNEC) Auditorium**
5:45 pm	**Keynote Address** Pamela Woodard Professor of Radiology, Chair of Dept. of Radiology and Director of the Mallinckrodt Institute of Radiology, Washington University School of Medicine *"Cardiac Disease and Oncology"*	
7:00 – 8:00 pm	**Buffet Dinner**	**Eric P. Newman Educational Center (EPNEC) Great Rooms A and B**
	Introductions and Brief Comments Steve Mennerick Associate Dean of the Roy and Diana Vagelos Division of Biology & Biomedical Sciences Washington University School of Medicine Ed Hansen, Director Midstates Consortium for Math and Sciences	
8:15 pm	**Janet Andersen Lecture** Dr. Devavani Chatterjea *"Bodies of fire: Inflammation and discovery research as life-changing forces"*	**Eric P. Newman Educational Center (EPNEC) Auditorium**
Following lecture	**Group Picture**	**EPNEC Lobby**

Saturday, November 11

All Saturday events are at the Eric P. Newman Educational Center (EPNEC)

All times are Central Time Zone

6:00 to 10:00 am	**Breakfast at hotel**	**DoubleTree Lobby**
8:15 am	*If checking out from hotel, there is a locked room for luggage and posters at EPNEC.*	**EPNEC Lobby**
8:15 am - 8:30 am	**Check set-up for oral presentations I.A, I.B, I.C** **All speakers in each session**	**Great Room A,** **Seminar rooms A & B**
8:30 am – 9:40 am	**Session I Oral Presentations of Student Papers** 15 min presentations, 2 min between talks Session I.A: (4) 8:30, 8:47, 9:04, 9:21 Session I.B: (4) Session I.C: (4)	 Great Room A Seminar Room A Seminar Room B
9:40am -9:55 am	**Break, Set-up for Poster Session 1 (P1)**	**Lobby, Great Room B**
9:55 am - 11:00 am	**Poster Session P1**	**EPNEC Great Room B**
11:00 am – 11:15 am	**Set-up for Poster Session 2 (P2)**	**EPNEC Great Room B**
11:15 am – 12:15 pm	**Poster Session P2**	**EPNEC Great Room B**
12:15 pm - 12:40 pm	**Buffet Lunch** *Take lunch to presentation of your choice*	**EPNEC Lobby**
12:40 pm - 1:30 pm	***Applying to Graduate School*** ***Graduate Student Panel*** ***Washington University in St. Louis*** *Moderator: Andrew Richards* **Graduate Student Panelists**	**Seminar Room B**
12:40 pm – 1:30 pm	**Consortium Faculty Gathering**	**Seminar Room A**
1:30 pm - 1:40 pm	**Check set-up for oral presentations II.D, II.E, II.F** **All speakers in each session**	**Great Room A,** **Seminar rooms A & B**

1:40 pm – 3:05 pm	**Session II Oral Presentations of Student Papers** 15 min presentations, 2 min between talks Session II.D (5) 1:40, 1:57, 2:14, 2:31, 2:48 Session II.E: (4) Session II.F: (5)	 Great Room A Seminar Room A Seminar Room B
3:05 pm - 3:20 pm	**Break, Set-up for Poster Session 3 (P3)**	**Lobby, Great Room B**
3:20 pm – 4:20 pm	**Poster Session P3** (32)	**EPNEC Great Room B**
4:20 pm – 4:40 pm	**Meeting Concludes** Remove posters & pick up box dinners Complete evaluations – available online	**EPNEC Lobby**

2023 Keynote Lecture

Pamela K. Woodard, MD
Director, Mallinckrodt Institute of Radiology
Elizabeth E. Mallinckrodt Professor of Radiology Chair, Department of Radiology
Professor of Biomedical Engineering
Head, Advanced Cardiac Imaging (CT/MR) Dr.

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Title: *Cardiac Disease and Oncology*

Biographical Sketch: Pamela K. Woodard, M.D. is the Elizabeth E. Mallinckrodt Professor of Radiology, Chair of the Department of Radiology, and Director of the Mallinckrodt Institute of Radiology, Washington University School of Medicine in St. Louis, where she is also Professor of Internal Medicine, Pediatrics, and Biomedical Engineering. She is a Siteman Cancer Center member. Dr. Woodard's undergraduate, medical (MD), and residency training was at Duke University. She completed her internship in Internal Medicine at the University of North Carolina at Chapel Hill, and did her fellowship in cardiothoracic imaging at the Mallinckrodt Institute of Radiology at Washington University. Dr. Woodard leads her own research group and is currently PI or MPI on three NIH R01 grants and a Department of Defense grant on imaging in cardiovascular disease. She has over 200 manuscripts, several patents, and has served as a standing member or chair on several NIH study sections. She is Director of the NIH-funded clinician-scientist T32 translational imaging research program, TOP-TIER, for residents and fellows. Her clinical and research area of expertise is cardiovascular imaging. She is a member of many professional organizations, including the American College of Radiology (ACR) where she serves on the Board of Chancellors, the Society for Coronary Computed Tomography (SCCT) where she serves on the Board of Directors, and the Radiological Society of North America (RSNA) where she serves on the Board of Trustees of the Research and Education Foundation. Dr. Woodard is a fellow of the American Heart Association (FAHA), American College of Radiology (FACR), Society of Coronary Computed Tomography (MSCCT), Society of Cardiac Magnetic Resonance (FSCMR), American Association for the Advancement of Science (FAAAS), and the American Institute for Medical and Biological Engineering (FAIMBE).

2023 Janet Andersen Lecture

Devavani Chatterjea, PhD, MPH
Biology Department,
Macalester College
Saint Paul, Minnesota

Title: *Bodies of fire: inflammation and discovery research as life-changing forces*

Abstract: We are constantly exposed to countless chemicals - in the air we breathe, the water we drink, and the important and useful objects that shape and support our daily lives. Though chronic pain is on the rise around the globe, it is not often thought to be an outcome of harmful chemical exposures. Our team studies the immune consequences of exposure to preservatives and their potential to cause long lasting chronic pain. The story of this research is also the story of the imagination, hard work, and dedication of numerous undergraduate students at Macalester College; from 2006 until now, they have been the life-force of these investigations and the discoveries you will hear about today.

About Professor Chatterjea: The letter nominating Dr. Chatterjea for the award emphasized her outstanding record in mentoring students and her impact on STEM education within the larger Macalester College community. Her scholarship occurs at the intersection of immunology, neuroscience and public health with a special emphasis on the environmental drivers of chronic pain. She has had an exceptionally prolific research program with over 100 research students mentored at Macalester in the last sixteen years. Her publication and fundraising record is remarkable, and especially impressive is her success at mentoring students from groups historically marginalized in STEM fields. She is known as an inspirational teacher who puts the welfare of her students front and center. Particularly relevant to the Janet Andersen Award is the broad range of interdisciplinary courses she has developed and taught. Dr. Chatterjea is known for her transformative leadership in promoting diversity, equity, and inclusion throughout the STEM program in Macalester and beyond by example and informal discussions, as well as formal workshops and presentations.

The Janet Andersen Lecture Award

Professor Janet Andersen was a beloved faculty member in the Hope College Mathematics Department and served enthusiastically as the Midstates Consortium Director for five years before her life ended tragically in an automobile accident in November 2005. As a teacher and scholar, Janet was devoted to providing creative, high quality learning experiences for her students, and she herself was always learning as she was teaching. As Consortium Director, she looked for ways to connect with and support natural science faculty, both new and experienced. To honor Janet's work with students and faculty in her teaching, research and service to the Consortium, the Janet Andersen Lecture Award was established in 2008. Each year, two faculty nominees from Consortium institutions are selected by the Executive Committee to present the Janet Andersen Lecture at one or both of the fall Undergraduate Research Symposia on a topic of his or her expertise.

Oral Session I Schedule

SESSION I.A: 8:30-9:40 am in Great Room A Moderator: Lyn Stahl			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.A.1	Jayitha Gaggenapally	Beloit College	Sense of Belonging and Existential Isolation
I.A.2	Morgan Ramirez	University of Chicago	Infectious Disease Impact on Cognitive Health and Alzheimer's Disease: Implications for Aging in Panama
I.A.3	Goichi Suganuma	Knox College	ADHD, boredom, impulsivity, and time perception
I.A.4	Finneas Frawley	Lawrence University	Validation of the Sexual Education Comprehensiveness Scale

SESSION I.B: 8:30-9:40 am in Seminar Room A Moderator: Elana Tonc			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.B.1	Kollin Kolb	Washington University	Cardiac Radiation Attenuates Cardiac Dysfunction and Macrophage Response in Mice with Cardiomyopathy
I.B.2	Tia Peterson	Colorado College	Presence of Pathogenic Variants in Circular RNA of Presenilin 1 and 2
I.B.3	Jo-Hsuan Chen	Macalester College	Investigating the Effects of Methylisothiazolinone (MI) on Mast Cells
I.B.4	Rajiv Swarup	Washington University	Choroid Plexus Cell Junction Breakdown in Post-Hemmorhagic Hydrocephalus

SESSION I.C: 8:30-9:40 am in Seminar Room B Moderator: Devanani Chatterjea			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.C.1	Marco Lopez G	University of Chicago	Taking the long way around: elucidating ecology from morphology in chondrichthyan cranial lateral line canals
I.C.2	Laken Hairston	Lawrence University	Exposure to parasitoid wasps induces thicker and stiffer cuticle in flies
I.C.3	Vu-Anh Le	Beloit College	Life Cycle Assessment of Biodegradable Plastic Packaging Subject to Comprehensive Organic Sorting
I.C.4	Madeline Chaplin	Gustavus Adolphus	Effects of Diurnal Cooling on RCH Induction in *Drosophila Melanogaster*

Oral Session II Schedule

SESSION II.D: 1:40-3:05 pm Great Room A Moderator: Travis Law			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.D.1	Mayher Kaur	University of Chicago	Metabolic Rewiring Supports Circulating Tumor Cells in Non-Small Cell Lung Cancer
II.D.2	Arjun Nair	Washington University	Impaired neurogenesis with reactive astrocytosis in the hippocampus in a porcine model of acquired hydrocephalus.
II.D.3	Genxuan Lian	Grinnell College	Telomere and Telomerase Hallmarks in Cancer Cell Regulation: Measurement, Gain-of-function Genotoxicity and the Novel Prisonbreak Model
II.D.4	Hoi Wan Lee	University of Chicago	Ephrin Receptor A4 is a novel mechanism of BACH1 driven metastasis in Triple-negative Breast Cancer
II.D.5	Sophie Hu	University of Chicago	A Drug Screening Approach for Enhanced Colorectal Tumor Killing of CAR-NK-92 Cells

SESSION II.E: 1:40-3:05 pm Seminar Room A Moderator: Pamela Kittelson			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.E.1	Kaia Meyer	Gustavus Adolphus College	Changes in metabolic rates of *Belgica antarctica* during recovery from sublethal freezing
II.E.2	John Georgiades	Washington University	Structural insights into flavin redox cycling in the *Helicobacter pylori* dihydroorotate dehydrogenase
II.E.3	Ella Sontowski	Gustavus Adolphus College	Investigating temperature tolerances on diploid versus polyploid germination: implications for cytogeographic patterns of *Solidago gigantea*
II.E.4	Levi Kaster	Washington University	A Text-Mining Model for Extracting Phenotypes from NF1 Clinical Notes

SESSION II.F: 1:40-3:05 pm Seminar Room B Moderator: Vince Eckhart			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.F.1	Lowell Finster	Washington University	Plasma cell-free DNA as a prognostic sepsis biomarker
II.F.2	Liam Leeming	University of Chicago	The Roles of Arp2/3 Nucleation Promoting Factors in Actin Cytoskeleton Self Organization
II.F.3	Sean Teng	Washington University	Crystal Structure of Unknown Mycolic Acid SAM methyltransferase UmaA from M. tuberculosis
		Over for II.F.4.4 & II.F.5	

II.F.4	Amelia Li	Washington University	Effects of wild-type and mutant cysteine string protein alpha in autophagy-lysosome phenotype in SH-SY5Y cells
II F.5	Megan Woelkers	University of Chicago	SaO2/FiO2 ratio as a marker of acute chest syndrome severity in sickle cell disease

Poster Session P1: 9:55 -11:00 am in Great Room B & Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.1	Jessica Schultz	Carthage College	Combating antibiotic resistance: The antimicrobial properties of L-leucine surfactants
P1.2	Cara Conforti	Washington University	Discovering SCN Network Organization through Enhanced Behavioral Feedback
P1.3	Anna Koppin	Hope College	Lysine 473 regulates the activity and trafficking of the cystine/glutamate transporter, System xc-.
P1.4	Ama Ameyaw	Beloit College	Identifying and Characterizing Antibiotics from Soil Microbes
P1.5	Blake Rose	Gustavus Adolphus College	The role of SLCO3A1 in macrophage efferocytosis
P1.6	Sophie Laye	Washington University	Role and mechanism of abnormal DNA methylation in Huntington's disease
P1.7	Aidan Wells	Colorado College	RNA splicing factor, MBL-1, is required for sensory neuron morphogenesis in *C. elegans*
P1.8	Arlet Montalvo-Mosso	Lawrence University	A mammalian system for expression and purification of the human ribonuclease/angiogenin inhibitor
P1.9	Ngoc Nguyen	Knox College	Effect of *Bacopa monnieri* extract on lipopolysaccharide-induced inflammatory response of J774A.1
P1.10	Mackenzie Joe	Washington University	Impact of Radio Drama on Mental Health Care Seeking Behaviors and Community Stigma in Ugandag
P1.11	Eunice Lim	Macalester College	Investigating Fibroblast Responses to Methylisothiazolinone Treatment
P1.12	Yalda Pourshaban	St. Olaf College	Mapping of Adaptor Protein Binding Along O-GlcNAc Transferase's (OGT) Tetratricopeptide Repeat (TPR) Domain
P1.13	Matthew Czmer Isabella Bozzi	Hope College	Semantic memory for religious concepts in undergraduate students
P1.14	Daleep Grewal	Washington University	Advantages of Enrolling Intellectual and Developmental Disorder Patients with Multiple Gene Variants to Clinical Studies
P1.15	Phoebe Holz	University of Chicago	Is Resting-State Gamma Production a Biomarker of Cognitive Deficits in People with Schizophrenia?
P1.16	Joe Ntayagabiri	Macalester College	GluN2B and ADC Expression in Spinal Cord of Mice with Inflammatory Pain
P1.17	Kevin Kyaw	Beloit College	Soil and Sediment samples had a similar number of Antibiotic-Producing Bacteria

Poster Session P1 (continued): 9:55 – 11:00 am in Great Room B & Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.18	Phoebe Gordon	Colorado College	Mayfly (Genus: *Neohagenulus*) food resource shift after hurricanes may increase rate of ecological recovery
P1.19	Moura Saad	Macalester College	Effects of demographics and lifestyle choices on spatial navigation ability in the aging brain
P1.20	Hrishi Kousik	Washington University	The Impact of Dysbiotic Gut Microbiota on Obesity and Glucose Intolerance
P1.21	Nicole Lagman	Lawrence University	Angiogenin Distribution in Mammalian Cells
P1.22	Nancy Garcia	Grinnell College	An analysis of the effect altered temperatures have on functional properties of *A. alternata* and neighbor species in *A. gerardi* litter
P1.23	Lexus Putt	Hope College	Modeling dopaminergic loss in the zebrafish olfactory system
P1.24	Divya Purswani	Washington University	Sex-specific programming of the Late Gestational Fetal Heart and Lungs with Prenatal T Excess
P1.25	Rahaf Qarabsa Blanca Torres Lopez	St. Olaf College	Is the Hawaiian acoustic parasitoid fly *Ormia ochracea* evolving its hearing capabilities to better detect rapidly evolving cricket songs?
P1.26	Erin Kim	Colorado College	Seasonal germination responses of *Liatris punctata* to heat and smoke
P1.27	Nathan Finegold	Lawrence University	Biophysical Characterization of Post Translational Modification within the Loop Region of Rop
P1.28	Saumith Menon	Washington University	The effects of neuromodulators tabernanthalog and ibogainalog on the α1β2γ2L GABAA receptor
P1.29	Natalie Olander	Hope College	Effects of delayed HCA exposure on a rat model of Bipolar Disorder
P1.30	Emma Uder	Washington University	Tyson Research Center Mosquito Diversity: Creating a Collection
P1.31	Alexandra Murphy	Beloit College	Isolating Potential Novel Antibiotic Compounds from Soil Bacteria
P1.32	Nancy Nabahire Ngutete	St. Olaf College	Characterization of a Stalkless Mutant in *C. crescentus*

Poster Session P2: 11:15 am – 12:15 pm in Great Room B & Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.1	Neil Panwalker	Washington University	Investigating Functional Roles of Orbitofrontal Cortex-Dorsomedial Striatum Projection during Economic Choice Task in Mice
P2.2	Satirtha Saha Protya	Beloit College	Computational approach to find difference between CCS values of all L vs D Amino Acid containing peptides and calculating peak resolving power
P2.3	Taylor Laurin	Hope College	Investigating the intersection of one carbon metabolism and mitochondrial genome maintenance
P2.4	Akwasi Amoah	Gustavus Adolphus College	Identifying the features responsible for Nonsense-mediated decay of the CEP3 mRNA
P2.5	Hannah Davis	Washington University	Improving KMT2A Rearrangement Detection in Leukemia
P2.6	Oliver Lagasse	Macalester College	Characterizing changes in the inflammatory potential of fibroblasts in response to repeated in-vivo methylisothiazolinone exposure
P2.7	Maverick Leer	Carthage College	Cladistic Ontogeny of *Eurypterus rempies*
P2.8	Mai Tien Nguyen	Colorado College	Inner kinetochore compositions across diverse centromere types in budding yeasts
P2.9	Joseph Kaczor	University of Chicago	Characterizing Photo-sensing in Non-photosynthetic Bacteria
P2.10	Wendy Wang	Washington University	Strategies for Including Individuals with Disabilities in Clinical Trials
P2.11	Sean Rogers	St Olaf College	Utilizing Patient DNA Sequencing Data to Evaluate 7 ADPKD Candidate Genes
P2.12	Davi Zola de Araujo	Hope College	Role of Temperature in Cluster K1 Mycobacteriophage Growth Properties
P2.13	Elizabeth Zeng	Washington University	How Tardigrade CAHS2 Protein forms Condensates to protect Cells from Reactive Oxygen Species induced Stress
P2.14	Alexandra Marcoullier	Knox College	Phytoextraction of Nickel by Brassiaceae and Asteraceae Species
P2.15	Caleb Yuan	Lawrence University	The Mindfulness-based Kindness Project: Resilience & Growth During the Pandemic
P2.16	Edgar Caracoza	Beloit College	Antibiotic-Producing Bacteria More Frequent in Soil than Water in Beloit, WI
P2.17	Kody Kobayashi	Macalester College	Identification and characterization of VGF in the nucleus accumbens

Poster Session P2 (continued) : 11:15 am -12:15 pm in Great Room B & Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.18	Allan Wang	Washington University	Uncovering enhanced Hsp104 NBD1 variants with improved substrate specificity
P2.19	Elianna Sandman	Hope College	Chemical defenses in the seeds of pioneer plants
P2.20	Trisha Vinay	University of Chicago	Investigation of the roles of MAL and MAL2 proteins in tumor immune evasion
P2.21	Mackenzie Horutz	Carthage College	Measuring functional recovery of vision after injury in zebrafish using the optokinetic response
P2.22	Shelly Xu	Washington University	Examining differential mitochondrial characteristics among retinal ganglion cell types
P2.23	Sydney Morris	Colorado College	The Effects of Burn Severity on Soil Chemistry and *Pinus ponderosa* Regeneration in Waldo Canyon, CO
P2.24	Ryan Saladin	Lawrence University	Musical improvisation decreases stress and music performance anxiety in classically trained vocalists
P2.25	Eric Kwon	Washington University	FLT-3 chimeric antigen receptors on conventional type 1 dendritic cells induce greater survival ability
P2.26	Anna Jonaus	Macalester College	Glucosinolates and Growth: Quantifying Allelopathy Resistance in Soybeans to Pennycress Glucosinolates
P2.27	Arya Murthy Feven Getachew	Grinnell College	The role of vimentin in zebrafish lateral line development
P2.28	Charlotte Ho	Lawrence University	Evolutionary conservation of WASp function during endocytosis in yeast
P2.29	Sai Prem	Washington University	Evaluating the radiosensitization potential of the antibody drug conjugate sacituzumab govitecan-hziy (IMMU-132)
P2.30	Sofia Rosenberger	Hope College	Ubiquitination of xCT: impacts on the protein's stability, turnover rate, and localization
P2.31	Emma Stock	Gustavus Adolphus College	ISGylation disrupts neuronal proteostasis & methods for quantifying miRNAs isolated from neuronal extracellular vesicles
P2.32	Zyva Sheikh	University of Chicago	Spheroid Viability Prediction with Deep Learning: Automating Quality Control in Tissue Engineering Applications
P2.33	Andrew Wong	Washington University	A Novel Droplet Digital PCR (DDPCR) Assay for the Detection of Tumor Cells and Predicting Metastasis in Breast Cancer Patients

Poster Session P3: 3:20-4:20 pm Great Room B & Lobby			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.1	Amanda Yang	Washington University	Cell-Cell Communication Analysis Using Single-Cell RNA Sequencing of Wildtype and CCR7 Knockout Human Trophoblast Organoids
P3.2	Tianlong Wang Takeshi Matsuda	Beloit College	Enhancing Heart Disease Prediction by Exploring Federated Learning in Machine Learning
P3.3	Frederick Melges Jacquelin D'Lamater	Hope College	Metabolic Diversity of *Escherichia coli*: Is there a Distinction Between Clinically-Derived and Water-Derived Strains?
P3.4	Michelle Osiro	Macalester College	Characterizing Early Immune Infiltration and Tumor Microenvironment Development in Pancreatic Cancer
P3.5	Victoria Afe	Washington University	Characterizing Acid Response Genes in *Klebsiella pneumoniae*
P3.6	Raymond Fleming Kaila Luell	Colorado College	Estadiol-mediated spinogenesis in avian NCM with novel sounf exposure during exposure to novel sound.
P3.7	Thy Le	Knox College	MicroRNAs in Cnidaria: Target Recognition and Conservation
P3.8	Madisyn Eyman	Lawrence University	Paternal Aggression Elicits an Increase in Corticosterone in California Mice
P3.9	Kira Jones	Washington University	Engineering substrate specific Hsp104 NBD1 variants selected by next-generation sequencing
P3.10	Hope Harrington	Grinnell College	Optimization of Recombination Techniques for *Bacillus subtilis* Cytochrome P450 protein
P2.11	Joshua Liu	Washington University	Modulation of Peripheral Ly6Chigh Monocytes Rescues Synapse Elimination during Recovery from Zika Virus Encephalitis
P3.12	Sara Hoggatt	University of Chicago	Investigating physical dynamics of single-cell host-pathogen interactions using Fluidic Force Microscopy
P3.13	Sophia Zhang	Washington University	Characterizing Engineered *Saccharomyces boulardii*: Interplay of Secretion Signals and Anti-infectious Protein Expression
P3.14	Avery Leigh	Knox College	Organic Matter Composition in Urban Ponds: Differences in Sample Methods and Trophic Gradients
P3.15	Xenia Sofianou	Macalester College	Lymph Node Stromal Cell Presentation Of Self Antigen With Or Without Immune Experience
P3.16	Cynthia Chang	Washington University	Characterizing protein amyloidogenesis in *Staphylococcus aureus* biofilms and countering biofilms with engineered protein disaggregases
P3.17	Kathryn Lillemon	Gustavus Adolphus College	Identification of potential TEN1 mutants induced by CRISPR/Cas9 in *Arabidopsis thaliana*

Poster Session P3 (continued): Time Room			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.18	Juan Alberto Gómez-Solis	Carthage College	Developing a reliable infection protocol for a synthetic virus in plants
P3.19	Jizhi Yan	University of Chicago	Glutamine Metabolism is Altered in Myeloproliferative Neoplasms and Represents a Potential Novel Therapeutic Target
P3.20	Ashley Trainor	Hope College	Social and Emotional Knowledge in Patient Populations
P3.21	Yifei Chen Sophia Coco	Washington University	Efficacy of Proofreading Strategies: Assessing Performance and Perceptions in Different Conditions
P3.22	Ella Homan	St. Olaf College	Galectins 1, 3, and 9: Role in Pregnancy Immune Suppression and Parallels in Cancer
P3.23	Alyson Hayashi	Macalester College	Oxytocin modulation and dopamine monitoring of mouse cooperative behavior
P3.24	Lane Nelson	Colorado College	Re-Understanding Cardiac Health: Exploring the Bidirectional Relationship Between Cardiovascular Disease and Social Support
P3.26	Sumana Turimella	University of Chicago	Evolution of Kinetic Proofreading in DNA Polymerases
P3.27	Chloe Traeder	St. Olaf College	Investigating the role of an sRNA in the bacterium *Caulobacter crescentus*
P3.28	Connor Bricco	Hope College	LC-MS/MS for proteomic analysis of post-translational modifications on xCT
P3.29	Paul Kang	Washington University	A single cell transcriptomic mapping of nasal epithelial cells from CF vs. non-CF patients
P3.30	Sharon Abraham	Lawrence University	Analyzing the Activation of G Proteins by PTH and PTH1R
P3.31	Julia Raddue	Colorado College	Caloric Expenditure During High Incline Handrail Supported & Unsupported Treadmill Walking
P3.32	Kendri Duran	Beloit College	Kinetics and Mechanism of the Reaction of Hydrogen Persulfide with Cobalamin in Aqueous Solution
P3.33	Rose Abarbanel	Washington University	Liquid-liquid phase separation in *Pseudomonas aeruginosa* biofilm matrices

Abstracts for all Sessions

Biological Sciences and Psychology
MCMS Undergraduate Research Symposium, Washington University
November 10-11, 2023

Presenter(s): Rose Abarbanel
School: Washington University
Session: Poster: P3.33
Title: Liquid-liquid phase separation in *Pseudomonas aeruginosa* biofilm matrices
Advisor(s): Courtney Reichhardt, Chemistry, Washington University in St. Louis
Co-Author(s): Nicole Fazio
Abstract: Biofilms cause chronic bacterial infections including chronic lung infections. Biofilms are bacterial communities that are embedded within an extracellular matrix that can contain exopolysaccharides (EPS), extracellular DNA (eDNA), and proteins. The biofilm matrix protects bacteria from antibiotics and host immune responses, making it a therapeutic target. Different matrix components co-localize with each other to structure and protect biofilms from degradation. We hypothesize that in some cases, liquid-liquid phase separation (LLPS) drives co-localization of biofilm matrix components. LLPS is a biophysical concept in which distinct liquids form phase separated droplets when mixed. We investigated if uncharged EPS and eDNA phase separate from the rest of the matrix. First, we utilized a two polymer system of polyethylene glycol (PEG) and dextran (DEX) to examine eDNA-polymer phase separation, and then to gain insight on how EPS and eDNA localize in the matrix, substituted the polymers with different biofilm matrix EPS. Our methods include differential interference contrast (DIC) microscopy, solid-state nuclear magnetic resonance (NMR), and confocal laser scanning microscopy (CLSM) of live biofilms to visualize localization of eDNA and specific matrix polymers. Our studies on eDNA-polymer associations will further our understanding of biofilm matrices, which is anticipated to aid the discovery of anti-biofilm therapeutics.

Presenter(s): Sharon Abraham
School: Lawrence University
Session: Poster: P2.15
Title: Analyzing the Activation of G Proteins by PTH and PTH1R
Advisor(s): Kelly Culhane, Biochemistry
Co-Author(s):
Abstract: PTH1R is a G protein coupled receptor, so the ligand, PTH, binds to the receptor, causing a conformational change. PTH1R activates an associated G protein by exchanging GDP to GTP, leading to a downstream signaling pathway. Previous studies show PTH interacts with the distinct conformations of PTH1R, leading to changes in signaling. Despite the knowledge that PTH interacts with the distinct conformations of PTH1R, what is not known is how the different conformations of the binding between PTH and its receptor affect how the different G proteins are selected. Therefore, we will use sensors to study which G protein is activated when PTH binds to PTH1R in different conditions**.**

Presenter(s): Victoria Afe
School: Washington University
Session: Poster: P:3.5
Title: Characterizing Acid Response Genes in *Klebsiella pneumoniae*
Advisor(s): Petra A. Levin, Biology, Washington University in St. Louis
Co-Author(s): Sarah D. Beagle
Abstract: The pH of the environment that a bacterium is growing can alter its physiology. Bacteria tend to prefer neutral environments as extremely low and high pHs are often unfavorable conditions for bacterial growth. *Klebsiella pneumoniae* is a Gram-negative human pathogen that has become

increasingly resistant to antibiotics. Growth in acidic pH increases K. pneumoniae's resistance to cell-wall-synthesis targeting antibiotics, but the mechanisms by which K. pneumoniae adapt to acid stress is under-researched. In *Escherichia coli*, the Acid Shock RNA (Asr) protein is critical to adapt to acidic pH stress. Asr is a periplasmic chaperone that helps maintain protein homeostasis during acid stress. RNA sequencing of K. pneumoniae grown in acidic pH revealed that K. pneumoniae possesses two acid-responsive copies of Asr, both of which are currently uncharacterized. To characterize these genes, single and double asr mutants were created and their response to acid stress was assayed. Timelapse microscopy and growth curves revealed that the double asr deletion mutant was more sensitive to acid stress than the wildtype strain. We are continuing to explore the role that these asr genes play in fitness and antibiotic resistance at low pH to better understand their contributions to adaptation to acid stress in Klebsiella.

Presenter(s): Ama Ameyaw
School: Beloit College
Session: Poster: P1.4
Title: Identifying and Characterizing Antibiotics from Soil Microbes
Advisor(s): Kristin Labby, Chemistry, Beloit College
Co-Author(s):
Abstract: The emergence of antibiotic resistance has given rise to a global crisis. To address this issue, the Tiny Earth Network focuses on identifying and characterizing new antibiotics from soil microbes. In this study, soil samples were collected from Riverside Park, Beloit, Wisconsin. Isolates cultured from the soil sample were tested against optimized concentrations of lab-safe relatives of ESKAPE pathogens for antibiotic activity. Four isolates named AA13, AA14a, AA14b, and AA17, demonstrated antibacterial activity against *Enterobacter aerogenes*, *Bacillus subtilis*, *Bacillus subtilis*, and *Mycobacterium smegmatis*, respectively.16s rRNA sequencing and BLAST analysis indicated that AA13, AA14a, AA14b, and AA17 had identity matches to *Luteibacter pinisoli* (98.11% identity), *Pantoea ananatis* (96.22% identity), *Bacillus mobilis* (96.81% identity), and *Bacillus mobilis* (98.55% identity) respectively. Chemical extractions of the natural products produced by these isolates were performed using ethyl acetate. The crude extract of these isolates were tested using a disk diffusion bioassay for antibiotic activity as well as intrinsic antibiotic resistance assay. Information on each isolate was entered into the Tiny Earth Database for further analysis.

Presenter(s): Akwasi Amoah
School: Gustavus Adolphus College
Session: Poster: P2.4
Title: Identifying the features responsible for Nonsense-mediated decay of the CEP3 mRNA
Advisor(s): Jeff Dahlseid, Biochemistry and Molecular Biology, Gustavus Adolphus College
Co-Author(s):
Abstract: The information that determines what a cell becomes – the specific structure it assumes and the functions it performs – is stored in its DNA. To access this information, the cell employs a series of processes, through which the information is conveyed from its DNA through the synthesis of a similar molecule, a messenger RNA (mRNA), and, finally, the mRNA programs the synthesis of protein. Our research focuses on mRNA, specifically how the cell degrades it. We utilize *Saccharomyces cerevisiae* (baker's yeast) as a model system. *S. cerevisiae* commonly uses an mRNA degradation pathway that has two rate-determining steps. Nonsense-mediated decay (NMD), a specialized mRNA degradation pathway, skips one of those steps, which results in faster mRNA degradation. NMD was initially discovered as a mechanism to target and eliminate mutated mRNA molecules, particularly those with features that prematurely halt protein synthesis.However, NMD also targets mRNA that lack those specific features, natural mRNA. Our research aims to uncover the features by which the NMD pathway recognizes and degrades these natural mRNA molecules, shedding light on how NMD influences the regulation of gene expression.

Presenter(s): Davi Zola de Araujo
School: Hope College
Session: Poster: P2.12
Title: Role of Temperature in Cluster K1 Mycobacteriophage Growth Properties
Advisor(s): Joseph Stukey, Department of Biology, Hope College
Co-Author(s):
Abstract: Mycobacteriophages are viruses that infect mycobacterial hosts. Over 2250 mycobacteriophages have been isolated and organized into 38 distinct “clusters" based on genetic similarity. Students in the Hope College SEA PHAGES program isolated mycobacteriophages of a particular cluster, K1, at a higher frequency (≈10x) after lowering the isolation temperature from 37°C to 32°C. This is particularly interesting because mycobacteriophages of cluster K1 generally show the ability to infect a wider range of bacterial hosts, including Mycobacterium tuberculosis, which is an important feature for future phage therapy efforts. We hypothesize that the elevated Cluster K1 phage isolation frequency is largely due to relatively better growth of these mycobacteriophages at lower temperatures. Seven K1 mycobacteriophages were tested for growth properties such as adsorption rates, burst size, and latent period and all results are consistent with our hypothesis. For one example, the K1 phage Ganymede infects *M. smegmatis* at 37°C producing 2-3 new phage per infection (burst = 2.5) in 128 minutes (latent period), while at 32°C the yield is ≈ 128 new phages in 129 minutes. These values resemble earlier findings on other K1 phages.

Presenter(s): Connor Bricco
School: Hope College
Session: Poster: P3.28
Title: LC-MS/MS for proteomic analysis of post-translational modifications on xCT
Advisor(s): Leah Chase-Waller, Chemistry, Biology, Neuroscience, Hope College
Co-Author(s):
Abstract: Membrane protein xCT and its heavy chain component 4F2 make up the xc- transport system. 4F2 may be necessary for membrane localization of the heterodimer and xCT is responsible for transport activity. Under basal conditions, xCT resides in endosomes, but upon oxidative insult, xCT moves to the membrane and functions to reduce oxidative stress. We hypothesize the movement of xCT to the membrane is directed by changes in post-translational modifications (PTMs) such as phosphorylation, ubiquitination and glycosylation. The overall goal of this project is to use mass spectrometry to detect the PTMs of xCT isolated from cells grown under basal conditions and those exposed to oxidative stress. We are optimizing a procedure to 1) maximize xCT expression in mammalian cells and 2) isolate xCT from cell lysates. In addition, we are evaluating the effectiveness of traditional urea/trypsin digests for preparation of xCT for mass spectrometry samples.

Presenter(s): Edgar Caracoza
School: Beloit College
Session: Poster: P2.16
Title: Antibiotic-Producing Bacteria More Frequent in Soil than Water in Beloit, WI
Advisor(s): Kristina Blanke, Biology, Beloit College
Co-Author(s):
Abstract: Soil erosion can drastically change the future of healthcare. The number of antibiotic resistant bacteria are increasing as antibiotics continue to be misused, which leads to the research question of where to find novel antibiotic-producing bacteria besides soil. This research identified antibiotic-producing bacteria in soil and water. The process started with collecting soil and water samples, plating serial dilutions on nutrient agar, and culturing bacteria with diverse colony morphologies. Then, select isolates were screened against tester bacteria, sequenced to determine the 16S rRNA, and biochemical tests were run to further classify the isolates. The soil samples contained five antibiotic-producing isolates and water samples contained two isolates. Three of the five isolates from the soil samples were of the *Calidifontibacillus* genus. There was a 150% increase in antibiotic-producing bacteria when soil

and water were compared, a 50% increase between the two soil locations, and only one isolate from each water source. In conclusion, there were more antibiotic producers in soil than water. This may be expected because water is more fluid, which reduces bacterial competition.

Presenter(s): Cynthia Chang
School: Washington University
Session: Poster: P3.16
Title: Characterizing protein amyloidogenesis in *Staphylococcus aureus* biofilms and countering biofilms with engineered protein disaggregases
Advisor(s): Meredith Jackrel, Chemistry, Washington University in St. Louis
Co-Author(s): Matthew Howard, Karlie Miller, Brian Sohn, Jeremy Ryan, Andy Xu
Abstract: Biofilms pose a major public health threat. They are sticky, polymeric mixtures produced by bacteria, which the bacteria then become embedded in. This environment enables strains to transition from a “free-floating” planktonic state to a “multicellular” sessile state, leading to social cooperation and antibiotic resistance, such as methicillin-resistant *Staphylococcus aureus* (MRSA). Since phenol-soluble modulins (PSMs) are the primary proteinaceous component stabilizing biofilms, my research investigates the properties of PSM peptides. I utilize a novel yeast model system to study the peptides, which closely recapitulates their known phenotypes. I have discovered that PSMs adopt an insoluble amyloid fold and confer varying degrees of toxicity toward yeast growth. I then characterized their aggregation, delineating differences in localization that correlate with the observed toxicities of different peptides. With this understanding, I hypothesized that we may be able to disrupt biofilm structure by disrupting the amyloid fold of PSMs. Thus, I have used potentiated variants of Hsp104, a hexameric AAA+ disaggregase native to yeast, to counter PSM aggregation and even dissolve preformed biofilm matrices. Ultimately, I hope to optimize Hsp104 disaggregases as a potential therapeutic to fight biofilm-related infections. Our yeast model can also be used to discover new agents to safely remove biofilms.

Presenter(s): Madeline Chaplin
School: Gustavus Adolphus College
Session: Oral I.C.4
Title: Effects of Diurnal Cooling on RCH Induction in *Drosophila Melanogaster*
Advisor(s): Yuta Kawarasaki, Biology, Gustavus Adolphus College
Co-Author(s):
Abstract: Rapid cold-hardening (RCH) is a type of phenotypic plasticity that allows insects to swiftly adjust their physiological states to a changing environmental condition. In *Drosophila melanogaster*, RCH is most traditionally induced by an exposure to 5ºC for 2 h. However, previous studies suggested that gradual ramp cooling that occurs during natural daily fluctuations in temperatures can also induce RCH. In this project, we examined the effects of gradual ramp cooling and reheating on the RCH induction in *D. melanogaster*. Compared to a control group that was directly exposed to -5.6ºC for 2 h, individuals that experienced one ramp cooling beforehand had a significantly enhanced survival rate (0% vs. 31.7±5.9%). Additionally, we demonstrated that the gradual cooling and classic RCH induction has a compound effect. Compared to individuals that experienced either mechanism of RCH induction, those experienced 1 ramp cooling cycle followed by classic RCH induction had a significantly improved survival rate of 81.3±4.4% at –5.6ºC. These results suggest that RCH induction via diurnal cooling is similar to classic RCH induction, but they enhance each other. Future studies will investigate the underlying mechanisms of RCH by classic induction versus diurnal cooling.

Presenter(s): Jo-Hsuan Chen
School: Macalester College
Session: Oral: IB.3
Title: Investigating the Effects of Methylisothiazolinone (MI) on Mast Cells
Advisor(s): Elena Tonc, Biology, Macalester College
Co-Author(s): Ahlaam Abdulwali

Abstract: Methylisothiazolinone (MI) is a preservative frequently found in household and personal care products. Repeated exposure to these products has been associated with an increased risk of developing vulvodynia, a vulvar chronic pain condition that has previously been linked to seasonal and contact allergies. Mast cells, which are skin-resident immune cells essential to allergic responses, accumulate in the painful tissues of patients and are key orchestrators of chronic pain in animal models of vulvodynia. We investigated the effects of MI on mast cells to elucidate the early inflammatory responses potentially leading to the development of vulvodynia. We treated bone marrow-derived mast cells with varying concentrations of MI and quantified cell viability using annexin V and propidium iodide (PI) staining by flow cytometry. We found that MI treatment decreased mast cell viability in a dose-dependent manner, which was supported by additional assays. Moreover, we found that MI treatment decreased mast cell expression of FcεRI, an IgE receptor implicated in mast cell activation and degranulation. In the future, we will continue investigating MI effects on mast cell viability and FcεRI expression. We will also assess their functionality in response to MI treatment, focusing on the secretion of inflammatory cytokines**.**

Presenter(s): Yifei Chen, Sophia Coco
School: Washington University
Session: Poster: P3.21
Title: Efficacy of Proofreading Strategies: Assessing Performance and Perceptions in Different Conditions
Advisor(s): Emily Cohen-Shikora, Psychological & Brain Sciences, Washington University in St. Louis
Co-Author(s): Grace Drake
Abstract: "This study aimed to assess the efficacy of different proofreading strategies and to discern differences between what strategies individuals perceive to be effective and their actual performance outcomes. We tested three proofreading strategies: reading aloud, in a disfluent font, and silently, elaborating on previous research by Cushing & Bodner (2022) in which participants read separate sets of texts in the same three conditions and recorded errors. We replicated their design and also introduced background noise to half our participants, simulating a real-world distraction and subsequent impact on cognitive load. While the distraction condition showed no significant impact on proofreading accuracy, our findings were similar to Cushing & Bodner (2022). Notably, proofreading aloud emerged as a superior strategy for detecting errors compared to proofreading silently, whereas proofreading in a disfluent font hindered performance relative to silent proofreading. These results aligned with participants' pre-task predictions, suggesting accurate preconceptions about proofreading strategies. Our study reinforces that proofreading aloud is effective and also raises questions about the efficacy of using disfluent fonts to increase deep processing in cognitive tasks, especially proofreading. We hope that our findings can inform the future work of psychologists and educators aiming to optimize textual comprehension and cognitive processing strategies."

Presenter(s): Cara Conforti
School: Washington University
Session: Poster: P1.2
Title: Discovering SCN Network Organization through Enhanced Behavioral Feedback
Advisor(s): Erik Herzog, Biology, Washington University in St. Louis
Co-Author(s): Nikhil Lokesh
Abstract: Circadian rhythms are 24-hour rhythms in physiology and behavior exhibited by nearly all organisms. Environmental and artificial light can entrain or disrupt circadian systems. We developed a novel system (Enhanced Behavioral Feedback or EBF) to study the behavioral effects of controlling one's own light cycle. Based on a computational model, we predicted that EBF with a 12-h delay would cause two bouts of activity per day (i.e., split circadian rhythms). We built 6 houses in which each mouse can access food, water, and a running wheel, and experiences light controlled by a Raspberry Pi based on prior locomotor activity. We found that mice exhibited two bouts of activity per day in EBF depending on the delay between locomotor offset and light onset. We next hypothesized that EBF rapidly

reorganizes the mouse circadian system into two anti-phase circadian pacemakers depending on light history. Our preliminary results show that EBF induced splitting ~2 days faster in mice exposed to long days (LD18:6) compared those exposed to short days (LD6:18). These results indicate that EBF provides a rapid, reliable way to study the behavioral, physiological, and molecular consequences of split circadian rhythms. Future studies will relate behavioral feedback regulation of light exposure to circadian system reorganization across seasons.

Presenter(s): Matt Czmer, Isabella Bozzi
School: Hope College
Session: Poster: P.13
Title: Semantic memory for religious concepts in undergraduate students
Advisor(s): Nathaniel Klooster, Psychology, Hope College
Co-Author(s): Isabella Bozzi, Ashley Trainor
Abstract: Semantic memory is the memory for facts that does not have a spatiotemporal factor. Although it has been shown that religious concepts consolidate into semantic memories, there is no research into what factors may affect these specific memories. The present work seeks to determine the effect of numerous factors including frequency of church services attendance, number of religion classes taken in college, and participants' majors. We will assess semantic memory using a word association task in which participants will be given two minutes to list as many associations to each of the 10 religious words (ie. God, Jesus, faith) and 10 control words, presented in random order. The participants will be recorded and their dialogue will be transcribed and coded to count the number of associations and to remove the subjective or incorrect responses. We expect to see that advanced undergraduate students have a richer semantic memory for these concepts, partly evidenced by an increased number of associations. Further, we expect that students who attend religious services more frequently and align more strongly with a faith will produce more associations. Future data collection will allow us to determine the effect of other factors that could influence these semantic memories.

Presenter(s): Hannah Davis
School: Washington University
Session: Poster: P2.5
Title: Improving KMT2A Rearrangement Detection in Leukemia
Advisor(s): Grant A. Challen, Division of Oncology, Washington University School of Medicine in St. Louis
Co-Author(s): Andrew L. Young
Abstract: Acute myeloid leukemia (AML) is an aggressive blood cancer diagnosed in approximately 120,000 people worldwide annually. One subtype of AML, known as therapy-related AML (t-AML) arises after prior chemotherapy treatment and is aggressive, treatment resistant and lethal. T-AML can be driven by chromosomal translocations involving the lysine methyltransferase 2A gene (KMT2A). Unlike other chromosomal translocations that have one gene fusion partner, KMT2A has 80 known gene fusion partners. For patients with KMT2A-rearranged t-AML, disease monitoring is complicated due to the heterogeneity of gene fusion partners. To address this problem, we developed a sensitive fusion detection assay using droplet digital PCR (ddPCR) that targets the five common fusion partners: AF9, AF6, AF4, ELL and ENL. We designed PCR primers and fluorescent probes that specifically target each fusion and benchmarked our assay using cell lines and t-AML patient samples. In our assay, if a droplet contains KMT2A-rearranged cDNA, a double positive fluorescent signal is identified and plotted by fluorescent intensity allowing for easy discernment of positive droplets. Our assay allows us to quantify transcript abundance, which we can then use to estimate disease burden. We anticipate our assay to have clinical applications in disease monitoring for t-AML patients.

Presenter(s): Kendri Duran
School: Beloit College
Session: Poster: P3.32
Title: Kinetics and Mechanism of the Reaction of Hydrogen Persulfide with Cobalamin in Aqueous

Solution
Advisor(s): Tawnya Cary. Biology, Beloit College
Co-Author(s): Jacek Zielonka
Abstract: Cobalamin (vitamin B12) is intriguing because of its redox activity and potential for sepsis management. Hydrogen sulfide is frequently elevated in patients with sepsis. Persulfides can serve as an H2S source. While cobalamin-sulfide interactions have been studied widely, cobalamin-persulfide interactions have not. This study aims to elucidate their reactivity, hypothesizing that cobalamin reacts with and metabolizes persulfide. The project focuses on reactions under pH conditions: 4.0 and 7.0. Through spectrophotometry, we were able to observe rapid consumption of cobalamin in the presence of persulfide. HPLC analysis revealed the formation of five distinct products when combining cobalamin and persulfide. Further analysis of the chromatograms provided insights into the stoichiometry of the reaction. The data suggests the reaction might involve the consumption of multiple persulfide molecules per cobalamin molecule—specifically two persulfide molecules per one cobalamin molecule, highlighting the complexity of the reaction and the involvement of multiple reactants. In conclusion, our investigation reveals a rapid reaction between cobalamin and persulfide, culminating in the formation of diverse products. Further investigations are needed to identify the specific products being produced.

Presenter(s): Madisyn Eyman
School: Lawrence University
Session: Poster: P3.8
Title: Paternal Aggression Elicits an Increase in Corticosterone in California Mice
Advisor(s): Elizabeth A. Becker, Department of Neuroscience and Psychology, Lawrence University
Co-Author(s): Jessica Hesling, Linda Muller
Abstract: Maternal aggression is defined as a mother protecting her offspring against a non-parental, commonly infanticidal intruder and is regulated by sensation and glucocorticoid hormones (Lonstein & Gammie, 2002). The mechanisms of paternal aggression are less understood. The aim of this study is to determine if paternal aggression elicits changes in corticosterone (cort). The monogamous and biparental California mouse (*Peromyscus californicus*) provide an excellent model for the study of paternal aggression because both parents are aggressive towards intruders, protecting their offspring. Paternal California mice are more aggressive than virgin male mice, demonstrating parallels with maternal aggression (Trainor et al., 2008). We assigned experienced fathers with a current litter to zero (control), one, or three paternal aggression tests. Plasma cort samples were collected at baseline and following final tests. Preliminary analyses demonstrate that cort is significantly elevated after paternal aggression tests compared to controls. Since in resident-intruder tests cort is not elevated in California mice, we suggest that paternal aggression may be mediated differently than other forms of aggression studied. Alternatively, it could be that the presence of pups provides sensory cues that elevates stress in fathers. Our findings suggest that paternal aggression against infanticidal conspecifics increases cort similarly to maternal aggression.

Presenter(s): Nathan Finegold
School: Lawrence University
Session: Poster: P1.27
Title: Biophysical Characterization of Post Translational Modification within the Loop Region of Rop
Advisor(s): Eva Gerber, Biophysics, UC Berkeley
Co-Author(s): Susan Marqusee
Abstract: Bacterial cells create a variety of ribosomal natural products, which are bioactive peptides that have undergone post-translational enzymatic modification. Strong antibiotic, antifungal, antiviral, and cytotoxic properties are present in several natural products, which has sparked interest in using biosynthetic enzymes to produce modified proteins with comparable capabilities. Previous research has yielded engineered biosynthetic enzymes, MicD-F, which has demonstrated site specific annulation of cysteine residues into thiazoline rings within the recognition sequence of "N-MCAYD-C" in fully folded proteins. However, it is unclear how the formation of heterocycles affects secondary and tertiary

structure of modified proteins. A combination of denaturant melts, mass spectrometry, and circular dichroism spectroscopy were used to determine the biophysical effect of heterocyclic post-translational modification within the loop region of a protein by comparing the thermodynamic and kinetic values of well-characterized proteins, such as the model protein ROP (Repression of Primer), with and without the thiazoline. Similar biophysical characterization was performed for another ROP construct, ROPC C44P, which was produced utilizing a conventional heterocycle proline inside the same recognition sequence as a point of reference.

Presenter(s): Lowell Finster
School: Washington University
Session: Oral: II.F.1
Title: Plasma cell-free DNA as a prognostic sepsis biomarker
Advisor(s): Aadel A. Chaudhuri, Radiation Oncology, Washington University in St. Louis
Co-Author(s): Nicholas P. Semenkovich, Peter K. Harris, Noah Earland, Andrew Chen
Abstract: Sepsis is the most common cause of hospital death in the United States. It is defined as life-threatening organ dysfunction caused by a dysregulated response to infection. The heterogeneity and pathophysiology of sepsis are why it lacks a reliable clinical biomarker.
Tissues throughout the body shed DNA into circulation, where it can be isolated from blood as cell-free DNA (cfDNA). cfDNA has been shown to predict sepsis mortality. Sequencing enables the detection of tissue-specific cfDNA via epigenetic marks like methylation, potentially enabling the prediction of sepsis severity and end-organ damage.
In this study, 62 patients being treated for sepsis underwent 1-6 blood draws. cfDNA was isolated from patient plasma, and isolated cfDNAs were run on a Bioanalyzer. cfDNA electropherograms rarely show high molecular weight genomic contamination, indicating that the DNA isolated is nucleosomal.
Initial, final, and maximum ng cfDNA isolated per mL plasma differ significantly between septic patients who survived and died. These cfDNA levels also discriminate effectively between survivors and non-survivors. Initial and final cfDNA levels predict overall survival, and final cfDNA level is significantly associated with increased risk of death in a multivariate regression analysis. Septic cfDNA levels may aid in clinical decision-making, trial design, and biomarker identification.

Presenter(s): Raymond Fleming, Kaila Luell
School: Colorado College
Session: Poster: P3.6
Title: Estadiol-mediated spinogenesis in avian NCM with novel sounf exposure during exposure to novel sound.
Advisor(s): Marcella Fernandez-Vargas, Psychology, Neuroscience Program, Colorado College
Co-Author(s): Jeremy Lewis, Anna Matsui
Abstract: The formation and growth of dendritic spines is emblematic of new synapses forming, and in the processes of cognition and memory, can be used as a measure of neuroplasticity. Previous research has demonstrated that novel song exposure can cause rapid dendritic spinogenesis within the avian secondary auditory cortex (caudomedial nidopallium, NCM) of male zebra finches. Other studies have found that brain estradiol can rapidly strengthen auditory encoding in songbirds. It was hypothesized that estradiol can facilitate novel song-evoked dendritic spine formation in the NCM of adult zebra finch males. To test this, subjects were administered estradiol or control orally 10 minutes prior to a 30-minute song exposure protocol mimicked from previous research. Following exposure to sound and treatment, the brains were trans-cardially perfused and extracted, then histologically processed using a rapid Golgi staining followed by sagittal sectioning (100 um) and mounting. Neurons were reconstructed in 3D using Neurolucida software, then used to quantify dendritic spine densities, branching, and spatial distribution (Sholl analysis). We identified at least three types of auditory neurons based on spine density, length, and diameter of dendrites and will present preliminary data comparing four experimental groups.

Presenter(s): Finneas Frawley

School: Lawrence University
Session: Oral:I.A.4
Title: Validation of the Sexual Education Comprehensiveness Scale
Advisor(s): Amanda Draheim, Psychology, Goucher University
Co-Author(s): Eli Miller
Abstract: Sex education has the potential to play a critical role in challenging myths that perpetuate stigma against many sexual identities, practices, and preferences, particularly for members of the LGBTQ+ community. Currently, sex education in American schools is pervasively lacking, likely due, in part, to legal policies preventing education beyond abstinence. Though people's experiences with sexual education in schools can inform their biases, attitudes, behaviors, and engagement with the medical community, no known measure of this construct exists. We created our own scale to measure the comprehensiveness of sex education during K-12 schooling in the United States and aim to demonstrate the validity of this scale using the Downing (2003) model. To ensure content validity, we based our items on the six key concepts of a comprehensive sex education outlined in the Sexuality Information and Education Council of the United States (SIECUS) guidelines for American primary and secondary schooling. Relationship to other variables will be demonstrated using correlations with measures of socioeconomic status, relationship satisfaction, political affiliation, religiosity, and anti-LGBTQ+ bias. Measures were disseminated to 204 participants using Prolific. Preliminary results in support of internal structure include excellent internal consistency ($\alpha = 0.90$). Clinical implications and future directions are discussed.

Presenter(s): Jayitha Gaggenapally
School: Beloit College
Session: Oral I.A.1
Title: Sense of Belonging and Existential Isolation
Advisor(s): Gloria Bradley, Assistant Dean of Students, Beloit College
Co-Author(s):
Abstract: Existential Isolation (EI) is described as the pervasive innate sense of disconnection between oneself and the world (Brown et al., 2021). Humans hold a unique internal world that is private and necessary for survival. However, it can lead to isolation if humans feel a lack of common ground with the people around them and the environment they live in. Recent studies examining EI have observed a consistent sex difference where men report higher levels of EI than women (Helm, 2018). Additionally, research suggests that members of minority races have more solidarity with members of their race than with other races (Helm, 2022). This study aims to examine the relationship between race, sex, and levels of EI among undergraduate college students. Participants completed several measures related to race, sex, and EI. We anticipate finding the results that male students experience higher levels of EI than their female counterparts. We also expect that members of minority races will experience higher EI when surrounded by individuals from demographics outside of their own. We further anticipate finding a relationship between EI and the well-being of students.

Presenter(s): Nancy Garcia
School: Grinnell College
Session: Poster: P1.22
Title: An analysis of the effect altered temperatures have on functional properties of *A. alternata* and neighbor species in *A. gerardi* litter
Advisor(s): Kathryn Jacobson, Biology, Grinnell College
Co-Author(s):
Abstract: Fungal communities play significant roles as decomposers in the prairie ecosystem, contributing to mineralization of organic matter and CO2 production. Studying the direct physiological responses of functionally relevant organisms like fungi is important when designing models of ecosystem response to environmental changes. Here, we assess the growth and decomposition rates of 4 prairie fungal isolates alone and in interaction. Fungi were grown on water agar containing plant

litter plates at 25, 30, and 35°C to measure 24-hour growth increments alone and during isolate interactions. Individual isolate growth was used to understand performance in competition and its effects on neighboring species during growth and decomposition assays. We hypothesized that fungal growth and decomposition would display similar trends and be optimized at 25 and 30°C, for both individual species and within interactions. We found that growth and decomposition varied across temperatures and isolates and was not solely optimized at 25 and 30°C. We also found that *Alternaria* genotypes perform very differently when interacting with other isolates, as they can compete with other isolates to maintain their performance or decomposition abilities. Altogether, this evidence suggests that with elevated temperatures, functional traits of fungi are not constrained, and different species and genotypes exhibit diverse responses that need to be further studied**.**

Presenter(s): John Georgiades
School: Washington University
Session: Oral: II.E.2
Title: Structural insights into flavin redox cycling in the *Helicobacter pylori* dihydroorotate dehydrogenase
Advisor(s): Craig L. Smith, Biology, Washington University in St. Louis
Co-Author(s): Ashna A. Agarwal, David D. Dranow, Donald D. Lorimer, Thomas Edwards, Peter J. Myler
Abstract: The Gram-negative bacterium *Helicobacter pylori* colonizes the gastrointestinal tracts of over half of the global population and can cause peptic ulcers and gastric cancer. Unfortunately, resistance to antibiotics is widespread among clinical strains of *H. pylori*, exposing a dire need for new drugs to combat this infection. Many drug development efforts have targeted the de novo pyrimidine biosynthesis pathway, as it is the exclusive means by which *H. pylori* accesses essential nucleotides. At the bottleneck of this pathway is dihydroorotate dehydrogenase (HpDHODH), the enzyme that catalyzes the flavin mononucleotide-dependent oxidation of dihydroorotate to orotate. We determined the first crystal structure of HpDHODH to 2.25 Å resolution and characterized the protein using bioinformatics approaches. We found that the active site of HpDHODH is highly similar to other isoforms and that it has the structural features necessary to form an interface with the bacterial membrane. In this membrane binding domain, we discovered a hydrophobic channel with direct access to the active site flavin. We believe that this feature allows ubiquinone to channel from its pool in the membrane to the active site, oxidizing the flavin, and resetting the enzyme for another round of catalysis.

Presenter(s): Phoebe Gordon
School: Colorado College
Session: Poster: P1.18
Title: Mayfly (Genus: *Neohagenulus*) food resource shift after hurricanes may increase rate of ecological recovery
Advisor(s): Boyce Drummond, Organismal Biology and Ecology, Colorado College
Co-Author(s):
Abstract: Due to climate change, hurricane frequency and intensity are expected to increase in Puerto Rico, creating a need to understand the dynamics of its ecosystems that may be affected by hurricane-induced disturbances. One such disturbance is canopy opening, which increases light availability in streams and may speed up algae growth, while decreasing the amount of leaf litter in streams. This shift from allochthonous carbon (leaf litter) to autochthonous carbon (algae) as a primary resource for stream communities may have effects on secondary production of aquatic macroinvertebrates. We explore the effects of canopy opening on *Neohagenulus julio* mayflies (Family Leptophlebiidae) by controlling food source and monitoring instantaneous growth rate. Specimens were collected from El Yunque National Forest, Puerto Rico. Half were given leaf litter, and the other half algae-coated rocks. Small, female individuals grew more quickly in algae treatment, and positive trends were visible in other groups despite a lack of statistical support. The positive response of growth rate to algae suggests that *N. julio* may benefit from increased algae productivity after canopy opening, which could have cascading

effects to the terrestrial ecosystem, which benefits from mayflies' increase secondary production.

Presenter(s): Daleep Grewal
School: Washington University
Session: Poster: P: 1.14
Title: Advantages of Enrolling Intellectual and Developmental Disorder Patients with Multiple Gene Variants to Clinical Studies
Advisor(s): Philip Payne, WashU's Institute for Informatics, Data Science, and Biostatistics, Washington University in St. Louis
Co-Author(s): Aditi Gupta, Inez Oh, Zachary Abrams
Abstract: The Brain-Gene Registry (BGR) was established to aggregate clinical data on Intellectual and Developmental Disorders (IDDs), primarily focusing on participants with single gene variants directly tied to their clinical phenotype. We aim to evaluate the advantages of enrolling participants with multiple versus single brain gene variants.
A gene enrichment analysis was conducted to compute the statistical likelihood of multi-gene pathways being involved in IDDs. A network graph using participants' genetic architectures pulled from their gene reports was developed to visualize the multi-gene networks in patients with IDDs.
The enrichment analysis demonstrated that many IDDs result from multi-gene variations rather than single gene mutations. The network graph reveals common brain gene variants among IDD patients.
Our results highlight the potential advantages of enrolling IDD patients with multiple variants. By incorporating these patients, we could improve our understanding of the genetic complexity behind these disorders, fostering better research and treatment approaches for IDD patients in the future.

Presenter(s): Laken Hairston
School: Lawrence University
Session: Oral I.C.2
Title: Exposure to parasitoid wasps induces thicker and stiffer cuticle in flies
Advisor(s): Shaun Davis, Biology, Lawrence University
Co-Author(s): Phuong Anh Bui
Abstract: Organismal survival depends upon the correct identification of environmental threats and the appropriate induction of defensive traits. Insects in nature, such as *Drosophila melanogaster*, readily encounter parasitoid wasps - small insects which use their needle-like ovipositor to inject an egg inside the fly's body. Upon hatching, the wasp eventually eats the host from the inside out. Flies have a variety of ways to protect themselves, including behavioral and immunological defenses. Here, we show that flies employ a third defensive mechanism by modifying their physical defenses. Fly larvae that were exposed to wasps developed thicker and more rigid cuticle compared to unexposed ones. We next questioned whether flies use olfaction to detect wasps. Homozygous orco2 mutant flies lack the odorant receptor co-receptor, rendering the flies unable to smell. These anosmic flies failed to alter their cuticle parameters when exposed to wasps. These data suggest that flies preemptively alter their physical defenses in anticipation of wasp attacks. We are now examining how wasp exposure changes the expression of cuticle-related genes that could contribute to their altered physical characteristics using wild type flies. In combination with the behavioral changes, these structural modifications are expected to aid in the survival of flies.

Presenter(s): Hope Harrington
School: Grinnell College
Session: Poster: P3.10
Title: Optimization of Recombination Techniques for *Bacillus subtilis* Cytochrome P450 protein
Advisor(s): Travis Hattery, Biology, Grinnell College
Co-Author(s):
Abstract: Cytochrome P450 enzymes (CYP450s) are involved in the metabolization of various xenobiotic compounds. Across humans, The CYP450 enzymes responsible for drug metabolism exhibit

substantial genetic variation, leading to a diverse spectrum of enzyme activity across individuals. This can have adverse consequences for patients that take concurrent medications when both are involved in the same CYP450 pathway, resulting in sub-optimal treatment. Bacterial CYP450 enzymes are still not well understood, despite the potential for heterologous expression of human CYP450s into bacterial organisms for simpler systems of study. Therefore, it's important to study the differences in DNA recombination techniques between naturally occurring CYP450s present in bacteria, in addition to heterologously-expressed human CYP450s into bacterial systems. It was our aim to provide an optimized protocol for DNA recombination techniques for bsu168 CYP450 enzymes in hopes of increasing the efficiency of bacterial CYP450 research. We confirmed successful ligation of the bsu168 cypB gene into our vector via gel electrophoresis. This work will increase the efficiency of bacterial CYP450 research.

Presenter(s): Alyson Hayashi
School: Macalester College
Session: Poster: P3.23
Title: Oxytocin modulation and dopamine monitoring of mouse cooperative behavior
Advisor(s): Marc Pisansky, Biology, Macalester College
Co-Author(s): Graham Yater
Abstract: Cooperation can be observed across species and is shown to be a critical part of functioning social groups. Mice are social creatures, yet there is little evidence that they can work cooperatively. To study this, we designed an experiment using Feeding Experimentation Devices (FEDs) that trained mice to make concurrent operant responses to earn a food reward. We then examined whether oxytocin, a hormone linked to prosocial behavior, would modulate cooperative behavior and reward sharing. We found that mouse cooperative behaviors vary by biological sex and may be altered by intranasal oxytocin. Because dopamine signaling mediates reward behaviors, we sought to build a fiber photometry system for simultaneous dopamine monitoring during the cooperation task. Mice were stereotaxically injected with an AAV encoding the dLight1.3b dopamine sensor into the nucleus accumbens brain region. We have confirmed dopamine monitoring in freely behaving mice and are currently examining dopamine signaling in the cooperation task.

Presenter(s): Charlotte Ho
School: Lawrence University
Session: Poster: P2.28
Title: Evolutionary conservation of WASp function during endocytosis in yeast
Advisor(s): Eric Lewellyn, Biology Department, Lawrence University
Co-Author(s):
Abstract: Endocytosis is a process that allows cells to internalize materials from the extracellular environment by deforming the membrane into a pit. We focused on Wiskott-Aldrich Syndrome protein (WASp), which is essential for the process. Much of our understanding of this topic derives from the study of yeast *Saccharomyces cerevisiae* (*S. cerevisiae*) because it is a tractable organism to study and often provides insight into endocytosis in many other organisms, including humans. However, it is crucial to investigate whether such processes in yeast are conserved so we know to what extent these discoveries are universal. Therefore, we aim to bridge the knowledge gap between the model organism *S. cerevisiae* with other species by endogenously encoding genes from other species into *S. cerevisiae* to observe the degree of functional conservation. Our specific goal is to investigate the subcellular localization of the WASp protein from *Schizosaccharomyces pombe* (*S. pombe*) in *S. cerevisiae* to see if it is the same as the *S. cerevisiae* WASp. To do this, we have edited the genome of S. cerevisiae to encode both the WASp gene from *S. pombe* and mark it with the gene for green fluorescent protein for imaging via fluorescence microscopy.

Presenter(s): Sara Hoggatt
School: University of Chicago

Session: Poster: P3.12
Title: Investigating physical dynamics of single-cell host-pathogen interactions using Fluidic Force Microscopy
Advisor(s): Aaron Esser-Kahn, Pritzker School of Molecular Engineering, University of Chicago
Co-Author(s): Elizabeth Mulder
Abstract: The innate immune system relies on cells like macrophages to detect signs of infections like bacteria. Macrophages detect bacteria using surface receptors that bind to ligands on the bacterium, activating the macrophage. However, the role of biophysical dynamics, such as contact time and area, in bacteria detection is unclear. This project aims to clarify the role of biophysical dynamics in the interaction between a bacterium and a single macrophage using Fluidic Force Microscopy (FluidFM). FluidFM consists of a force-sensitive probe with a hollow pipette-like tip that can dispense nano-scale quantities of fluid or pick up single cells. We used FluidFM to pick up a single bacterium and approach a macrophage, precisely controlling the contact time, area, approach speed, number of contacts, and number of bacteria in the interaction. Macrophages most consistently activated after 30-minute contact with live bacteria. Greater numbers of bacteria lead to greater macrophage activation. Multiple short contacts and contacts with recently frozen bacteria did not lead to consistent macrophage activation. Identifying which physical dynamics lead to bacterial detection contributes to a better understanding of how macrophages detect bacteria, leading to improved techniques to fight bacterial infections.

Presenter(s): Juan Alberto Gómez-Solis
School: Carthage College
Session: Poster: P3.18
Title: Developing a reliable infection protocol for a synthetic virus in plants
Advisor(s): Erin Weber, Chemistry, Darthage College
Co-Author(s):
Abstract: Potato virus Y (PVY) is a virus that infects potatoes, leading to a decrease of up to 80% in crop yield. This single-stranded RNA virus has five dominant strains that elicit a range of symptoms among different potato varieties. To determine the role of the strain-specific viral proteins in infectivity and symptoms requires a virus that can be intentionally mutated and the impact on infection monitored. Unfortunately, PVY is toxic to *E. coli*, limiting the use of common molecular biology tools. Instead, we have developed a full-length PVY genome in yeast. Using this synthetic virus will allow the eventual determination of strain-specific viral proteins in PVY infection. Currently, we are working on identifying a method of infecting tobacco plants, a common model organism, with the synthetic PVY. This work focuses on screening different modes of infecting plants, including direct application, and screening of Agrobacterium tumefaciens.

Presenter(s): Phoebe Holz
School: University of Chicago
Session: Poster: P1.15
Title: Is Resting-State Gamma Production a Biomarker of Cognitive Deficits in People with Schizophrenia?
Advisor(s): Molly Erickson, Psychiatry & Behavioral Neuroscience, University of Chicago
Co-Author(s):
Abstract: Impaired resting-state gamma (30-50 Hz) activity within the electroencephalogram (EEG) is a proposed biomarker of cognitive deficits found in people with schizophrenia (PSZ). However, prior comparisons of resting-state gamma in PSZ with healthy controls (HCs) have found gamma to be at times elevated, lowered and not significantly different. Furthermore, recent work indicates that traditional methods for measuring gamma power may be contaminated by aperiodic parameters such as offset and exponent slope of the EEG spectra. In the present study we attempt to explain the mixed state of the literature by analyzing gamma's test-retest reliability and by applying a novel method of spectral power analysis (FOOOF) which accounts for aperiodic parameters. We compare resting-state gamma collected from 9 PSZ and 24 HCs. Using traditional analysis methods we replicate prior

research which has found nominally, but not significantly, elevated gamma power in PSZ. Using FOOOF analysis we find nominally lowered gamma power in PSZ, which rises to significance in posterior channels. We also find high test-retest reliability in both groups. Our results suggest that resting-state gamma can be reliably elicited and that mixed results may be due to aperiodic contamination, supporting the hypothesis that impaired gamma activity underlies cognitive deficits in PSZ.

Presenter(s): Ella Homan
School: St. Olaf College
Session: Poster: P3.22
Title: Galectins 1, 3, and 9: Role in Pregnancy Immune Suppression and Parallels in Cancer
Advisor(s): Svetomir Markovic; Kim Kandl, Department of Oncology Research; Biology, Mayo Clinic Graduate School of Biomedical Sciences; St. Olaf College
Co-Author(s): Zach Nevala
Abstract: Immunosuppression is vital in pathophysiology of cancer, pregnancy, and related pregnancy complications. Pregnancy is a normal, biological process that can be studied as a model which mimics the immunosuppressive pathways of cancer. Pregnancy complications like Villitis of Unknown Etiology (VUE) and Chronic Histiocytic Intervillositis (CHI) consist of the breakdown of immunotolerance which can help identify the mechanisms involved in cancer immune evasion and targets of immunotherapy.
Cancer systemically shifts the immune response to an immunosuppressive tumor-supportive microenvironment. This is analogous to pregnancy in the sense that it is unfavorable for the immune system to attack the fetus. In pregnancy complications, we see a shift from TH2/M2 to an induced immune activation response, TH1/M1.
Galectins, part of the lectin superfamily, extensively studied in pregnancy, play a role in the immune suppression of cancer. These proteins decipher information encoded by glycosylation machinery via a conserved carbohydrate recognition domain (CRD) which translates to proper cellular function. Dependent on the cancer, and tumor microenvironment, the upregulation of certain galectins is associated with both immune activation and suppression. In pregnancy, galectins are recognized as an important factor in establishing immune tolerance at the feto-maternal interface and successful pregnancy.
To understand the microenvironment in pregnancy and cancer, multi-plex immunofluorescence (MxIF) was utilized on pregnancy and tumor slides. Multiple tumor and trophoblast cell lines were cultured and treated with galectins with various in vitro assays. ELISA and flow cytometry were utilized to measure cytokines and cell surface markers, respectively.
MxIF demonstrates that immune tolerance pathways at the feto-maternal interface and tumor microenvironment are similar in the upregulation of galectins and CD206 in both normal pregnancy and cancer as opposed to Th1/M1 upregulation in pregnancy complications and lymph nodes without tumors. In vitro assays suggest that galectins promote Th2 and M2 upregulation in T-cells and macrophages, respectively.

Presenter(s): Mackenzie Horutz
School: Carthage College
Session: Poster: P2.21
Title: Measuring functional recovery of vision after injury in zebrafish using the optokinetic response
Advisor(s): Steve J. Henle, Neuroscience, Carthage College
Co-Author(s): Sarah Young
Abstract: The structure of zebrafish eyes is similar to humans, which makes them a favorable animal model for studying vision. While structurally similar, zebrafish have one function that humans do not possess; the ability to regenerate. While measuring vision in human beings can be achieved through the simple means of an eye chart, zebrafish are not able to complete these kinds of tests. Instead, vision is measured using the optokinetic response (OKR); where your eyes innately track a moving stimulus. After injuring the optic nerve of a zebrafish, we can measure the regeneration by monitoring the return of the OKR. Previous work analyzing vision in zebrafish has focused on the anatomical process of

regeneration. We have developed a 3D-printed and optimized device and are working to further develop computational tools to improve the efficiency and accuracy of the OKR assay. Using the OKR assay allows us to analyze the functional process of regeneration. Understanding the functional regeneration of optic nerves in zebrafish will aid in developing treatments for humans with optic nerve injuries.

Presenter(s): Sophie Hu
School: University of Chicago
Session: Oral: II.D.5
Title: A Drug Screening Approach for Enhanced Colorectal Tumor Killing of CAR-NK-92 Cells
Advisor(s): Xiaoyang Wu, The Ben May Department for Cancer Research, The University of Chicago
Co-Author(s):
Abstract: Chimeric antigen receptor (CAR)-engineered immune cells have had limited therapeutic efficacy with solid tumors due to hostile tumor microenvironment and poor trafficking to tumor sites. Apart from CAR-T cells, natural killer (NK) cells represent promising alternative effectors cells that can be engineered with CAR technology with several advantages over CAR-T cells. Importantly, NK cells can be utilized as allogeneic off-the-shelf products with a reduced risk of toxicities. However, many are not sufficiently effective and researchers have proposed that combined treatment with chemotherapeutic drug compounds may help to remedy this. Here we propose to target colorectal cancer and its peritoneal metastasis by designing CAR-modified NK-92 cells against novel epitopes. Also, we will identify potential chemical compounds enhancing the therapeutic potential of CAR-modified NK-92 cells against colorectal cancer. A high-throughput screening will be done to identify candidate drugs for our study. Then, the cytotoxicity of different combinations of CAR-NK-92 cells and chemical compounds will be assessed, both in vitro and in vivo. We expect to find a combination therapy with synergistically enhanced efficacy. Results may elucidate a novel molecular mechanism and carry clinical relevance.

Presenter(s): Mackenzie Joe
School: Washington University
Session: Poster: P1.10
Title: Impact of Radio Drama on Mental Health Care Seeking Behaviors and Community Stigma in Ugandag
Advisor(s): Anna Jacobsen, Anthropology, Washington University in St. Louis
Co-Author(s): Yang Jae Lee
Abstract: Mental illness accounts for a significant portion of the global burden of disease. In Uganda, listening to the radio is a popular social activity in rural and urban areas. Thus, this project studied whether a community-designed radio-based intervention can decrease mental illness stigma and lead to improved health-seeking behaviors. Qualitative methods, such as focus groups and in-depth interviews, were performed to determine acceptance or rejection. Based on preliminary data from Tanzania, an arts-based intervention had promising results for increasing HIV/AIDS treatment. Working alongside Ugandan students, the protocol required three listening sessions, each one week apart. The first session required listening to a 30-minute control audio, followed by a structural questionnaire. The second session was either a control or experimental audio, depending on the village. The last session was another 30-minute control audio with the final structured questionnaire. A total of 206 participants in 24 villages were studied. The preliminary results have demonstrated that radio positively impacts mental illness stigma and increases seeking treatment. Ethnographic data demonstrates communities' response to listening to the radio and their drive toward accessing healthcare services. This aligns with our prediction. Further statistical analysis will be performed to fully evaluate the data**.**

Presenter(s): Anna Jonaus
School: Macalester College
Session: Poster: P2.26
Title: Glucosinolates and Growth: Quantifying Allelopathy Resistance in Soybeans to Pennycress

Glucosinolates
Advisor(s): Lucas Roberts, Agronomy and Genetics, University of Minnesota
Co-Author(s):
Abstract: During the winter, farmers in the Midwest often end up with empty fields between planting corn and soybeans. To change this, the USDA NIFA CAP project IPREFER was created with the goal of making pennycress, a common weed, into a marketable oilseed crop used on formerly fallow fields during winter months. One issue with this is the presence of glucosinolates: stinky compounds found in Brassicas like brussels sprouts and horseradish that have the potential to inhibit germination and negatively affect plant growth. When herbivores damage plant tissue, glucosinolates and myrosinase are able to interact and form highly damaging hydrolysis products. This deters further consumption and harms surrounding plants, thus minimizing resource competition. In pennycress, the glucosinolate sinigrin hydrolyzes into allyl isothiocyanate (AITC), a compound that also makes wasabi spicy! In the Upper Midwest, soybeans must be planted several weeks before pennycress is harvested to give them enough time to grow over the summer. This system of relay cropping means that soybeans are most exposed to these compounds during early development. My research looks at how these two compounds affect early soybean growth in order to effectively breed tolerant soybeans for this cropping system.

Presenter(s): Kira Jones
School: Washington University
Session: Poster: P3.9
Title: Engineering substrate specific Hsp104 NBD1 variants selected by next-generation sequencing
Advisor(s): Meredith Jackrel, Chemistry, Washington University in St. Louis
Co-Author(s): Karlie Miller, Shamika Bhandarkar, Allan Wang
Abstract: Neurodegenerative diseases are associated with toxic protein misfolding which forms stable amyloid structures leading to proteotoxicity in neurons, and my research seeks to solubilize these toxic aggregates to reduce proteotoxicity. In yeast, the Hsp104 protein disaggregase solubilizes native protein aggregates and reactivates unfolded proteins; no human Hsp104 homolog exists. Neurodegenerative proteins can be expressed in yeast models where mutated Hsp104 variants are tested for solubilization of the aggregates and re-localization. Mutations in the middle domain (MD) of Hsp104 were found to rescue proteotoxicity but disaggregated other folded proteins essential to cell function, causing off-target cell toxicity. This toxicity has inspired different regions of Hsp104, like the nucleotide bonding domain 1 (NBD1), to be explored for mutations that can disaggregate and refold toxic proteins while leaving native proteins unscathed. From a large library of Hsp104 NBD1 variants, I am testing those showing high enrichment scores, correlating with greater probability that the variant is effective against the protein aggregates. Understanding their solubilization activity will provide information about how aggregation and neuronal loss are related and insight into the structural interactions within Hsp104 proteins. No technology accurately predicts neurodegeneration, so developing a therapy targeting proteotoxic accumulation after detection can provide treatment to patients.

Presenter(s): Joseph Kaczor
School: University of Chicago
Session: Poster: P2.9
Title: Characterizing Photo-sensing in Non-photosynthetic Bacteria
Advisor(s): Sampriti Mukherjee, Molecular Genetics and Cell Biology, University of Chicago
Co-Author(s): Erin Higgins
Abstract: Bacteria possess photo-sensing cascades to control collective behaviors, like biofilms. Specifically, a light-sensing pathway that is extensively studied is the BphP-AlgB cascade in the non-photosynthetic bacterium *Pseudomonas aeruginosa*. In this pathway, the photoreceptor BphP, when bound to its ligand biliverdin and activated by light, phosphorylates the downstream response regulator AlgB. AlgB then activates and represses biofilm and virulence genes. The transcription factors that

regulate the BphP operon have yet to be discovered. To reveal potential activators and repressors that control bphP expression, a transposon mutagenesis screen is being performed to find the candidate genes. In addition, the BphP-AlgB pathway is conserved in a diverse set of non-photosynthetic bacteria, including the bacterium *Pseudomonas putida*. It was discovered that the BphP of *P. aeruginosa* can phosphorylate the AlgB of *P. putida*. However, *P. putida* has been hypothesized to have two homologs of *P. aeruginosa*'s bphP, bphP1 and bphP2 of which the function of both is unknown. I am characterizing bphP1's and bphP2's functions from *P. putida* using protein purification, reporter assays, and phenotypic arrays. Learning about the BphP-AlgB system in a new species allows for comparative studies between *P. putida* and *P. aeruginosa*, giving insight into unexplored conserved features of the pathway.

Presenter(s): Paul Kang
School: Washington University
Session: Poster: P3.29
Title: A single cell transcriptomic mapping of nasal epithelial cells from CF vs. non-CF patients
Advisor(s): Yan Xu, Neonatology and Pulmonary Biology, University of Cincinnati
Co-Author(s): Yina Du, John Brewington
Abstract: Cystic Fibrosis (CF) is a genetic disorder resulting from a mutation in the Cystic Fibrosis Transmembrane conductance Regulator (CFTR) gene. CF-related lung disease is the primary cause of morbidity and mortality due to inflammation and impaired mucociliary clearance. CFTR modulators are CF treatments that restore salt and water transport in epithelia by aiding in protein trafficking to the cell surface and improving conductance across the channel. Recent developments in CF treatments have greatly improved the prognosis for CF patients, but transcriptional changes in these modulators have yet to be thoroughly explored. We performed single-cell RNA-seq (scRNA-seq) to investigate changes in gene expression in nasal epithelial cells (NECs) across wild-type (WT), CF, and treatment conditions.

Presenter(s): Levi Kaster
School: Washington University
Session: Oral: IIE.4
Title: A Text-Mining Model for Extracting Phenotypes from NF1 Clinical Notes
Advisor(s): Aditi Gupta, Institute for Informatics, Data Science, and Biostatistics, Washington University in St. Louis
Co-Author(s): Rui Mu, Ethan Hillis, Inez Oh, Stephanie M. Morris, David H. Gutmann, Randi E. Foraker, Philip R. O. Payne
Abstract: Neurofibromatosis Type 1 (NF1) is a syndrome caused by mutations in the NF1 gene, resulting in heterogeneous outcomes across individuals. Current management of NF1-related conditions is reactive due to the lack of early risk stratification tools. This study addresses this gap by extracting clinically relevant phenotypes from progress notes to facilitate development of risk stratification models for NF1. A 4-step pipeline was developed to extract NF1-related phenotypes, identified by expert physicians as being of interest, from clinical progress notes from Washington University School of Medicine/Barnes-Jewish Hospital (WUSM/BJH) electronic health records (EHRs). Progress notes were extracted for 380 individuals with NF1. Leveraging medspaCy for implementation, the pipeline consisted of 1) sentence segmentation, 2) pattern-based logic to identify phenotype references, 3) pattern-based logic to identify negation and contextual information, and 4) a final determination about phenotype presence/absence for each individual utilizing output from the previous steps. Pipeline results were compared to gold-standard annotations from an existing NF1 registry, and F1-scores were calculated. These scores indicate that our text-mining pipeline was successful at phenotyping NF1 patients from unstructured progress notes, with 8/13 high-prevalence phenotypes having an F1-score >.8.

Presenter(s): Mayher Kaur
School: University of Chicago

Session: Oral: II.D.1
Title: Metabolic Rewiring Supports Circulating Tumor Cells in Non-Small Cell Lung Cancer
Advisor(s): Brandon Faubert, Section of Hematology/Oncology, University of Chicago Medicine, University of Chicago
Co-Author(s): Nia Hammond
Abstract: During metastasis, cancer cells detach from the primary tumor and migrate through the circulatory system. Most cancer cells die from oxidative stress during this process. How the remaining cells adapt to survive this stress is largely unknown, but a key hypothesis is that circulating tumor cells (CTCs) rewire metabolic programs to adapt to these stresses. In this work, we investigated the metabolic differences between anchorage-dependent and anchorage-independent growth in non-small cell lung cancer (NSCLC). A key limitation in this area is that standard cell culture conditions do not accurately recapitulate the in vivo
environment. To more accurately model the in vivo environment, we cultured NSCLC cells in human plasma-like media (HPLM), which better recapitulates the physiological nutrient concentrations of the blood. To investigate differences in metabolic activity between anchorage-dependent and independent growth, we cultured cells under standard or physiologically relevant conditions. We performed stable isotope labeling with key nutrients (glucose, lactate, glutamine, etc.), and preliminary results indicate key metabolic and proliferative differences across these conditions. Cells cultured in HPLM use less glucose and glutamine to fuel the TCA cycle compared to standard culture conditions, and non-adherent cells are primarily using glutamine to fuel TCA intermediates. We are currently leveraging these metabolic differences to identify novel therapeutic strategies to target CTCs. We anticipate that these assays will be a starting point for more sophisticated, in vivo models of circulating tumor cells, and that this metabolic reprogramming may lead to context-specific therapeutic vulnerabilities.

Presenter(s): Erin Kim
School: Colorado College
Session: Poster: P1.26
Title: Seasonal germination responses of *Liatris punctata* to heat and smoke
Advisor(s): Shane Heschel, Organismal Biology & Ecology, Colorado College
Co-Author(s):
Abstract: *Liatris punctata*, commonly known as the dotted gayfeather, is an herbaceous perennial of the Asteraceae family native to North America. While non-threatened, *L. punctata* plays a critical role as the primary nectar source to the threatened Pawnee montane skipper butterfly (*Hesperia leonardus montana*). This butterfly subspecies is endemic to the South Platte River drainage system in Colorado, specifically near Deckers and Cheesman Reservoir in dry, open Ponderosa pine woodlands. Despite the importance of *L. punctata* to the butterfly's preservation, the plant's germination requirements remain poorly understood. Previous studies have indicated that butenolide, a compound found in smoke, promoted germination—a finding that aligns with the species' occurrence in Ponderosa forest habitats, where occasional low-intensity fires are known to have played a natural role. Moreover, gibberellins, specifically GA4+7, have been found to have also significantly increased germination. By applying different combinations of smoke and heat treatments on seeds, this study aims to elucidate the effects of low-grade fire on *L. punctata* germination and understand the underlying mechanisms of this phenomenon, exploring individual factors such as smoke, gibberellins, and heat.

Presenter(s): Kody Kobayashi
School: Macalester College
Session: Poster: P2.17
Title: Identification and characterization of VGF in the nucleus accumbens
Advisor(s): Lucy Vulchanova, Department of Neuroscience, University of Minnesota
Co-Author(s): Anisha Adke, Patrick Rothwell
Abstract: VGF is a neuropeptide precursor that is cleaved into biologically active products. The nucleus accumbens (NAc) is central to modulating reward and pain-related behaviors. Prior work demonstrated

that, following interrupted opioid exposure, VGF transcription is upregulated in the NAc. Preliminary data showed that knockdown of VGF in the NAc attenuates the behavioral adaptations that reflect maladaptive plasticity associated with opioid withdrawal. Our overarching goal is to investigate how VGF functions in synaptic plasticity in the NAc in neuropathic pain and opioid withdrawal. This project aimed specifically to validate the presence of VGF-derived peptides in the NAc and determine how the levels change following interrupted opioid exposure and nerve injury. We hypothesize that VGF levels will increase in the NAc following either interrupted opioid exposure or peripheral nerve injury in mouse models. We induced nerve injury and used western blots to analyze the levels of VGF-derived proteins in the NAc. In separate cohorts, mice were administered oxycodone or saline, and the effects of oxycodone were interrupted using naloxone. This study will help highlight mechanisms of opioid and pain-related plasticity to ultimately identify a new therapeutic target for opioid withdrawal and addiction treatment.

Presenter(s): Kollin Kolb
School: Washington University
Session: Oral I.B.1
Title: Cardiac Radiation Attenuates Cardiac Dysfunction and Macrophage Response in Mice with Cardiomyopathy
Advisor(s): Carmen Bergom, Radiation Oncology, Washington University in St. Louis
Co-Author(s): Lauren N. Pedersen, Amanda Klaas, Felicia Grogan, Abigail Heck, Kory Lavine, Ali Javaheri
Abstract: Purpose: There is an urgent need to develop new therapies for patients with heart failure (HF). Preliminary data suggests that patients with cardiomyopathy receiving cardiac radiotherapy for ventricular tachycardia have improved cardiac function. Therefore, we hypothesized that cardiac radiation would attenuate cardiac dysfunction in HF mice, which would be associated with altered myocardial macrophage content. Methods: ACSL1TG mice, which have cardiac lipid overload and HF, underwent 5 Gy cardiac radiation (RT) or sham. At 6 and 12 weeks post-treatment, echocardiography assessed cardiac function. At 6 weeks post-treatment, cardiac tissue was collected. Trichrome staining was performed to evaluate fibrosis. To assess cardiac macrophages, CD68 immunofluorescence was performed at 1-, 4-, and 6 weeks post-treatment and flow cytometry of heart tissue was performed at 6 weeks post-treatment. CCR2+ macrophage radiolabeling with subsequent PET/CT was performed at 1- and 3 weeks post-treatment. Results: RT improved survival and attenuated cardiac dysfunction and fibrosis vs. sham. RT reduced cardiac macrophages at post-treatment time points vs. sham, which was confirmed by CCR2+ radiolabeling. Conclusions: In HF mice, cardiac radiation improves survival and attenuates cardiac dysfunction, which may be associated with reduced cardiac macrophages. Future investigation will characterize how macrophages contribute to the RT-induced cardioprotection observed.

Presenter(s): Anna Koppin
School: Hope College
Session: Poster: P1.3
Title: Lysine 473 regulates the activity and trafficking of the cystine/glutamate transporter, System xc-.
Advisor(s): Leah Chase, Chemistry, Biology, and Neuroscience, Hope College
Co-Author(s):
Abstract: System xc- is a membrane transport system that plays a critical role in mitigating oxidative stress. Past work in our lab has shown that System xc- localizes to the plasma membrane allowing for increased activity to support production of antioxidants during oxidative stress. In this study, we sought to determine if post-translational modification (PTM) of the transporter regulates its trafficking. A C-terminal 3KR mutant (K422,472,473R) exhibited decreased membrane localization and activity, suggesting that PTM at one of these sites increases activity. Further, we observed that K473R exhibits a 7 kD decrease in the molecular weight, indicating that K473 may be modified under basal conditions. We determined that this loss in molecular weight is not due to ubiquitination. In addition, we found that

K473R exhibited complete loss of xCT activity and loss of membrane expression. K473Q, an acetylated lysine mimic, appears to lead to an intermediate molecular weight loss, an intermediate level of membrane expression, and complete loss of xCT activity. We are currently working to identify the PTMs that K473 acetylation might regulate. Regardless, these preliminary data suggest that acetylation at K473 could serve as a potential mechanism by which System xc- activity and trafficking is regulated.

Presenter(s): Hrishi Kousik
School: Washington University
Session: Poster: P1.20
Title: The Impact of Dysbiotic Gut Microbiota on Obesity and Glucose Intolerance
Advisor(s): Devesha Kulkarni, Gastroenterology, Washington University in St. Louis
Co-Author(s): Elizabeth Joyce, Alexandria Floyd, Brigida Rusconi, Dalia Harris, Bejan Mahmud, Gautam Dantas, Khushi Talati, Samuel Klein, Rodney D Newberry
Abstract: As one of the most prevalent chronic diseases in the United States, obesity reduces life expectancy and quality on a widespread scale. Many factors including diet, lifestyle, genetics, and microbiota contribute to the development of obesity and obesity-related dysfunction. Not all obese individuals develop metabolic disease, however. Individuals with metabolically unhealthy obesity (MUO) characterized by high visceral fat content, insulin resistance, and adipose tissue (AT) inflammation disproportionately comprise the population suffering from metabolic diseases. In contrast, individuals with metabolically healthy obesity (MHO) experience little to no obesity-related dysfunction. Seminal animal studies correlate dysbiotic gut microbiota with MUO, yet the causal influence of gut microbiota on metabolic health remains unknown. To address this, a humanized microbiota-associated model was established: colonizing wild-type C57BL/6 mice with fecal specimens collected from MUO, MHO, or lean human subjects. Cytokine assays performed on mouse serum and small intestinal tissues showed increased levels of pro-inflammatory cytokines (e.g. Il-1β, TNFα) in mice colonized with MUO microbiota. MUO-colonized mice also exhibited glucose intolerance and insulin resistance. However, both MUO and MHO-colonized mice had similar levels of weight gain after 5 weeks. These studies demonstrate that microbiota independent of diet, genetic background, and environment, drives metabolic dysfunction.

Presenter(s): Eric Kwon
School: Washington University
Session: Poster: P2.25
Title: FLT-3 chimeric antigen receptors on conventional type 1 dendritic cells induce greater survival ability
Advisor(s): Carl DeSelm, Radiation Oncology, Washington University School of Medicine
Co-Author(s): Shelby Namen, Solomon Kang
Abstract: Dendritic cells, specifically the conventional type 1 dendritic cells (cDC1s), are a key component of the adaptive immune system, providing the crucial ability to cross present antigens on MHC molecules for downstream effectors to eliminate threats. In this poster, I will explore a novel chimeric antigen receptor (CAR) containing FLT-3, an important receptor that has downstream survival and functional effects when actively signaling in cDC1s. We hypothesized that this FLT-3 CAR construct should exhibit a significantly higher survival ability and presence of activation markers. Although these expectations were not met, the FLT-3 CAR cDC1 did have near-significant differences in survival rates than non-signaling CAR constructs and control non-CAR cDC1s at 24 hours post-incubation with tumor. Similarly, differences in levels of CD40+/CCR7+ cDC1s and CD40+/CD86+ cDC1s amongst the FLT-3 CAR and non-signaling CAR conditions were nearly significant. Interestingly, looking at the phagocytotic activity of these constructs, there was no significant difference between them. Further study of this FLT-3 CAR is needed to explore their impact on the survival capacity of cDC1s in a tumor microenvironment, but the introduction of CARs into dendritic cells provides a promising pathway for potential immunotherapies.

Presenter(s): Kevin Kyaw
School: Beloit College
Session: Poster: P1.17
Title: Soil and Sediment samples had a similar number of Antibiotic-Producing Bacteria
Advisor(s): Kristina Blanke, Biology, Beloit College
Co-Author(s):
Abstract: The fight against antibiotic resistance has accelerated the need for effective antibiotics. Currently, two-thirds of our antibiotics come from *Acinetomycetes* that are primarily found in soil. This research focused on freshwater sediment as a novel environment to find antibiotic-producing bacteria. Sediment experiences aquatic environmental conditions and was hypothesized to contain antibiotic-producing bacteria that differ from those found in soil. Sediment and soil samples were collected from local parks with water bodies around Beloit, Wisconsin, and plated on tryptic soy agar to culture bacteria. These colonies were screened against tester bacteria with similar characteristics to antibiotic resistant bacteria to find effective antibiotic-producing isolates. Nine antibiotic producers were found in soil samples and ten were found in sediment samples. Further genetic analysis of the antibiotic producing bacteria showed that the soil samples generally contained Bacillus and Pseudomonas genera, with sediment samples additionally including the *Planococcus* genus. In conclusion, antibiotic producers were found in both soil and sediment. Future studies will continue to explore the prospect of sediment as a novel source for antibiotic-producing bacteria. Freshwater sediment around Beloit, Wisconsin, will be used to find antibiotic-producing bacteria that will be further analyzed via genetic sequencing and the antibiotic metabolite will be chemically identified.

Presenter(s): Oliver Lagasse
School: Macalester College
Session: Poster: P2.6
Title: Characterizing changes in the inflammatory potential of fibroblasts in response to repeated in-vivo methylisothiazolinone exposure
Advisor(s): Elena Tonc, Biology, Macalester College
Co-Author(s): Eunice Lim
Abstract: Vulvodynia is a chronic vulvar pain condition estimated to affect roughly 10% of woman-identifying individuals in the United States. Vulvodynia has been associated with a history of allergies and exposure to common household cleaning and personal care products. Methylisothiazolinone (MI), a preservative often found in these products, elicits inflammatory responses in allergic individuals. In our murine model of vulvodynia, dermal application of MI results in enduring anogenital hypersensitivity and other clinical findings. This suggests MI has the potential to lead to chronic pain. Vulvar fibroblasts from patients diagnosed with vulvodynia express higher levels of inflammatory cytokines upon activation in in-vitro cultures. With this in mind, we investigate how the in-vitro inflammatory potential of fibroblasts is altered in response to repeated in-vivo exposure to MI. We find heightened IL-6 and TNF-α but not IL-Iβ production in response to in-vitro activation of fibroblasts. This suggests that in-vivo MI treatment increases the inflammatory potential of fibroblasts and could initiate a cascade of events that lead to chronic pain development, including inflammation in the tissue. We are currently further profiling the changes in the biology of fibroblasts from our animal model to help elucidate the hitherto obscure etiology of vulvodynia.

Presenter(s): Nicole Lagman
School: Lawrence University
Session: Poster: P1.21
Title: Angiogenin Distribution in Mammalian Cells
Advisor(s): Kimberly Dickson, Biochemistry, Lawrence University
Co-Author(s):
Abstract: Angiogenin (ANG) is a ribonuclease holding an important role in angiogenesis which is the formation of blood vessels. Besides its angiogenic activity, its other cellular function includes its

regulation of ribosomal RNA transcription by cleaving certain non-coding RNA molecules such as pRNA and tRNA. Previous studies have also suggested that mutations in ANG are associated with amyotrophic lateral sclerosis (ALS) indicating its involvement in neuronal health. Much is known about ANG, but its relative cellular distribution as well as its movements to and from the nucleus in response to changing cellular conditions is poorly understood. Our overarching goal is to characterize the cellular distribution of ANG along with its nuclear import and export through an optimized cellular fractionation protocol in tandem with western blots. We have successfully cloned an epitope tagged ANG which will be utilized to study the uptake and movement of exogenous ANG in HeLa cells. Our current goal is optimizing our cellular fractionation protocol so that we can quantify ANG levels in cellular compartments via downstream western blot experiments.

Presenter(s): Taylor Laurin
School: Hope College
Session: Poster: P2.3
Title: Investigating the intersection of one carbon metabolism and mitochondrial genome maintenance
Advisor(s): Kristin Dittenhafer-Reed, Chemistry, Hope College
Co-Author(s):
Abstract: Mitochondria contain their own DNA (mtDNA), and while the regulation of nuclear DNA is well understood, the regulation of mtDNA is not. Interestingly, four mitochondrial proteins known to associate with mtDNA are also part of one-carbon metabolism (MTHFD1L, SHMT2, ALDH1L2, PRDX5). One-carbon metabolism is a biosynthetic process that produces nucleotides and nitrogenous bases which serve as building blocks for DNA and RNA. We hypothesize that the proximity of one-carbon metabolic proteins to mtDNA is required to relay nutrient status signals that regulate mtDNA maintenance and expression. To investigate this, the expression levels of MTHFD1L, SHMT2, ALDH1L2, and PRDX5 were altered in HeLa cells, and qPCR was used to assess mtDNA content and RNA transcript levels. Results indicate that overexpressing ALDH1L2 and PRDX5 decrease mtDNA content. siRNA knockdown has variable effects, with loss of MTHFD1L decreasing mtDNA content, and loss of ALDH1L2 increasing mtDNA content.

Presenter(s): Sophie Laye
School: Washington University in St. Louis
Session: Poster: P1.6
Title: Role and mechanism of abnormal DNA methylation in Huntington's disease
Advisor(s): Hiroko Yano, Neurosurgery, Washington University in St. Louis
Co-Author(s): Maryam Borhani-Haghighi, Andrew Speidell, Yanchun Pan
Abstract: It has been shown that patients with Huntington's disease (HD), an invariably-fatal neurodegenerative disease, present with abnormal epigenetic modifications, including changes to DNA methylation patterns. The Yano lab has previously shown pharmacological inhibition of DNA methyltransferases (DNMTs), responsible for DNA methylation, and genetic inhibition of DNA-methyltransferase-3-alpha (DNMT3A) provided a neuroprotective effect in HD model primary neurons, suggesting DNMT3A's abnormal methylation plays a critical role in HD neurodegeneration through an unknown mechanism. Due to DNMT3A forming a multiprotein complex, we hypothesize that specific DNMT3A-binding proteins transport it to sites of abnormal methylation. Through cell-free binding assays and co-immunoprecipitation/immunoblotting using HEK293 cells, protein-DNMT3A binding was investigated, and three proteins, which play roles in chromatin interaction and/or transcription regulation, were identified as DNMT3A interactors. Additionally, a preclinical study of a known DNMT inhibitor in R6/2 HD mice showed that this compound improved motor function for the model HD mice compared to saline via rotarod assays. Taking all this together suggests the importance of DNMTs, specifically DNMT3A, in progression of disease, highlighting a need to continue to study the mechanism of action of these proteins to provide a more thorough understanding of the causes of HD on a molecular level.

Presenter(s): Thy Le
School: Knox College
Session: Poster: P3.7
Title: MicroRNAs in Cnidaria: Target Recognition and Conservation
Advisor(s): Matthew Jones-Rhoades, Biochemistry, Knox College
Co-Author(s):
Abstract: MicroRNAs are small (21-22nt) non-coding RNAs that regulate mRNAs post-transcriptionally. In bilateral animals (e.g. insects and mammals), miRNAs bind to the 3' UTR region of regulatory targets via the "seed", a 7nt sequence at the 5'-terminus of miRNAs (position 2-7), resulting in mRNA destabilization and decay. In plants, miRNAs bind extensively (position 2-22) to the coding region of the targets, resulting in target slicing. MicroRNAs in cnidarian animals (e.g. jellyfish and corals) are less well studied compared to those in bilaterians and plants. Some cnidarian miRNAs have been shown to cleave targeted transcripts like plant miRNAs. This project aims to verify the regulation activity of cnidarian miRNAs and their conserved targets using comparative genomics. Potential mRNA targets were predicted using an extensive search for perfect and near-perfect Watson-Crick pairing. To control for complementary matching by chance, near perfect matches were also identified for sets of control RNAs. Dinucleotide controls consist of short sequences with the same dinucleotide composition as bona fide miRNAs while trinucleotide controls consist of those with the closest mRNA-matching likelihood to the miRNAs.

Presenter(s): Vu-Anh Le
School: Beloit College
Session: Oral: I.C.3
Title: Life Cycle Assessment of Biodegradable Plastic Packaging Subject to Comprehensive Organic Sorting
Advisor(s): Mehmet Dik, Mathematics and Computer Science, Beloit College
Co-Author(s): David Zoro, Mike Waggoner, Christine Ortiz
Abstract: Organic waste rotting into methane in landfills cause approximately 14% of methane emissions in the United States, and a significant portion of the world's energy is used to generate plastic packaging. A holistic solution for reducing energy in packaging and organic waste could have significant environmental benefits. This paper presents a potential solution called "The Big Green Loop" (BGL), in which high performance organic packaging is generated from organic waste diverted from landfills. This value chain is enabled by recent advances in organic waste valorization and a high value packaging technology developed by a startup, Corumat, Inc. This new packaging technology enables high performance packaging to be made from as little as one third the material of competitive technologies, and prototypes have been made from organic waste diverted from landfills. The paper systematically analyses each step in the BGL process value chain and calculates the impacts based on various scenarios and scopes. Calculations estimate that sourcing organic waste diverted from landfills, displacing traditional packaging with reduced amounts of environmentally friendly material, and enabling the diversion of additional organic material through superior value chain economics could reduce greenhouse gas emissions and may also have other positive environmental effects.

Presenter(s): Hoi Wan Lee
School: University of Chicago
Session: Oral II.D.4
Title: Ephrin Receptor A4 is a novel mechanism of BACH1 driven metastasis in Triple-negative Breast Cancer
Advisor(s): Marsha Rosner, The Ben May Department for Cancer Research, The University of Chicago
Co-Author(s): Wenchao Liu
Abstract: Metastasis, the leading cause of cancer-related mortality, is particularly difficult to treat in Triple-negative Breast Cancer (TNBC), an aggressive cancer subtype with limited therapies. BACH1 is a transcription factor that drives TNBC metastasis, but directly targeting it is challenging as it lacks clear

binding sites. Therefore, novel strategies are needed to selectively identify and target BACH1-expressing cells and downstream proteins in the BACH1-regulated metastasis pathway. This study identifies Ephrin receptor A4 (EPHA4), a receptor tyrosine kinase, as a potential downstream target of BACH1-driven metastasis. BACH1 is sufficient to induce EPHA4 in MDA-MB-231 cells, and is necessary for EPHA4 expression in BM1 cells. EPHA4 knockout and knockdown decreased invasion of MDA-MB-231 and MDA-MB-436 cells respectively. Additionally, the mechanism of BACH1's regulation of EPHA4 was explored, revealing that BACH1 may indirectly regulate EPHA4 through BACH1/NRF2-downstream pathways. NRF2, a transcription factor that competes to promote a set of genes that BACH1 represses, was found to repress EPHA4 in MDA-MB-231 cells. This suggests that BACH1 may repress a factor promoted by NRF2, which subsequently represses EPHA4. This study found EPHA4 to potentially be a mechanism of BACH1-driven metastasis, offering a new avenue for the inhibition of the BACH1 metastasis pathway via EPHA4 inhibition.

Presenter(s): Liam Leeming
School: University of Chicago
Session: Oral: II.F.2
Title: The Roles of Arp2/3 Nucleation Promoting Factors in Actin Cytoskeleton Self Organization
Advisor(s): David R. Kovar, Molecular Genetics and Cell Biology, University of Chicago
Co-Author(s): Sarah Yde, Rachel Kadzik
Abstract: How do inputs from different branched actin nucleation promoting factors (NPFs) combine spatially and temporally to induce the Arp2/3 activity that the cell needs to function? Using the single-cell *C. elegans* embryo as a model system, we investigated the localization of two NPFs, WASP and WAVE complex, to different F-actin structures using two-color TIRF microscopy. WASP localized to F-actin mini-comets as well as dynamically in filopodia. WAVE was enriched at the tips of filopodia and a subset of actin comets which had different dynamics that those associated only with WASP. RNAi depletion of WAVE decreased the numbers of both filopodia and WAVE rich comets, while depletion of WASP decreased the number of comets not enriched with WAVE and increased the time filopodia are present at the cortex.
These results suggest that there are two distinct populations of mini-comets in the *C. elegans* zygote. Filopodia may contain multiple branched F-actin networks, nucleated by different NPFs and playing distinct, possibly antagonistic, roles in regulating filopodial assembly. However, because we do not observe Arp2/3 at the tips of filopodia, it is also plausible that WAVE complex plays an Arp2/3 independent role in filopodia, possibly in conjunction with the formin cyk-1.

Presenter(s): Maverick Leer
School: Carthage College
Session: Poster P:2.7
Title: Cladistic Ontogeny of *Eurypterus rempies*
Advisor(s): Thomas Carr, Biology, Carthage College
Co-Author(s):
Abstract: This study was done to recover a growth series for *Eurypterus remipes* using cladistic ontogeny, which has previously been unexplored in eurypterids. Any ontogenetic studies have focused on size or character changes separately, but cladistic ontogeny brings the two types of data together. These methods use cladistic algorithms to recover growth, and in order to have confidence in the results for *E. remipes*, a similar process was used for a closely related extant taxa*, Centruroides vittatus.* In doing these tests, it is hypothesized that growth and maturity will be correlated. The recovery of the growth series is the main objective, but there is also the goal to perform descriptive statistics and a Spearman test on the data matrices to evaluate the correlation between size and maturity variables. This study began with a literature review to collect data to work with, followed by the assembly of a data matrix in a software called Mesquite and the analysis of the matrix in a software called PAUP. SPSS was used for the descriptive statistics and Spearman test. The recovered growth series for *E. remipes* had six growth stages, and it was found that growth and maturity are correlated.

Presenter(s): Avery Leigh
School: Knox College
Session: Poster: P3.14
Title: Organic Matter Composition in Urban Ponds: Differences in Sample Methods and Trophic Gradients
Advisor(s): Jess Briggs and Grace Wilkinson, Center for Limnology, University of Wisconsin-Madison
Co-Author(s): Helen Schlimm, Cami Schroeder
Abstract: Urban ponds contain large amounts of dissolved organic matter (DOM), a heterogeneous mixture of organic molecules. The composition of DOM is heavily influenced by its source and the productivity of the pond, which in turn affects the greenhouse gas production in urban ponds. Allochthonous DOM, produced by terrestrial sources (soil, leaves, grass), is more complex and has more aromatic rings. Autochthonous DOM has a more simple chemical structure and is produced by aquatic sources within the water body (macrophytes, microbes, algae). To examine the differences in composition between three different DOM pools, we collected water column samples and sediment cores from seven urban ponds with differing nutrient levels. We found that the three pools - water column, sediment pore water, and sediment water soluble DOM - were all significantly different in their dissolved organic carbon (DOC) concentrations but were not significantly different in their SUVA254 values, a DOC normalized calculation of aromaticity based on wavelength measurements. In addition, we compared the DOM composition to the nutrient levels of the urban ponds. We found that as ponds became more eutrophic, their autochthonous DOM increased, unless their DOM was being more heavily impacted by other factors (such as water basin size and intended use).

Presenter(s): Amelia Li
School: Washington University
Session: Oral: II.F.4
Title: Effects of wild-type and mutant cysteine string protein alpha in autophagy-lysosome phenotypes in SH-SY5Y cells
Advisor(s): Bruno A. Benitez, Neurology, Harvard Medical School
Co-Author(s): Matthew J. Rosene
Abstract: Cysteine string protein α (CSPα) is a co-chaperone protein located in the endolysosomes and presynaptic terminal of neurons. Our group discovered CSPα mutations (p.L115R and p.L116Δ) causing adult-neuronal ceroid lipofuscinosis (AD-ANCL). Biopsy from an early-stage AD-ANCL patient suggests early dopaminergic neuron loss, yet CSPα's precise role in their endolysosomal pathway remains unclear. My project assesses SH-SY5Y neuroblastoma cells' susceptibility to CSPα mutations and evaluates related changes in the autophagy-lysosome pathway.
We created SH-SY5Y neuroblastoma cell lines stably expressing CSPα-p.L115R or p. L116Δ or wild-type via lentiviral transduction. We found that CSPα mutants produced an accumulation of CSPα aggregates absent in cells transduced with the empty vector control. We also found that mutants changed the cytosolic distribution of CSPα to exhibit visible aggregates. CSPα mutants also produced depalmitoylated CSPα monomer and higher molecular weight aggregates. Altered cellular distribution of LAMP1, a lysosomal marker, was found in cells overexpressing WT and mutant CSPα compared to the empty vector. Mutants also exhibited changes in LC3 and P62 levels, suggesting disruption to autophagic flux and likely mediating their disease-inducing effect through this role.
These findings reveal CSPα mutations' disruption of the autophagy-lysosome pathway in neuron-like cells, shedding light on AD-ANCL pathophysiology.

Presenter(s): Genxuan Lian**,**
School: Grinnell College
Session: Oral II.D.3
Title: Telomere and Telomerase Hallmarks in Cancer Cell Regulation: Measurement, Gain-of-function Genotoxicity and the Novel Prisonbreak Model

Advisor(s): Lu Chen, Epigenetics Institute, Fox Chase Cancer Center
Co-Author(s): Musinu Zakari, Ashley Park, Julia Hoopman, Abby Fowler, Rachana Thang
Abstract: Telomeres maintain chromosomal integrity and shorten due to the end replication problem. To circumvent the loss and the ensuing replicative senescence, telomerase is recruited by shelterin to elongate telomeres, which is a hallmark for 90% of human cancers. In this study, we applied flow fluorescence in situ hybridization (flow FISH) to measure telomere length (TL), alongside the telomerase repeated amplification protocol (TRAP) to measure telomerase activity. Further, we improved TRAP into the "TRAP-vs" assay, which allows specific detection of template-mutated telomerase when co-expressed with their wildtype counterpart. Utilizing this assay, we examined the dominant-acting effects of a telomerase RNP mutant, DN-TERT, a catalytic-dead mutant of the protein subunit. We observed that the transient DN-TERT expression induces immediate cytotoxicity in leukemia cell lines with long telomeres. This observation contradicts the common belief that telomerase inhibition only leads to cancer cell death when telomeres shorten over multiple cell divisions. Our results suggest that DN-TERT operates in a neomorphic and gain-of-function manner, inducing a non-canonical mode of genotoxicity at long telomerases. Moreover, with our novel understanding of telomerase RNP prisonbreaking from phase-separated nuclear body, we examined its combination effect on noncoding RNA structure, trafficking, and genomic functions through various techniques.

Presenter(s): Kathryn Lillemon
School: Gustavus Adolphus College
Session: Poster: P3.17
Title: Identification of potential *TEN1* mutants induced by CRISPR/Cas9 in *Arabidopsis thaliana*
Advisor(s): Katherine Leehy, Biology, Gustavus Adolphus College
Co-Author(s):
Abstract: The CST complex in *Arabidopsis thaliana* is made up of three genes (*CDC1*, *STN1*, and *TEN1*) and has an important role in the maintenance of telomeres in plants and other eukaryotic organisms. *CDC1* and *STN1* are relatively well characterized for their roles in regulating telomere maintenance, but *TEN1* has been studied very little. Previous research suggests that mutating the *TEN1* gene produces several stem-cell related morphological, developmental, and molecular defects like fused stems and genomic instability in *Arabidopsis*. Using CRISPR/Cas9, several guide RNAs have been designed to target the exon regions of *TEN1* in *Arabidopsis*. Five candidate lines have been identified with mutations in exon 3 of *TEN1*, and one candidate line with a 4-amino acid deletion has been identified in exon 1 of *TEN1*. Future work will include characterizing the phenotypes of candidate mutant lines and performing molecular analyses to determine the effect of CRISPR/Cas9 editing on different regions of the *TEN1* gene.

Presenter(s): Eunice Lim
School: Macalester College
Session: Poster: P1.11
Title: Investigating Fibroblast Responses to Methylisothiazolinone Treatment
Advisor(s): Elena Tonc, Biology Department, Macalester College
Co-Author(s): Eunice Lim, Oliver Lagasse, Mady Chen, Ahlaam Abdulwali, Devavani Chatterjea
Abstract: Methylisothiazolinone (MI) is a common chemical preservative. Past studies have linked contact allergies and MI exposure to a chronic pain condition, vulvodynia. Studies have also shown that repeat dermal application of MI to murine labia leads to long-term tactile sensitivity and low-grade inflammation, mirroring clinical findings from vulvodynia. Clinical findings implicate fibroblasts in the pathophysiology of vulvodynia, so we investigated the effects of MI on fibroblasts. While MI has a negative effect on liver and bronchial epithelial cell viability, the effect of MI on fibroblasts has never been investigated. To study these responses, primary fibroblasts from naive mice were treated with varying concentrations of MI. Cell viability was assessed by annexin V and propidium iodide staining using flow cytometry, and metabolic activity was determined using colorimetric MTT assay.
Our results indicate a decrease in cell viability after treatment with higher concentrations of MI,

supporting our hypothesis that MI has a cytotoxic effect on fibroblasts. Currently, we are investigating the inflammatory responses of fibroblasts to MI and the cell death mechanism at play. These results will help elucidate whether early fibroblast responses to MI are involved in the initiation of cellular events that contribute to the development of vulvodynia.

Presenter(s): Joshua Liu
School: Washington University
Session: Poster: P2.11
Title: Modulation of Peripheral Ly6Chigh Monocytes Rescues Synapse Elimination during Recovery from Zika Virus Encephalitis
Advisor(s): Robyn S. Klein, Medicine, Washington University
Co-Author(s): Jeremy Hill, Adham Fani-Maleki, Shenjian Ai
Abstract: Zika virus (ZIKV) encephalitis is an acute neurological disease that leads to long-term cognitive deficits, including memory loss and reduced spatial learning. Effective control of ZIKV within the central nervous system relies on appropriate innate and adaptive antiviral immune responses, including the infiltration of inflammatory Ly6Chigh monocytes and CD8+ T cell responses. Our previous research demonstrates that the cytokine interferon-gamma (INF-γ), produced by CD8+ resident memory T cells (Trm), triggers the elimination of synapses. In peripheral tissues, Ly6Chigh monocytes play a crucial role in facilitating CD8+ Trm differentiation. While inflammatory monocytes infiltrate the CNS during viral encephalitis, their impact on CD8+ Trm differentiation and the development of cognitive impairment remains unknown. Muramyl dipeptide (MDP) is a peptide that mediates the conversion of Ly6Chigh inflammatory monocytes to Ly6Clow anti-inflammatory monocytes via the NOD2 receptor. In this study, we investigated the effects of MDP treatment on the neuropathology of a mouse model of ZIKV encephalitis. We hypothesized that MDP treatment would modulate the innate immune system by converting infiltrating monocytes from an inflammatory to an anti-inflammatory phenotype and would result in enhanced long-term neurological outcomes by preserving synapses. Our data revealed that MDP treatment limited the elimination of post-synaptic termini during recovery. Additionally, there was a decrease in the total number of CD8+ T cells, but MDP treatment did not alter the proportion of CD8+ resident T cells. Collectively, these findings suggest a role for Ly6Chigh inflammatory monocytes in the phagocytosis of synapses during acute ZIKV infection, which persists beyond viral clearance.

Presenter(s): Marco Lopez G
School: University of Chicago
Session: Oral: I.C.1
Title: Taking the long way around: elucidating ecology from morphology in chondrichthyan cranial lateral line canals
Advisor(s): Michael Coates, Department of Organismal Biology, The University of Chicago
Co-Author(s): Vishruth Venkataraman
Abstract: The lateral line canals of the Bonnethead Shark (*Sphyrna tiburo*) differ wildly from the expected morphology relative to its close and distant relatives, even accounting for differences in head shape. Instead of being markers of phylogenetic constraint, the morphological characteristics of the lateral line system may reflect, and thus be a proxy for, fish ecology. Conserved in all fish, the mechanosensory lateral line organ is essential for behaviors like schooling, predation, predator avoidance, and navigation. The diverse forms of the system have been investigated phylogenetically, but little research has been done to determine how the pattern and structure of the line correlates with an animal's behavior and life history. With an ecomorphological disparity comparable to mammals, morphological convergence in distant lineages, and a well-conserved canal pattern throughout, sharks are used as the model clade for analyzing and comparing the lateral line organ. Using a representative sample of sharks, non-invasive and non-destructive digital data of the system is acquired from tomographic reconstructions of contrast-stained heads for testing the connection between ecology and lateral line canal morphology. Length, depth, caliber, and surface area analyses of the system are used to understand the canals between taxa and in different regions of the head.

Presenter(s): Alex Marcoullier
School: Knox College
Session: Poster: P2.14
Title: Phytoextraction of Nickel by Brassiaceae and Asteraceae Species
Advisor(s): Stuart Allison, Biology, Knox College
Co-Author(s):
Abstract: Several plants that exhibit phytorextraction are members of the Brassicaceae and Asteraceae families. However, few metallophytes are native to North America. Nickel chloride is a heavy metal commonly found in the flowback water of hydraulic fracturing and can cause a variety of health issues. To test if certain plant species (*B. rapa*, *C. bursa-pastoris*, *E. cheiri*,. *H. maximiliani*, *T. arvense*), were able to uptake nickel, individuals were grown and exposed to two concentrations of nickel chloride solution over 8 weeks. The plant's physical health was observed for any changes in the aerial parts of the plant throughout exposure. The soil was analyzed using pXRF to determine if plants were taking up or resisting the nickel. The pXRF results were analyzed using a two-way ANOVA ($p < 0.05$) and the results were statistically significant, indicating that the plants were taking up a significant amount of nickel from the soil. The qualitative results however, indicate that some species may not be able to survive higher concentrations of nickel and would not be suitable for real world applications. *C. bursa-pastoris, E. cheiri*, and *T. arvense* had minimal reactions to the nickel and may be successful in phytoextraction in areas contaminated by heavy metals.

Presenter(s): Frederick Melges, Jacquelin D'Lamater
School: Hope College
Session: Poster: P3.3
Title: Metabolic Diversity of *Escherichia coli*: Is there a Distinction Between Clinically-Derived and Water-Derived Strains?
Advisor(s): Aaron Best, Biology, Hope College
Co-Author(s): Samuel Leslie, Clayton Piehl, Benjamin Turner, Natalie Huisman, Brent P. Krueger, Mike Pikaart
Abstract: *Escherichia coli* is a coliform bacteria predominantly found in the digestive systems of animals and humans. Strict regulations exist for *E. coli* in recreational waters, stemming from the assumption that *E. coli* is confined to the body and the presence in the environment is a result of fecal contamination. Longitudinal monitoring of the Macatawa Watershed has resulted in the isolation of over 10,000 strains of water-derived *E. coli* and sequencing of over 500 strains. To understand potential differences between clinically-derived and water-derived *E. coli* strains, we are characterizing the metabolic diversity of the watershed populations through 1) experimental determination of growth properties on 192 substrates provided as sole carbon sources for growth and 2) computational prediction of metabolic capabilities using genome scale metabolic modeling based on genome sequences of strains. Results indicate a high level of diversity in the water-derived strains that show distinct growth patterns from each other and from a laboratory strain, supporting the hypothesis that endemic strains of *E. coli* exist in recreational waters not indicative of fecal contamination. This has implications for regulatory monitoring approaches of recreational waters for public health purposes and improves our understanding of metabolic diversity in closely related strains of bacteria.

Presenter(s): Saumith Menon
School: Washington University
Session: Poster: P1.28
Title: The effects of neuromodulators tabernanthalog and ibogainalog on the α1β2γ2L GABAA receptor
Advisor(s): Gustav Akk, The Department of Anesthesiology, Washington University School of Medicine in St. Louis
Co-Author(s): Sophia Q. Xu
Abstract: GABAA receptors are ligand-gated ion channels located primarily on the postsynaptic

membrane of neurons. The receptor's primary role is to regulate neuronal excitability by mediating inhibitory neurotransmission. The main physiological purposes of this receptor include preventing overexcitation, anxiety and stress regulation, sleep promotion, pain modulation, mood regulation and memory. The primary objective of this project was to investigate the pharmacological properties and structural interactions of two newly developed neuromodulators, tabernanthalog (TBG; 8-methoxy-3-methyl-1,2,3,4,5,6-hexahydroazepino[4,5-b]indole fumarate) and ibogainalog (IBG; 9-methoxy-3-methyl-1,2,3,4,5,6-hexahydroazepino[4,5-b]indole hydrochloride), on the α1β2γ2L GABAA receptor. The main method of experimentation was double voltage-clamp electrophysiology on Xenopus laevis oocytes. Our functional assessments have revealed that both TBG and IBG exhibit inhibitory effects on the α1β2γ2L GABAA receptor. The results further showed that IBG yielded a higher IC50, which refers to the ligand concentration that produces 50% binding inhibition, in comparison to TBG (380 and 90 µM respectively).

Presenter(s): Kaia Meyer
School: Gustavus Adolphus College
Session: Oral: II.E.1
Title: Changes in metabolic rates of *Belgica antarctica* during recovery from sublethal freezing
Advisor(s): Yuta Kawarasaki, Biology. Gustavus Adolphus College
Co-Author(s):
Abstract: Terrestrial midge, *Belgica antarctica*, is the only species of true insect that is native to Antarctica, and is found exclusively along the west coast of the Antarctic Peninsula. As polyextremophiles, larvae of the Antarctic midge are capable of surviving a wide variety of environmental stresses including freezing of their body fluids. Although the limit of their survival is as low as -18 °C, the midge larvae rarely experience temperatures below -10°C in their natural habitat. Therefore, the objective of this study was to examine the changes in metabolic rates after the midge larvae were exposed to a more ecologically-relevant temperature condition of -5°C for 24 h. We found that metabolic activity of larvae was significantly elevated immediately after freezing at -5°C, and remained increased during recovery for up to 12 days. Compared to the resting rate of 3.2 nl O2 consumed per mg-1 FW per min-1, the average oxygen consumption of larvae was elevated to ~4.0 nl O2 consumed per mg-1 FW per min-1 by freezing. Our results suggest that although larvae of the Antarctic midge are capable of enduring freezing at -5°C, such an exposure can have a prolonged impact on their metabolic functions.

Presenter(s): Sydney Morris
School: Colorado College
Session: Poster: P1.18
Title: The Effects of Burn Severity on Soil Chemistry and *Pinus ponderosa* Regeneration in Waldo Canyon, CO
Advisor(s): Roxaneh Khorsand, Organismal Biology & Ecology, Colorado College
Co-Author(s):
Abstract: High severity fires can be detrimental to forest types that have not historically experienced these conditions, leading to a low likelihood of forest regeneration and the development of novel post-fire ecological trajectories. Pinus ponderosa forest is a dominant forest type in the western United States and is poorly adapted to regenerate following high severity fires. While factors such as elevation and climate are known to affect *P. ponderosa* regeneration post-fire, less is known regarding how fire-altered soils may impact forest regrowth, specifically in relation to the soil's chemical properties. In this study, I investigate how soil nitrogen, carbon, and aluminum oxide across high and low burn severity sites may be correlated with *P. ponderosa* regeneration. I quantified soil nutrients and sapling abundance in the historic 2012 Waldo Canyon burn scar in Colorado. Aluminum oxide levels were measured using an XRF while nitrogen and carbon levels were recorded using NC 2100 Soil analysis. Given the prediction that high severity fires will increase as the climate continues to warm, understanding the relationship between *P. ponderosa* regeneration and soil chemistry has major implications for land management

and conservation in the Rocky Mountain West.

Presenter(s): Arlet Montalvo-Mosso
School: Lawrence University
Session: Poster: P1.8
Title: A mammalian system for expression and purification of the human ribonuclease/angiogenin inhibitor
Advisor(s): Kimberly Dickson, Biology/Biochemistry, Lawrence University
Co-Author(s):
Abstract: The human ribonuclease/angiogenin inhibitor (RNH1) is a horseshoe-shaped, leucine-rich repeat protein that inhibits the activity of pancreatic-type RNases (RNase). The binding of RNH1 to its target RNases is among the tightest interactions known in biology. RNH1 is also rich in cysteine, which must be reduced for RNH1 to maintain its structure and inhibitory function. RNH1 has a potential role as an oxidative stress sensor in the cell. The degree to which cys influences the structure, stability, and binding affinity for RNases is poorly understood. This project aims to better understand the role of cysteines in RNH1 by constructing variants in which cysteines are replaced with leucines. We engineered several variants of RNH1 with some or all of the cysteines substituted with leucines and incorporated a cleavable N-terminal twin Strep-tag®. We have successfully expressed wtRNH1 in CHO-K1 cells and purified the protein using StrepTactin® XT resin. Our future work will include purifying wt and variant RNH1 and characterizing their structural stability, sensitivity to oxidation, and inhibition of target RNases. The biochemical properties of variant RNH1 will enable us to decipher the role of cysteines in its structure and function in vitro and provide tools for investigating these questions in vivo.

Presenter(s): Alexandra Murphy
School: Beloit College
Session: Poster: P1.31
Title: Isolating Potential Novel Antibiotic Compounds from Soil Bacteria
Advisor(s): Kristin Labby, Chemistry, Beloit College
Co-Author(s):
Abstract: To combat the antibiotic crisis, Tiny Earth aims to isolate novel natural products from soil bacteria. Various soil samples were collected from surrounding areas including Beloit College. These samples were plated and cultured following Tiny Earth research protocols. Colonies of interest were isolated and further analyzed by screening against lab-safe ESKAPE relatives. It was found that isolates “DV12” and “DV8” were highly effective at reducing the growth of *E. raffinosus*, *B. subtilis, A. baylyi*, *P. putida*, and *M. smegmatis*. Using PCR and BLAST, the isolate DV8 was found to match Pseudomonas reineki (97.53% identity). By using liquid-liquid extraction from DV12 cultured in 500mL of PDB medium, 44.3 mg of extract was isolated and further analyzed by thin layer chromatography (TLC) and disk-diffusion bioassays. In future work, DV12 as well as DV8 will continue to be studied and their extracts will be further analyzed by HPLC and NMR spectroscopy.

Presenter(s): Arya Murthy, Feven Getachew
School: Grinnell College
Session: Poster: P2.27
Title: The role of vimentin in zebrafish lateral line development
Advisor(s): Pascal Lafontant, Biological Chemistry, Grinnell College
Co-Author(s):
Abstract: The lateral line is a mechanosensory system in fish and amphibians comprised of neuromasts innervated by sensory neurons. Neuromasts are deposited by migrating primordia originating from cephalic placodes soon after fertilization. Vimentin, a type III intermediate filament expressed in neuronal progenitor cells, is associated with epithelial mesenchymal transition, matrix remodeling, and migration. However, the role of vimentin in lateral line development has not been investigated. Using

zebrafish that express a vimentin-RFP fusion protein, we found that vimentin is highly expressed in the neuron-like fiber migrating along the path of the lateral line. Using the pan-neuronal marker Zn-12, and neuromast marker DASPEI, we have confirmed that the vimentin expressing cells are lateral line nerves innervating the neuromasts. In addition, using live imaging we have found that these sensory neurons co-migrate with a population of sox-10 expressing neural crest cells. We have generated vimentin mutants using CRISPR gRNA. Preliminary data suggests that vimentin-null zebrafish have no apparent phenotypic changes in the lateral line, suggesting possible compensation by a number of vimentin-related genes such as Vimr1. Additional mutations in these will provide insight into the role of the vimentin family of genes in lateral line development.

Presenter(s): Arjun Nair
School: Washington University
Session: Oral II.D.2
Title: Impaired neurogenesis with reactive astrocytosis in the hippocampus in a porcine model of acquired hydrocephalus**.**
Advisor(s): James P. McAllister, Neurosurgery, Washington University in St. Louis
Co-Author(s): Arjun Nair, Maria Garcia-Bonilla, Jason Moore, Leandro Castaneyra-Ruiz, Sarah H. Zwick, Ryan N. Dilger, Stephen A. Fleming, Rebecca K. Golden, Michael R. Talcott, Albert M. Isaacs, David D. Limbrick Jr
Abstract: Hydrocephalus is a neurological disease with an incidence of 80-125 per 100,000 births in the United States characterized by ventriculomegaly and ventricular zone disruption.
We hypothesized that hippocampus structure and neurogenesis are altered in untreated hydrocephalus and correlate with recognition memory deficits. Intracisternal kaolin injections induced hydrocephalus in domestic juvenile pigs (43.6□9.8 days). Age-matched sham controls received similar saline injections. MRI volumetric analysis determined ventricular volumes, and/or hippocampal and perirhinal sizes 14□4 days and 36□8 days (sacrifice) post-induction. Recognition memory was assessed one week before and after kaolin induction. Histology and immunohistochemistry were performed on the hippocampus post-sacrifice. Hippocampal width and perirhinal cortex thickness were decreased ($p<0.05$) in hydrocephalic pigs 14□4 days post-induction. Significant cerebral ventricle expansion was observed in hydrocephalus pigs at sacrifice, and dorsal hippocampus area was reduced by 23.4% ($p=0.035$) in hydrocephalic pigs. Reactive astrocytes were increased ($p=0.041$) by 48.7% in the dorsal hippocampus of hydrocephalic pigs. Doublecortin+ cells and neurons decreased ($p<0.01$) by 32.35%, and 19.74%, respectively, in the subgranular zone of the dorsal hippocampus. No difference in the recognition index, a summative measure of recognition memory, was observed. In untreated juvenile pigs, acquired hydrocephalus caused morphological alterations, reduced neurogenesis, and reactive astrocytosis in the hippocampus**.**

Presenter(s): Lane Nelson
School: Colorado College
Session: Poster: P3.24
Title: Re-Understanding Cardiac Health: Exploring the Bidirectional Relationship Between Cardiovascular Disease and Social Support
Advisor(s): Eryn Murphy, Human Biology and Kinesiology, Colorado College
Co-Author(s):
Abstract: Background: This study aims to elucidate the relationship between social support, cardiac function, and incidence of cardiovascular disease among active older adults.
Methods: We recruited 15 participants from Colorado College's Fit4Life group (avg. age = 74.9 years ± 6.32; n=8 females). Participants completed a series of semi-balanced conditions, including eyes-open and eyes-closed balance after seated and supine rest. Concurrent data collection included cardiac output and associated measures. Additionally, the Duke Social Support Index (DSSI) was administered to each participant upon intake. Independent t-tests compared groups with and without cardiovascular disease, as well as top and bottom 50% of scores on the DSSI.

Results: Results indicate a statistically significant difference between individuals that rank in the top and bottom 50% of DSSI scores and their incidence of cardiovascular disease. Additionally, there is a statistically significant difference between the individuals with and without history of cardiovascular disease and their level of social support. There was no significant difference across any groups in measures of cardiovascular function.
Conclusions: These results confirm the bidirectional relationships between cardiovascular disease and social support, even among well-supported older adults. Further research is warranted to investigate the relationship between social support and metrics of cardiac function.

Presenter(s): Nancy Nabahire Ngutete
School: St. Olaf College
Session: Poster: P1.32
Title: Characterization of a Stalkless Mutant in *C. crescentu*s.
Advisor(s): Lisa Bowers, Biology, St. Olaf College
Co-Author(s):
Abstract: *Caulobacter crescentus* is a non-pathogenic stalk-forming bacterium with a dimorphic life cycle. A stalk is a protrusion of the cell envelope at one pole of the cell and is a canonical feature of this species of bacteria. *Caulobacter crescentus* and another stalk-forming bacterium, *Hyphomonas neptunium,* share 8 transcription factor genes that are not found in closely related non-stalk-forming bacteria. A deletion of one of these genes, cc_1664, resulted in Caulobacter cells that were missing their stalks. Our aim was to construct a plasmid that will add the gene back with high expression levels. We constructed a new plasmid by adding the gene, cc_1664, with a strong promoter to the knockout cells. This resulted in the cells making stalks again, both in rich and low-phosphate media. We will also be identifying the genes regulated by this transcription factor in order to learn more about the role of cc_1664 in the stalk formation pathway. We plan to perform an RNA-sequencing experiment and a ChIP-seq experiment to help us determine the genetic pathway leading to stalk formation in low-phosphate media.

Presenter(s): Mai Tien Nguyen
School: Colorado College
Session: Poster: P2.8
Title: Inner kinetochore compositions across diverse centromere types in budding yeasts
Advisor(s): Sara Hanson, Molecular Biology, Colorado College
Co-Author(s): Jennifer Garcia
Abstract: NOTE: The kinetochore, a multiprotein structure, links centromeres to microtubules during eukaryotic cell division, ensuring accurate chromosome segregation. Centromeres are specific chromosomal regions that serve as platforms for kinetochore assembly. While functionally conserved, kinetochore composition and centromere organization exhibit diversity in eukaryotes. In budding yeasts (subphylum Saccharomycotina), centromeres vary from short, sequence-specific point centromeres to larger regional centromeres. To inventory inner kinetochore compositions in budding yeasts with varying centromere types, we developed “mign”, a tool written in Python, to automate the homolog identification of 20 inner kinetochore proteins in 338 species. During the homolog identification process, certain inner kinetochore proteins in budding yeasts exhibit greater similarity to fission yeast *Schizosaccharomyces pombe*, as opposed to *Saccharomyces cerevisiae*. The resulting inventory reveals that proteins previously recognized to be linked with point centromeres are also present in species featuring regional centromeres. Additionally, the inner kinetochore inventory in the Saccharomycodaceae family positions it as a candidate for centromere type research, given the limited knowledge of centromere types within this family. Understanding inner kinetochore compositions in relation to centromere types offers insight into the coevolution of centromeric DNA sequences and associated proteins. The data obtained here provide directions for future wet lab projects.

Presenter(s): Ngoc Nguyen
School: Knox College
Session: Poster: P1.9
Title: Effect of *Bacopa monnieri* extract on lipopolysaccharide-induced inflammatory response of

J774A.1
Advisor(s): Janet Kirkley**,** Biochemistry, Knox College
Esther Penick, Neuroscience, Knox College
Co-Author(s):
Abstract: Inflammation is the response of the immune system to the pathogen. It is induced when the receptors on macrophages recognize the invading pathogen, leading to the release of inflammatory mediators. At later stages of inflammation, macrophage secretes anti-inflammatory cytokines to suppress the responses, which helps prevent uncontrolled acute inflammation. Since *Bacopa monnieri* is widely used in traditional medicine for its anti-inflammatory activity, the role of bacopa in altering the response of macrophages to lipopolysaccharide (LPS), an inflammatory stimulus, is important to examine. It is possible that bacopa regulates the inflammation by inhibiting the secretion of pro-inflammatory mediators, increasing the secretion of anti-inflammatory mediators, or some combination of the two. Here, this study aims to understand the impact of *Bacopa monnieri* extract (BME) on the production of nitric oxide (NO), the expression of inducible nitric oxide synthase (iNOS), and the secretion of inflammatory cytokines including tumor necrosis factor-α (TNF-α) and interleukin-6 (IL-6) from LPS-stimulated J774A.1 macrophages.

Presenter(s): Joe Ntayagabiri
School: Macalester
Session: Poster: P1.16
Title: GluN2B and ADC Expression in Spinal Cord of Mice With Inflammatory Pain
Advisor(s): Carolyn Fairbanks, Pharmacology, University of Minnesota
Co-Author(s): J. K. Ntayagabiri, T. Xie, C.D. Peterson, C. Barajas, K.F. Kitto
Abstract: Chronic pain is a great public health burden, requiring effective long-term treatments. Previous studies have shown that NR2B subunit of the (N-methyl-D-aspartate) NMDA receptor is increased in animals with chronic pain. Previous studies in our lab have demonstrated that decarboxylated L-arginine, agmatine, reverses nerve-injury induced mechanical hyperalgesia, in a manner dependent on NR2B-subunit containing NMDA receptors. Agmatine is an endogenous neuromodulator presumably synthesized via arginine decarboxylase (ADC). We have previously shown that elevated ADC level attenuated mechanical hyperalgesia in animals with peripheral neuropathy. This study aims to determine the impact of CFA (Complete Freud's Adjuvant)-induced inflammatory hypersensitivity on the expression of NR2B-subunit containing NMDA receptors and ADC in the spinal cord. Male ICR (Institute of Cancer Research) mice were divided into naïve, sham, CFA-injected, CFA-injection with intrathecal saline, CFA-injection with intrathecal agmatine. The tactile hypersensitivity was measured before and after CFA and drug injections using the von Frey monofilament stimulation. Mice were perfused with 4% paraformaldehyde, spinal cords extracted and prepared for analysis. We hypothesize that expression of GluN2B and ADC would be altered in CFA treated animals compared control subjects and CFA-treated subjects with intrathecal agmatine.

Presenter(s): Natalie Olander
School: Hope College
Session: Poster: P1.29
Title: Effects of delayed HCA exposure on a rat model of Bipolar Disorder
Advisor(s): Leah Chase, Departments of Biology, Chemistry, and Neuroscience, Hope College
Co-Author(s): Eden Comer
Abstract: Bipolar disorder (BD) features cyclical periods of depressive and manic behaviors. The Chase lab aims to develop a reliable animal model for BD to characterize its critical neurological triggers. Previous work has shown daily injection of rat pups from postnatal days 3 through 19 (P3-P19) with homocysteic acid (HCA) produces a mixed manic and depressive state that can be reversed by lithium treatment. Despite this model's reproducibility, critical behavioral changes were observed during summer 2021, such that animals exhibited more manic than depressive behaviors. Investigation of pup weight and timing of eye opening suggested older pups than indicated by the vendor. Our current study

therefore measures behavior in rats given HCA injections from P5 to P21, mimicking exposure of the 2021 cohort, to assess effects of a delayed treatment period. We aim to understand how HCA exposure timing impacts behavior and determine its implications for BD.

Presenter(s): Michelle Osiro
School: Macalester College
Session: Poster: P3.4
Title: Characterizing Early Immune Infiltration and Tumor Microenvironment Development in Pancreatic Cancer
Advisor(s): Emma Dawson, Biology, Massachusetts Institute of Technology
Co-Author(s): Tyler Jacks
Abstract: Pancreatic Ductal Adenocarcinoma (PDAC) is a lethal disease with a 12.5% five-year survival rate due to late diagnosis and poor therapeutic responses. PDAC features a highly fibrotic and inflamed tumor microenvironment (TME) that excludes anti-tumor immune cells in late stage disease. However, immune infiltration and TME development in early stages of PDAC progression is poorly understood. Here, we utilized a murine pancreatic KP (KrasG12D/+; Trp53 fl/fl) organoid model which is transplanted orthotopically into syngeneic mice resulting in advanced disease 8 weeks post-transplantation. We performed immunohistochemistry analysis of lesions 1-4 weeks post-transplantation and observed notable innate and adaptive immune responses by monitoring macrophage and CD8+ T cell populations, respectively. We observed a strong macrophage response that was then steadily maintained, likely constituting the tumor-associated macrophage population. Interestingly, despite previous data showing that CD8+ T cell depletion does not affect tumor burden, we observed significant CD8+T-cell infiltration which rapidly decreased with disease progression indicating a trend towards a dysfunctional anti-tumor immune response. Our data also indicates early fibrosis and increased cell proliferation in the TME compared to adjacent normal pancreas tissue. Additionally, as small early lesions are difficult to visualize within tissue, we concurrently engineered KP organoids to express a Zsgreen fluorophore to ease their future identification. Our data demonstrates a reproducibly robust adaptive and innate immune response in early PDAC development, emphasizing the need for further investigation to improve diagnosis and prevent disease progression.

Presenter(s): Neil Panwalker
School: Washington University
Session: Poster: P2.1
Title: Investigating Functional Roles of Orbitofrontal Cortex-Dorsomedial Striatum Projection during Economic Choice Task in Mice
Advisor(s): Camillo Padoa-Schioppa, Neuroscience, Washington University in St. Louis
Co-Author(s): Manning Zhang, Mary Carter, Camillo
Abstract: The orbitofrontal cortex(OFC) plays an important role in economic decision-making. Numerous neurophysiology studies indicate that the OFC gathers information relating to the values of individual offers and compares these values to generate economic choices. However, we do not know how the OFC cooperates with other parts of the brain to accomplish this economic choice task. In this study, we aimed to demonstrate the role of the output projection from OFC to the dorsomedial striatum (DMS) during economic choice behavior. To answer this question, we successfully trained two mice to perform the economic choice task. In the task, they chose between two different rewards by trading between juice types and quantities. We also performed surgeries on two mice by injecting retrograde pAAV-CAG-tdTomato virus in DMS to label the output projection from OFC to DMS, and pAAV.Syn.GCaMP6f virus in OFC for recording the neurons. Furthermore, we used two-photon (2P) calcium imaging with gradient-index (GRIN) lenses to image OFC neurons during the economic choice tasks. By analyzing their activities, we found neurons in OFC encode different task-related variables. From this project, we established the stage for further studying the functional roles of OFC-> DMS projection neurons.

Presenter(s): Tia Peterson
School: Colorado College
Session: Oral: I.B.2
Title: Presence of Pathogenic Variants in Circular RNA of Presenilin 1 and 2
Advisor(s): Meredith Course, Molecular Biology, Stanford University
Co-Author(s): Ian Johnson
Abstract: Alzheimer's Disease (AD) is the most common form of neurodegeneration, currently affecting over 6 million Americans. Previous research suggests that circular RNAs (circRNAs) are heavily implicated in neuronal gene regulation; however, their precise role in AD pathogenesis has yet to be established. In this study, we examined circRNA of two AD-causing genes, presenilin 1 and 2 (PSEN1 and PSEN2), for the presence of pathogenic variants. cDNA from individuals with familial AD (FAD) was PCR amplified using divergent primers to target back-spliced regions specific to circRNAs, and the purified PCR product was subsequently Sanger sequenced. Four variants, I143T, S212Y, V272A in PSEN1, and N141I in PSEN2, were identified in circRNAs. The presence of pathogenic variation in circRNAs marks a crucial first step in determining their role in AD pathogenesis. To our knowledge, this research is the first of its kind to identify pathogenic variants in circRNAs of AD risk genes.

Presenter(s): Yalda Pourshaban
School: St. Olaf College
Session: Poster: P1.12
Title: Mapping of Adaptor Protein Binding Along O-GlcNAc Transferase's (OGT) Tetratricopeptide Repeat (TPR) Domain
Advisor(s): Cassandra M Joiner, Chemistry Department, St. Olaf College
Co-Author(s): Rose Lopez, Meghan Moore
Abstract: O-GlcNAc Transferase (OGT) is a mammalian enzyme responsible for the addition of N-acetylglucosamine (GlcNAc) to serine and threonine residues on over 1,000 nuclear and cytoplasmic proteins. Misregulation of protein O-GlcNAc levels is implicated in cancer, diabetes, and neurodegeneration. However, it is unknown how OGT selects its substrates. OGT has two domains, the catalytic domain that mediates sugar transfer and the tetratricopeptide repeat (TPR) domain that mediates protein-protein interactions. It is hypothesized that adaptor proteins recruit specific substrates to OGT through binding interactions along the TPRs, but the location of these interactions is unclear. Our project aims to map the binding sites of known adaptors along the TPRs, using a library of OGT mutants with a photoactivatable unnatural amino acid, Bpa, inserted into 26 locations along the domain. Using this library, we covalently captured the interactions between OGT and two adaptors, CARM1 and mSin3a, at different sites along the TPRs.

Presenter(s): Sai Prem
School: Washington University
Session: Poster: P2.29
Title: Evaluating the radiosensitization potential of the antibody drug conjugate sacituzumab govitecan-hziy (IMMU-132)
Advisor(s): Vaishali Kapoor, Department of Radiation Oncology, Washington University in St. Louis School of Medicine
Co-Author(s):
Abstract: Within the medical field, the application of radiation-sensitizing chemotherapy in cancer treatment has displayed encouraging potential. However, the administration of chemotherapy at elevated dosages is impeded by harmful side effects. Antibody-drug conjugates (ADCs) have been identified as a groundbreaking and highly innovative class of targeted therapeutics that combine the specificity of monoclonal antibodies with the potent cytotoxic effects of chemotherapy drugs, resulting in the ability to selectively deliver powerful drugs to cancer cells while sparing healthy tissues. Thus, we hypothesized that the antibody-drug conjugate IMMU-132 will enhance the efficacy of radiotherapy (RT). Although the U.S. Food and Drug Administration has approved the ADC, for the

treatment of patients with triple-negative breast cancer, its ability to enhance the sensitivity of cancer cells to radiotherapy has not been assessed.

Presenter(s): Satirtha Saha Protya
School: Beloit College
Session: Poster: P2.2
Title: Computational approach to find difference between CCS values of all L vs D Amino Acid containing peptides and calculating peak resolving power
Advisor(s): Jonathan Sweedler, Analytical Chemistry, University of Illinois Urbana-Champaign
Co-Author(s): Samuel Okyem
Abstract: This poster introduces a computational methodology to discern Collision Cross-Section (CCS) value disparities between peptides composed exclusively of L-amino acids and those featuring a combination of L and D-amino acids (DAACPs). Amino acids naturally occur in enantiomeric pairs, influencing peptide structure profoundly. The enzymatic post-translational modification of all-L-amino acid peptides in animals leads to the creation of a unique class of DAACPs, posing a challenge for accurate detection due to their identical mass to their all-L-amino acid counterparts. Leveraging advanced analytical instruments, we explored differences in CCS values between these peptide variants.
We employed ChimeraX software and the PeptideConstructor Python Library to generate essential Protein Data Bank (PDB) files. PeptideConstructor offers a versatile and efficient solution for creating PDB files for both L and D-amino acid-containing peptides. ChimeraX, an interactive visualization program, provides a comprehensive suite of tools for structure modification and PDB file generation.
Through the manipulation of PDB files, we outlined workflows for creating DAACPs, incorporating Iso-Aspartate residues, implementing C-terminus amidation, and adding hydrogen atoms to the structure. We also emphasized the vital step of converting PDB files to XYZ format using Open Babel. Using the PSA web server, the computational CCS value was calculated. Afterward, we calculated the peak resolving power to identify DAACP peaks in mass spectrometry data. Moreover, we will conduct a comprehensive analysis of CCS values at varying charge states, enabling a detailed comparison between experimentally derived and computationally calculated CCS values. This comparison will yield insights into the presence of DAACPs in mammalian systems.

Presenter(s): Divya Purswani
School: Washington University
Session: Poster: P1.24
Title: Sex-specific programming of the Late Gestational Fetal Heart and Lungs with Prenatal T Excess
Advisor(s): Arpita Vyas, Pediatrics, Washington University in St. Louis
Co-Author(s): Mary Jabari, Vasantha Padmanabhan
Abstract: Cardiovascular disease is the leading cause of death worldwide. Nearly 545 million individuals live with a chronic respiratory condition. Intrauterine growth restriction due to in-utero insult has been associated with cardiopulmonary disease postnatally. Utilizing an ovine model of prenatal exposure to excess testosterone (T), we have reported sex-specific adverse cardiac left ventricle remodeling in early fetal life. This study investigates the sex-specific effect of prenatal T excess on right ventricle (RV) and lungs in late gestation.
Pregnant ewes were injected with 100 mg of testosterone twice weekly from gestational days 30-90. At day 120, tissues were weighed and processed for molecular studies (RT-PCR and Western Blot).
Body weight (BW) was decreased with T-treatment in both sexes (MC 3.38±0.15 vs. MT 2.68±0.14, p=0.003, Cohen's effect size: d=1.29; FC 3.27±0.21 vs. MC 2.72±0.11, p=0.02, d=1.08). RV to BW ratio in both sexes significantly increased with T-excess (MC 0.23±0.01 vs. MT 0.27±0.06, p = 0.0538, d=0.84; FC 0.23± 0.08 vs. FT 0.27±0.03, p = 0.0675, d= 0.72). Glucose transporter (GLUT4) demonstrated a large magnitude reduction in FT RV. In the lungs, FT had a moderate magnitude increase in collagen gene unlike males. Our preliminary data indicates sex-specific adverse programming of fetal cardiopulmonary system.

Presenter(s): Lexus Putt
School: Hope College
Session: Poster: P1.23
Title: Modeling dopaminergic loss in the zebrafish olfactory system
Advisor(s): Erika Calvo-Ochoa, Biology, Hope College
Co-Author(s): Samantha Groenwold, Ted Lockett, Nathaniel Vorhees
Abstract: Zebrafish provide an ideal model to study neurodegenerative diseases and regenerative processes as they present neurogenesis and a high degree of neuroplasticity throughout their lifespan. It has been suggested that dopamine has an important role in regulating olfaction. We aimed to study the structural and functional effects of dopaminergic loss in the olfactory system. We injected 6-hydroxydopamine (6-OHDA) int the ventricular zone of adult zebrafish at the interphase between the olfactory bulbs and the telencephalon to target dopaminergic neurons in the olfactory bulb. Then, we assessed dopaminergic neural loss, markers of inflammation, morphological changes of olfactory axons, and synaptic connections. Olfactory function was evaluated using behavioral assays. 6OHDA injections cause an increase in apoptosis (TUNEL) in the olfactory bulb as well as a significant loss of dopaminergic neurons (TH) at 1- and 3- days post injection (dpi), confirming the success of our approach. Morphological changes in the olfactory glomeruli were discovered by differences in the distribution of the presynaptic marker, SV2. Astroglial activation (GFAP) and cell proliferation (PCNA) were also increased. Furthermore, we found disturbances in olfactory-mediated behavior that suggest olfactory functional alterations. Further studies will explore the relationship between olfactory function, dopaminergic neurons, and the adverse effects of 6-OHDA.

Presenter(s): Rahaf Qarabsa, Blanca Torres Lopez
School: St. Olaf College
Session: Poster: P1.25
Title: Is the Hawaiian acoustic parasitoid fly *Ormia ochracea* evolving its hearing capabilities to better detect rapidly evolving cricket songs?
Advisor(s): Norman Lee, Biology and Neuroscience, St Olaf College
Co-Author(s): Quang Vu, Jimena Dominguez
Abstract: Natural selection imposed by the acoustic parasitoid flies *Ormia ochracea* has resulted in the rapid evolution of cricket-calling songs among some populations of field crickets on the Hawaiian Islands. Some Hawaiian field crickets have lost the ability to produce calling songs, while others have evolved songs that are less intense and with emphasized frequency components that diverge from ancestral calling songs. This is in stark contrast to other populations of host field crickets found in the continental US, where they are not found to be evolving novel cricket songs. In this study, we investigate whether Hawaiian *O. ochracea* uniquely exhibits heightened sensitivity to novel cricket-calling songs compared to continental populations of *O. ochracea*. If Hawaiian *Ormia ochracea*
possesses heightened auditory sensitivity to maintain their ability to locate host crickets with novel calling songs, then Hawaiian *O. ochracea* may exhibit lower auditory thresholds at key sound frequencies emphasized in novel cricket songs compared to continental populations of *O. ochracea*. In behavioral and neurophysiological experiments, we established auditory response thresholds in response to varying calling song carrier frequencies and intensities. Our results indicate little difference in auditory thresholds among three populations of Hawaiian flies (Kauai, Hilo, Oahu) and Floridan *O. ochracea.* These results suggest that the auditory system of *O*. ochracea is not currently evolving its auditory sensitivity to better detect novel cricket songs. Hawaiian *O. ochracea* can still detect novel calling songs, but likely from limited hearing distances.

Presenter(s): Julia Raddue
School: Colorado College
Session: Poster: P3.31
Title: Metabolic Cost of High-Incline Handrail Supported & Unsupported Treadmill Walking

Advisor(s): Anthony Bull, Department of Human Biology and Kinesiology, Colorado College
Co-Author(s): Jacob Moore
Abstract: In fitness centers, people often use treadmill handrails, especially on steep inclines and at higher walking speeds. This study compared the metabolic cost of treadmill walking with and without front handrail support at 12% incline in healthy participants. While previous research focused on populations needing handrail assistance, little data exists for healthy individuals during fast-paced, high-incline workouts. Using a Cosmed CPET metabolic measurement system to determine metabolic cost, 18 healthy participants ages 18-25 completed two randomly ordered incline treadmill trials, each with 5-minute stages at 12% incline. In one trial, participants began with handrail-supported walking at 3.7 km/h (2.3 mph) and 5.63 km/h (3.5 mph), followed by unsupported stages at speed increments of 0.48 km/h (0.3 mph), from 3.7 to 5.63 km/h. In the other trial, the order was reversed, with supported stages occurring after the final unsupported stage. Results indicated a significant reduction (-24.57%, $p<0.001$) in metabolic cost with handrail support at 5.63 km/h and 12% incline. Walking at 5.63 km/h with handrail support was metabolically similar to walking unsupported at about 4.2 km/h (2.6 mph) at 12% incline. These findings suggest refraining from handrail use during treadmill workouts to maximize metabolic and cardiorespiratory fitness benefits.

Presenter(s): Morgan Ramirez
School: University of Chicago
Session: Oral: I.A.2
Title: Infectious Disease Impact on Cognitive Health and Alzheimer's Disease: Implications for Aging in Panama
Advisor(s): Rima McLeod, Biological Sciences Division; Toxoplasmosis Research Institute and Center, University of Chicago
Co-Author(s): Kristen Wroblewski, Alcibiades Villareal, Berta Muñoz, Kira Wiesinger, Giselle Rangel, Gabrielle B. Britton
Abstract: Background: Global aging presents considerable health challenges due to rising age-related dementias and cognitive impairment. Panama's no exception, with 1 in 4 Panamanians projected to be 65 or older by 2050. Studies have linked infections as risk factors for neuroinflammation and neurodegenerative disorders. Here, we evaluate seven pathogens evidencing cognitive decline's purported infectious etiology among Panamanians 60 and older; *Toxoplasma gondii*, *Trypanosoma cruzi,* HSV-I, *Cytomegalovirus*, *Helicobacter pylori*, *Chlamydophila pneumoniae* and *Treponema pallidum*.
Methods: Case-cohort study of 165 participants from Panama Aging Research Initiative Health Disparities cohort compared cognitive impairment among individuals with/without serum IgG/IgM antibodies to above microorganisms. Sociodemographic, clinical, cognitive-functional, psychiatric evaluations were analyzed. Covariables: age, sex, education. Data analyzed using ANOVA and logistic regression in STATA 18.
Findings: Frequency of clinically diagnosed cognitive impairment cases increased with more coinfection pathogens. Younger age($p=0.038$) & education($p=0.002$) were protective against neurodegeneration. Additional clinical infections increased likelihood of neurodegenerative disease diagnosis(OR=1.48 95% CI, $p=0.048$). Most common simultaneous seroreactivity IgG antibody included *Toxoplasma*, HSV, CMV, *Helicobacter*, and *Chlamydophila*. Among simultaneous coinfections, the most frequent individual pathogen was HSV, then *Chlamydophila*, CMV, *Toxoplasma*, and *Helicobacter*. *Chlamydophila* presence in coinfections increased cognitive impairment diagnosis probability($p=0.029$). Individual pathogen association/neurodegeneration diagnosis Odds Ratios(95% CI; $p>0.05$): HSV(OR=2.50), *Chlamydophila*(OR=2.4), *Treponema*(OR=1.6), *Toxoplasma*(OR=1.2), *Heliobacter*(OR=1.2).

Presenter(s): Sean Rogers
School: St. Olaf College
Session: Poster: P2.11

Title: Utilizing Patient DNA Sequencing Data to Evaluate 7 ADPKD Candidate Genes
Advisor(s): Peter C. Harris, Nephrology and Hypertension, Mayo Clinic College of Medicine and Science
Co-Author(s):
Abstract: Autosomal Dominant Polycystic Kidney Disease (ADPKD) is a common genetic disease, characterized by the development of kidney cysts. Most cases are due to pathogenic variants of PKD1 or PKD2 (>95%). Additional disease-causing genes have been identified, while a small proportion of cases remain unresolved. Sequence data was employed to test an association between ADPKD and the candidate genes, IFT172, WDR19, IFT43, NOS3, TRPV2, C5orf42, and SEC62. Variants were excluded if they were common in the normal population, as determined by the gnomAD database. In silico pathogenicity prediction tools and the variant database ClinVar were used to select variants of interest (VOI). Patients with VOIs were examined for variants in other genes that might contribute to the phenotype. Patient phenotypic data, including abdominal imaging and estimated glomerular filtration rate, was collected from electronic health records. Limited evidence was found connecting NOS3, TRPV2, C5orf42, and SEC62 with ADPKD. Patients with WDR19 and IFT43 VOIs did not display a consistent phenotype, while IFT172 patients displayed milder phenotypes featuring small kidney cysts. This indicates the greatest likelihood of a causative role in ADPKD is for IFT172, however, further populations need to be screened to determine if it is a monogenic cause of kidney cysts.

Presenter(s): Blake Rose
School: Gustavus Adolphus College
Session: Poster: P1.5
Title: The role of SLCO3A1 in macrophage efferocytosis
Advisor(s): Wai Kee Eddie Ip, Department of Immunology and Division of Gastroenterology and Hepatology, Mayo Clinic
Co-Author(s): Tiffany Cassmann, Weiwei Shi
Abstract: Macrophages are an important part of the innate immune system, responsible for phagocytosis as well as pro- and anti-inflammatory signaling. One target of phagocytosis is apoptotic cells (ACs) in a process known as efferocytosis. Efferocytosis is known to contribute to anti-inflammatory signaling. Ineffective efferocytosis can lead to inflammation as ACs enter secondary necrosis. Macrophages find and identify dying cells in two steps: the first is extracellular signals that guide the macrophage to the cell; the second is surface signal recognition by the macrophage to initiate engulfment of the cell. Breakdown of ingested ACs within the phagosome upregulates expression of genes associated with efferocytosis and anti-inflammatory polarization. Efferocytosis and immune tolerance are important in the gut, where there is constant cell turnover and the immune system must tolerate the gut microbiome. AC metabolites have been shown to promote efferocytosis and mediate immune tolerance in macrophages. The expression of metabolic transporters in macrophages is therefore important for sensing AC-derived signals. One transporter found to be highly expressed in gut macrophages is SLCO3A1, a member of a transporter family responsible for transporting large hydrophobic and amphiphilic molecules, including cholesterol. It was therefore hypothesized that SLCO3A1 is required for regulating efferocytosis and immune tolerance.

Presenter(s): Sofia Rosenberger
School: Hope College
Session: Poster: P2.30
Title: Ubiquitination of xCT: impacts on the protein's stability, turnover rate, and localization
Advisor(s): Leah Chase, Department of Biology, Chemistry, Neuroscience, Hope College
Co-Author(s):
Abstract: System x_c^- imports cystine and exports glutamate. Its presence on the plasma membrane has been shown to increase directly with oxidative insults. Ubiquitin, a small protein, is directly involved in the trafficking and degradation of numerous proteins within cells and has been shown to bind to System x_c^-. Moreover, upon oxidative insult, protein ubiquitination increases. However, it is not understood how ubiquitination of the transporter impacts its activity. Therefore, the objective of this

project is to directly assess how ubiquitination affects the protein's stability, turnover rate, and localization in the context of oxidative stress. We expressed System x_c^- in COS7 cells transfected with increasing levels of ubiquitin and observed a decrease in xCT expression and increase in xCT turnover rate. However, we also observed an increase in membrane localization. Ultimately, this work will allow us to better understand the mechanisms by which System x_c^- activity is regulated under oxidative stress.

Presenter(s): Moura Saad
School: Macalester College
Session: Poster: P1.19
Title: Effects of demographics and lifestyle choices on spatial navigation ability in the aging brain
Advisor(s): Michael Borich, Department of Rehabilitation Medicine, Emory University
Co-Author(s): Yasmine Bassil
Abstract: Advancing age is reliably associated with deficits in spatial navigation ability, an early indicator of aging-related cognitive decline and neurodegenerative pathologies. To characterize aging-related navigational differences between younger and older adults, we previously developed a naturalistic, city-like, virtual reality maze called "NavCity." In this study, we sought to explore the influence of demographics and lifestyle, specifically of gender, exercise, and sleep quality, on NavCity performance. We hypothesized that, regardless of age, men would have improved navigational ability compared to women, and lifestyles with increased exercise and better sleep quality would correlate with better navigation ability.
Younger and older adults self-reported gender identity and exercise type and frequency, and completed the Pittsburgh Sleep Quality Index to measure sleep quality. Participants completed 3 repetitions of finding 8 different buildings in NavCity. Navigational ability was quantified as the mean distance traveled across 3 blocks. Training effects were quantified as the change in distance traveled (block 3-1). Unpaired t-tests, two-way ANOVAs, and Spearman correlations were conducted. Younger adults showed better navigation ability, but similar training effects compared to older adults. Gender, exercise, and sleep quality were not related to navigation ability, suggesting age as the primary factor associated with spatial navigation ability.

Presenter(s): Ellianna Sandman
School: Hope College
Session: Poster: P2.19
Title: Chemical defenses in the seeds of pioneer plants
Advisor(s): Elizabeth Sanford, K. Greg Murray, Chemistry, Biology, Hope College
Co-Author(s): Nicholas T. Weigle, Eleda V. Plouch
Abstract: The seeds of the pioneer plant *Phytolacca americanin* are known for their prolonged survivability in the seed bank until there is a transition from low light to high light intensity that triggers their germination. The persistence of these seeds suggests that they possess forms of chemical defense against microbial predators. This research seeks to identify potential compounds responsible for chemical defense against fungi. Methanolic extraction is used to isolate compounds of interest from the seed. Preparative HPLC is utilized to separate the components. 1H-NMR and LC/MS are used in tandem to determine the structure of the unknown components. Regioisomers Americanin A and Isoamericanin have been separated and identified from the seed mixture utilizing these methods. The anti-fungal properties of these and additional isolated compounds will be analyzed using bioassays. The results from this study will then be extended to identify the antifungal components of *P. americana*'s Costa Rican counterpart, *Phytolacca rivinoides*, to understand the role of pioneer plants in the rainforest ecosystem.

Presenter(s): Ryan Saladin
School: Lawrence University
Session: Poster: P2.24
Title: Musical improvisation decreases stress and music performance anxiety in classically trained

vocalists
Advisor(s): Elizabeth Becker, Neuroscience, Psychology, Lawrence University
Co-Author(s): Madisyn Eyman, Dana Abbo, Eleanor Rudoff, Karen Leigh-Post, Andrew Sage
Abstract: Up to 60% of performing musicians report experiencing music performance anxiety (MPA), a state of intense worry surrounding performance outcomes. Flow, a state of heightened attention considered optimal for performance, is negatively correlated with MPA. Musical improvisation may induce flow and therefore may help decrease MPA and stress and enhance performance quality outcomes. In the present study, we examined the effects of a musical improvisation intervention on flow, state anxiety, and performance quality in a mock audition among classically trained conservatory voice students. Participants performed in two mock auditions, one before and another after the intervention. At each professionally adjudicated audition, participants answered digital adaptations of the State-Trait Anxiety Inventory-State (STAI-S) and Occupational Flow State Scale, measuring state anxiety in the context of their performance and flow respectively, and provided saliva samples to be assayed for Cortisol and Alpha-Amylase. At baseline and again following the completion of the study, participants answered the Kenny Music Performance Anxiety Inventory (K-MPAI). Preliminary analyses show a significant decrease in average STAI-S scores and Cortisol levels across auditions, suggesting an attenuation of anxiety and stress levels surrounding performance. We suggest further research into the potential for musical improvisation to reduce MPA.

Presenter(s): Jessica Schultz
School: Carthage College
Session: Poster: P1.1
Title: Combating antibiotic resistance: The antimicrobial properties of L-leucine surfactants
Advisor(s): Deborah Tobiason, Biology, Carthage College
Co-Author(s):
Abstract: Since their commercialization began in the 1940s, antibiotics have been overused and inappropriately prescribed, leading to increased antibiotic resistance cases seen now in thousands of bacterial strains. Without new treatments, by 2050, an estimated 10 million people will perish annually due to antibiotic resistant bacterial infections. One of the ways to combat the rise in antibiotic resistant pathogens occurring worldwide is to develop new antimicrobials, such as amino acid-based surfactants, to eliminate bacterial populations. Surfactants are amphiphilic molecules that have hydrophobic and hydrophilic components that can be chemically modified to target bacteria and inhibit growth. A novel L-leucine surfactant has been synthesized at Carthage College and tested for potential antimicrobial activity. The L-leucine surfactant is effective in inhibiting bacterial growth in both Gram-negative and Gram-positive bacteria, such as *Escherichia coli*, *Acinetobacter baylyi*, *Staphylococcus aureus*, and *Enterococcus faecalis*, which are non-pathogenic relatives of antibiotic-resistant bacteria. Antimicrobial activity was measured using a standard serial dilution assay to determine the L-leucine surfactant's minimum inhibitory concentration (MIC) needed to inhibit bacterial growth. Analysis of the surfactant's activity will help determine its future potential use as an antimicrobial agent.

Presenter(s): Zyva Sheikh
School: University of Chicago
Session: Poster: P2.32
Title: Spheroid Viability Prediction with Deep Learning: Automating Quality Control in Tissue Engineering Applications
Advisor(s): Narutoshi Hibino, University of Chicago
Co-Author(s):
Abstract: Spheroids, which are three-dimensional aggregates of cells, have been essential for biomaterial-free tissue engineering, as they are often used as the building blocks for 3D bio-printed tissue patches. An accurate assessment of spheroid viability is essential to ensure the success of these patches. Still, current viability assay methods are time-consuming, necessitate significant manual labor, require specialized training, and are subject to human bias. In this study, I propose the development of

a deep learning model to predict the viability of spheroids, addressing the challenges associated with manual assessment methods.
The proposed deep learning model leverages convolutional neural networks (CNNs) to analyze high-resolution images of spheroids obtained through microscopy. A comprehensive dataset comprised of a range of mMSC spheroid sizes with corresponding viability percentages is used for training and validation. The model is trained to automatically detect and classify the spheroids into a specific range of viabilities based on morphological and structural features, such as cell density, size, and shape. This deep learning model provides a reliable and efficient tool for spheroid viability prediction.

Presenter(s): Xenia Sofianou
School: Macalester College
Session: Poster: P3.15
Title: Lymph Node Stromal Cell Presentation of Self Antigen With or Without Immune Experience
Advisor(s): Vaiva Vezys, Center for Immunology, Department of Microbiology and Immunology, University of Minnesota
Co-Author(s): Meagan Rollins
Abstract: The hygiene hypothesis posits an inverse correlation between microbial exposure and development of autoimmunity, yet the underlying mechanisms are poorly understood. This poster explores the impact of infections and other types of immune experience on self-antigen presentation by Lymph Node Stromal Cells (LNSC) at T cell priming sites.
Preliminary data indicate that prior induction of T cell immunity diminishes CD8+ T cells' ability to mount future harmful responses against self-antigens.
We utilize the iFABP-ova mouse model, producing ovalbumin (OVA) in mature small intestinal epithelial cells. Our results reveal increased LNSC cell counts in infected mice. Using flow cytometry, we will phenotype LNSC for PD-L1, PD-L2, CD80/86, MHC I, and other markers. This will show if phenotypic changes in these cells, in combination with numerical changes already observed are impacting self-specific CD8 T cell priming.
We intend to co-culture LNSC with naïve OTI-T cells which recognize the OVA peptide and are labeled with CTV fluorescent dye. We anticipate elevated antigen presentation by infected mice's LNSC, which will correspond to increased T cell proliferation peaks on the flow cytometry histograms. This heightened self-antigen levels will ultimately skew differentiation to less pathogenic T cells, diminishing their capacity to initiate autoimmune responses.

Presenter(s): Ella Sontowski
School: Gustavus Adolphus College
Session: Oral: II.E.3
Title: Investigating temperature tolerances on diploid versus polyploid germination: implications for cytogeographic patterns of *Solidago gigantea*
Advisor(s): Angela Walczyk, Biology, Gustavus Adolphus Colleg**e**
Co-Author(s):
Abstract: Polyploidy (whole genome duplication) is a large-scale genomic mutation that can alter plant morphology and physiology, potentially changing abiotic and biotic stress tolerances between diploids and polyploids. Ploidy-variants of a species can separate geographically (cytogeographic separation), but the causes are not well-known. *Solidago gigantea* (giant goldenrod), is a North American perennial exhibiting cytogeographic separation: diploids occupy the south-eastern USA, tetraploids the Great Lakes, and hexaploids the Great Plains. Since this correlates with spring climate patterns, we hypothesized that germination success of *S. gigantea* cytotypes differs depending upon temperature.
We germinated diploid, tetraploid, and hexaploid *S. gigantea* in three temperatures (cold=12°C, ambient=22°C, hot=32°C) and quantified germination and seedling metrics.
Regardless of temperature, hexaploids had 1) the fastest germination, 2) the greatest daily germination percentage, and 3) the largest seedlings. Diploids had the greatest final germination percentage, but only under hot treatments.

Our results suggest that *S. gigantea* cytotypes possess local adaptations strategies. The faster germination rates of hexaploids may be advantageous in the short growing seasons of the Great Plains, while diploid germination success in hot temperatures could be an adaptation to the south-eastern USA's climate. Future studies would benefit by evaluating potential cytotype-differences in adult *S. gigantea.*

Presenter(s): Emma Stock
School: Gustavus Adolphus College
Session: Poster: P2.31
Title: ISGylation disrupts neuronal proteostasis & methods for quantifying miRNAs isolated from neuronal extracellular vesicles
Advisor(s): Charles L Howe, Department of Neurology, Mayo Clinic
Co-Author(s): Rioghna Pittock, Sara Muhammad, Benjamin D S Clarkson
Abstract: ISG15 is a ubiquitin-like protein that functions in a cell's innate immune response. The conjugation of this system has been termed ISGylation and involves a cascade of three enzymes that are linked to biological functions including proteasome and mitochondrial degradation. When the ISG pathway is expressed, mitophagy is deregulated. This pattern holds true in ALS and other neurodegenerative pathways. This was studied using adeno-associated virus (AAV) vectors. They are a common mode of gene therapy and are able to show regions of mitochondrial turnover. When cells are tagged with GFP or mCherry fluorescent proteins, the level of degradation can be viewed via the fluorescence overlay. The leftover signals show where mitochondrial degradation is occurring, which in turn shows the effectiveness of the ISG pathway.
In addition, we studied and developed methods in which miRNAs can be isolated from extracellular vesicles. miRNAs are about 20 base pairs in length and function in regulation of gene expression. Some, once engineered, are hypothesized to have neuroregenerative effects. To test this we examined the product of cellular supernatant, isolating EVs and miRNAs for further quantification and analysis. The application of these miRNAs involves lentivector transduction and may lead to novel Multiple Sclerosis treatments.

Presenter(s): Goichi Suganuma
School: Knox College
Session: Oral: I.A.3
Title: ADHD, boredom, impulsivity, and time perception
Advisor(s): Heather Hoffmann, Psychology, Knox College
Co-Author(s):
Abstract: Decision-making and interpersonal interactions are significantly impacted by time perception, a fundamental cognitive process. Deficits in time perception have been associated with attention-deficit/hyperactivity disorder (ADHD), boredom proneness, and impulsivity. This study explored the complex interplay between those variables and time perception. In this study, 101 participants from a diverse population took part in a novel online survey design. They filled out the Adult ADHD Self-Report Scale-v.1.1, the 8-item Boredom Proneness Scale-Short Form, and the Barratt Impulsiveness Scale-Brief before being asked to estimate how long they spent answering them. The study found a positive correlation between ADHD symptoms, boredom proneness, and impulsivity, which is consistent with previous studies. Notably, a statistically significant positive correlation between the time estimation discrepancy and the hyperactive motor symptoms of ADHD was found, suggesting that people with hyperactive motor symptoms tend to overestimate the time spent on the task. Other ADHD symptom subtypes weren't shown to have a similar relationship. This research implies that altered time perception may be a basic symptom of ADHD, presumably due to a faster internal clock, adding a new perspective to the existing attentional gate model. This study illuminates a previously unrecognized facet of ADHD symptomatology and inspires further research into its implications.

Presenter(s): Rajiv Swarup

School: Washington University
Session: Oral: I.B.4
Title: Choroid Plexus Cell Junction Breakdown in Post-Hemmorhagic Hydrocephalus
Advisor(s): David D. Limbrick, Neurosurgery, Virginia Commonwealth University
Co-Author(s): Maria Garcia-Bonilla, Owen W. Limbrick, Jayne Crouthamel, Jason Moore, James P. McAllister
Abstract: Introduction: Posthemorrhagic hydrocephalus (PHH) is a condition characterized by ventricular enlargement usually following intraventricular hemorrhage (IVH). The pathophysiology of PHH following IVH in preterm infants is complex, multidimensional, and poorly understood. We hypothesized that neuroinflammation and alterations in choroid plexus (ChP) junctional biology are associated with PHH.
Methods: At 3 days post-natal (P3), mice received bilateral intraventricular injections of 5 ul lysed blood or saline to induce PHH or reflect sham controls, respectively. At P6 and P8, 5 behavioral tests were conducted. At P10, MRI neuroimaging was performed, and mice were euthanized. Brains were fixed, paraffin-embedded, and immunoassayed. Evans ratio (ER) calculations were performed on MRI scans to quantify ventriculomegaly.
Results: After 7 days post-induction, ventriculomegaly was confirmed in PHH cases (0.45 ± 0.06) compared to sham (0.24 ± 0.06) controls; preliminary data from behavior analyses suggest no conclusive differences. A significant decrease in ZO-1 was detected in ChP epithelial cells in PHH, in addition to increased GFAP+ astrocytes and iba1+ microglia/macrophages in ChP stroma.
Conclusion: These results demonstrate, for the first time, significant alterations in ChP junctional biology, specifically tight junction disruption. These results open the possibility of exploring novel treatment approaches to prevent PHH pathogenesis and development.

Presenter(s): Sean Teng
School: Washington University
Session: Oral: II.F.3
Title: Crystal Structure of Unknown Mycolic Acid SAM methyltransferase UmaA from *M. tuberculosis*
Advisor(s): Craig L. Smith, Biology, Washington University in St. Louis
Co-Author(s): Jie Wang, C. D. Sroge, Jan Abendroth, Donald D. Lorimer, Peter S. Horanyi, Thomas Edwards, Peter J. Myler
Abstract: *Mycobacterium tuberculosis* is a Gram-positive bacillus that causes tuberculosis, which is a leading cause of mortality worldwide. This disease is a growing health threat due to the occurrence of extensively drug-resistant tuberculosis and there is a need to identify new drug targets and develop novel drugs. A promising target is a family of S-adenosylmethionine-methyltransferases (SAM-MTases) that modify mycolic acids, important cell envelope lipids. UmaA is the least understood in this family of enzymes. We conducted an in-depth study of the X-ray crystallography structure of UmaA (PDB: 7lxi). UmaA consists of a SAM binding domain and a substrate binding domain, which is composed of a Rossmann-like fold and a helical lid, respectively. The structure is complexed with SAH, NO3-, and PEG-6. The binding interactions for these ligands were examined using PyMOL. A structural alignment conducted using DALI revealed that the SAM-binding region is highly conserved among different species, while the auxiliary substrate-binding domain is highly variable. UmaA contains a region that binds CO32- (mimicked by NO3-), which is characteristic of all known mycolic acid cyclopropane synthases. Further investigation revealed that the N-terminus is flexible and that SADAE may act as a bifunctional inhibitor for UmaA.

Presenter(s): Chloe Traeder
School: St Olaf College
Session: Poster: P3.27
Title: Investigating the role of an sRNA in the bacterium *Caulobacter crescentus*
Advisor(s): Lisa Bowers, Biology, St. Olaf College
Co-Author(s):

Abstract: *Caulobacter crescentus* is a non-pathogenic gram negative bacterium that is commonly found in nutrient-poor freshwater environments. Caulobacter cells have tightly regulated transporters on their cell surface that help take in scarce nutrients through the outer membrane. A previous study identified an operon responsible for sucrose uptake and catabolism. Within this operon, there is predicted to be a gene, R0135, that encodes a small RNA. Small RNAs are often responsible for regulating expression of neighboring genes but the function of this predicted small RNA is unknown. This study attempts to determine the function of R0135 through measuring its expression in Caulobacter grown in environments containing different nutrients, in order to investigate its hypothesized role in the use of sucrose by the cell. This process involved purification of RNA harvested from wild-type Caulobacter, and RTqPCR in order to measure the expression of the R0135 gene.

Presenter(s): Ashley Trainor
School: Hope College
Session: Poster: P3.20
Title: Social and Emotional Knowledge in Patient Populations
Advisor(s): Nathaniel Klooster, Psychology, Hope College
Co-Author(s): Olivia Onderdonk
Abstract: The hippocampus has been found to play a role in general semantic knowledge but it is unclear if it plays a role in social and emotional semantics. This study seeks to evaluate the role of the hippocampus in social and emotional semantics through the study of patients with hippocampal amnesia. Although previous literature has shown that individuals who have damage to their hippocampus show deficits in neutral words, we expect that the hippocampal amnesic group should show the same social-emotional knowledge as the brain-damaged and healthy comparison groups. Participants from the hippocampal amnesic (n=5), ventromedial prefrontal cortex (vmPFC) damaged (n=5), and healthy control (NC) (n=16) groups completed feature and sense-listing tasks. Within these tasks, responses for social and emotional words were noted. For the senses task, the amnesic group produced significantly fewer features compared to the vmPFC and NC groups. For the senses task, the amnesic group produced significantly fewer senses compared to the vmPFC and NC groups. These findings suggest that patients with hippocampal amnesia show deficits in social and emotional knowledge. Further, this may indicate that the hippocampus plays a role in social and emotional knowledge and memory.

Presenter(s): Sumana Turimella
School: University of Chicago
Session: Poster: P3.26
Title: Evolution of Kinetic Proofreading in DNA Polymerases
Advisor(s): Arvind Murugan
Co-Author(s):
Abstract: DNA replication faithfully transmits genetic information across generations. Our study reevaluates the classical kinetic proofreading paradigm, suggesting that increased DNA replication speed may enhance, not compromise, fidelity. Using a novel cytoplasmic virus-based system in yeast, we will controllably select on speed and accuracy across a barcoded library of DNA polymerase variants. Mutation rates will be assessed via a novel high-throughput Luria-Delbruck assay. This investigation could redefine our understanding of DNA replication's speed-accuracy relationship, hypothesizing that faster replication might actually reduce mutation rates, which bolsters genomic stability.

Presenter(s): Emma Uder
School: Washington University
Session: Poster: P1.30
Title: Tyson Research Center Mosquito Diversity: Creating a Collection
Advisor(s): Kim Medley, Katie Westby, Biology, Washington University

Co-Author(s):
Abstract: Roughly 3500 species of mosquitoes exist worldwide. Fifty of those species are estimated to be found in Missouri. At Tyson Research Center, the total number of mosquito species present is still unknown. From June-August, several previously unrecorded species were found on-site through collection methods. Methods included pulling larvae from sources in the field and rearing to adulthood in the lab, capturing adults with light traps, and capturing individual adults using a manual aspirator. Captured mosquitoes were then identified and preserved as adults. This is part of an ongoing project to create a collection of mosquitoes. The collection contains ten species of mosquito found at Tyson Research Center, although there are several more known species to be collected. The collection consists of pinned adult mosquitoes of every recorded species on the property, and both sexes when possible. The current record of mosquitoes includes ten species. As it continues to grow, the collection will be made more accessible with detailed photographs and descriptions. This project is meant to create a teaching tool for researchers and act as a bridge into mosquito diversity studies. The ability to identify mosquitoes is important for the ability to study these creatures now and in the future.

Presenter(s): Trisha Vinay
School: University of Chicago
Session: Poster: P2.20
Title: Investigation of the roles of MAL and MAL2 proteins in tumor immune evasion
Advisor(s): Yuxuan Miao, Ben May Department of Cancer Research, University of Chicago
Co-Author(s): Matthew Ji
Abstract: Recent studies show that a subset of TGF-β-responding tumor-initiating cells (TICs) is the main driver of immune evasion and tumor survival in squamous cell carcinoma (SCC). However, the mechanism via which these TGF-β-responding TICs cause immune evasion is still unclear. Here, I will show how SOX2, a commonly overexpressed gene in cancer, functions in TICs to suppress the immune response by upregulating MAL and MAL2. These genes encode cellular trafficking proteins that transport membrane and secretory proteins to and from the cell surface. Through this trafficking, I will show how MAL and MAL2 are able to promote tumor survival via the suppression of cytotoxic CD8+ T cells. Given that TICs have intact tumor-associated antigen presentation, the mechanism of suppression is more complex than the removal or blockage of MHC I. Instead, it suggests that MAL and MAL2 may be suppressing CD8 T cells through a more direct interaction via the trafficking of an immune-modulating ligand. My project aims to determine the specific role of MAL and MAL2 in conferring this immune resistance, identify the ligand(s) being trafficked, and the mechanism by which this drives immune evasion with the hopes of finding a potential target to improve cancer immunotherapy efficacy.

Presenter(s): Allan Wang
School: Washington University
Session: Poster: P2.18
Title: Uncovering enhanced Hsp104 NBD1 variants with improved substrate specificity
Advisor(s): Meredith Jackrel, Chemistry, Washington University in St. Louis
Co-Author(s): Karlie Miller
Abstract: Hsp104 is a hexameric AAA+ protein that disaggregates proteins trapped in low energetic configurations, such as amyloid fibrils and amorphous aggregates. While highly conserved in bacteria, fungi, and plants, Hsp104 is absent from metazoa. We aim to redirect this disaggregase activity towards TDP-43, FUS, and a-Synuclein, as they are hallmarks of neurodegenerative disorders in humans (ALS and Parkinson's Disease, respectively). We set out to engineer improved Hsp104 variants via mutations in the first nucleotide-binding domain (NBD1). With a library of mutations of all possible natural amino acids along NBD1, we utilized next-generation sequencing (NGS) to efficiently screen and identify variants that were active against our target substrates while having low off-target effects.
Hsp104:G188C and Hsp104:G188T are a pair of such hits. Initial protein structure analysis suggests changing glycine to a polar sidechain near the ATP binding pocket may modulate the binding affinity of

Hsp104 for ATP. To further test this hypothesis, these variants are being purified and will be assessed with ATPase assays and a luciferase reactivation assay. We suggest that mutating NBD1 may give rise to finely tuned, substrate-specific Hsp104 variants that may become a future remedy for neurodegenerative diseases.

Presenter(s): Tianlong Wang, Takeshi Matsuda
School: Beloit College
Session: Poster: P3.2
Title: Enhancing Heart Disease Prediction by Exploring Federated Learning in Machine Learning
Advisor(s): Eyad Haj Said, Mathematic and Computer Science, Beloit College
Co-Author(s):
Abstract: Heart disease remains a leading global cause of mortality, prompting the exploration of innovative approaches for diagnosis and risk assessment. Traditional methods such as Electrocardiogram and angiography are often costly, invasive, and reliant on specialized expertise. In contrast, non-invasive techniques like machine learning offer promising avenues, with Federated Learning (FL) emerging as a particularly compelling option. Our deep learning models, including Convolutional Neural Networks and Recurrent Neural Networks, requiring only clinical information from patients, offer a cost-effective and easily deployable solution. Our study focuses on the application of FL to the UCI Heart Disease dataset, which contains 920 records from Cleveland, Virginia, Hungary, and Switzerland, aiming to demonstrate its robustness and effectiveness. Importantly, the FL aspect of the models maintains data integrity and confidentiality by allowing training on decentralized data sources without data sharing. Our FL architecture achieves remarkable results, ranging from 79% to 88%, surpassing the baseline models that scored between 77% and 85%, all while preserving data privacy. By showcasing the suitability of FL for this purpose, our tool can enhance medical diagnosis processes or serve as an independent system for public access, simplifying heart disease prevention and prediction while reducing costs and the need for specialized expertise.

Presenter(s): Wendy Wang
School: Washington University
Session: Poster: P2.10
Title: Strategies for Including Individuals with Disabilities in Clinical Trials
Advisor(s): Amanda Price, Parisa Parsafar, NIH Office of Health Equity
Co-Author(s):
Abstract: The Americans with Disabilities Act describes a disability as any mental health or physical condition that can cause impairment when performing major life activities. Disabilities often co-occur with chronic illnesses. People with disabilities are regularly excluded from research that typically focuses on a single specific condition. Exclusion poses a challenge to advancing care - it reduces scientific attention to people with disabilities, which contributes to a lack of data about this population, limiting their prioritization in health research. The risk associated with excluding individuals with disabilities from participation in clinical trials perpetuates health disparities by limiting the generalizability of findings and having clinical trial results that do not accurately reflect the efficacy of treatment for populations with diverse health care needs. For this project, a literature, policy, and resources review was conducted to identify strategies for improving the inclusion of persons with disabilities in clinical trials. Recommendations highlight methods for improving inclusivity and proposing new solutions with an emphasis on increasing the communication of resources for individuals with disabilities to access clinical trials. The discussion focuses on how implementing these changes can further the mission of improving healthcare equity and enhancing the safety and effectiveness of treatments for everyone.

Presenter(s): Aidan Wells
School: Colorado College
Session: Poster: P1.7
Title: RNA splicing factor, MBL-1, is required for sensory neuron morphogenesis in *C. elegans*

Advisor(s): Darrell Killian, Department of Molecular Biology, Colorado College
Co-Author(s): Meena Kim
Abstract: Neuron morphology is important for neuronal function. Therefore it is important to identify genes that regulate neuron morphology. Loss of *C. elegans* mbl-1 produces a nervous system phenotype characterized by defects in dendrite patterning and synapse formation. We found that mbl-1 mutants exhibit reduced terminal branching of dendrites in the PVD sensory neuron, with terminal branching becoming progressively more sparse with increasing distance from the cell body. Loss of mbl-1 function does not affect the stereotyped patterning of PVD muscle-skin interface innervation and no defects in the macrostructure of the body wall muscle were evident in the mutant. Work from other labs has shown that mbl-1 mutants fail to properly transport axonal and dendritic proteins into their respective compartments in some types of neurons. We are testing this hypothesis in PVD neurons using fluorescently-labeled axon/dendrite markers to observe where they localize. mbl-1 encodes an RNA-binding protein that is predicted to regulate alternative RNA splicing. To learn more about the molecular function of MBL-1 protein, we biochemically isolated RNAs bound by MBL-1. The forthcoming sequencing analysis of these bound RNAs may suggest mechanisms by which mbl-1 regulates neuron morphology.

Presenter(s): Megan Woelkers
School: University of Chicago
Session: Oral: II.F.5
Title: SaO2/FiO2 ratio as a marker of acute chest syndrome severity in sickle cell disease
Advisor(s): Gabrielle Lapping-Carr, Section of Hematology, Oncology and Stem Cell Transplant in the Department of Pediatrics, the University of Chicago
Co-Author(s): Austin Wesevich
Abstract: Introduction
Acute chest syndrome (ACS) is a potential deadly complication of sickle cell disease (SCD) diagnosed based on chest imaging and symptoms.
Methods
This retrospective cohort study of adult ACS admissions at the University of Chicago in 2017-21 examined oxygenation status, specifically the ratio of arterial oxygen saturation (SaO2), estimated by pulse oximetry (SpO2), to fraction of inspired oxygen (FiO2). We dichotomized the lowest SaO2/FiO2 ratio per admission to severe (< 243) versus mild/moderate (>243). Chi-square, Fisher's exact, and Wilcoxon rank-sum tests assessed associations between severity and clinical outcomes.
Results
Of 231 ACS admissions, 51 (22%) were severe. Severe ACS was associated with higher rates of blood transfusion (96% vs 77%, p=0.002), red cell exchange transfusion (47% vs 4%, p<0.001), and ICU transfers (76% vs 7%, p<0.001), and longer length of stay (11.2 vs 8.8 days, p=0.0002). Mortality rate (6% vs 1%, p=0.07) trended towards differing based on ACS severity. Readmission rate was 23% in both groups.
Conclusions
SaO2/FiO2 was associated with important admission-specific clinical outcomes and could be a useful bedside marker for pending ICU transfer or even death. Future study could evaluate SaO2/FiO2 ratio cutoffs to guide earlier red cell exchanges.

Presenter(s): Andrew Wong
School: Washington University
Session: Poster: P2.33
Title: A Novel Droplet Digital PCR (DDPCR) Assay for the Detection of Tumor Cells and Predicting Metastasis in Breast Cancer Patients
Advisor(s): Mark Watson, Department of Pathology and Immunology, Washington University in St. Louis
Co-Author(s): Jackie Snider, Rebecca Aft
Abstract: Metastasis is the most common cause of mortality in breast cancer patients. A key step of

the metastatic process is the dispersal of disseminated tumor cells (DTCs) and circulating tumor cells (CTCs) into the bone marrow and bloodstream of patients, respectively. The presence of these cells is a known predictor of early disease relapse, although they can remain dormant for years before reemerging. Previous work by our group identified an 8-gene expression panel (EPCAM, PDGFRB, SNAI2, SMO, SRC, CAV1, PTCH1, and ERBB2) that, when detected in the bone marrow of triple-negative breast cancer (TNBC) patients, predicts time to relapse. To improve the sensitivity, specificity, and precision of this assay and to validate initial findings, we have adopted the gene panel to a novel droplet-digital PCR (ddPCR) platform. With results obtained on this platform, we identified several distinct gene expression profiles using a hierarchical clustering model, and correlated expression levels with likelihood of and time to recurrence.

Presenter(s): Shelly Xu
School: Washington University
Session: Poster: P2.22
Title: Examining differential mitochondrial characteristics among retinal ganglion cell types
Advisor(s): Philip Williams, John F. Hardesty, MD, Department of Ophthalmology & Visual Sciences, Washington University School of Medicine
Co-Author(s):
Abstract: Retinal ganglion cells (RGCs) are a diverse group of neurons with varied morphologies and firing patterns, with certain types being more resilient to degeneration than others. RGCs require considerable amounts of energy to maintain electrical gradients and conduct neuronal signals through unmyelinated sections of their axons. Because of the energy-demanding nature of RGCs, major ATP-producing pathways like the electron transport chain (ETC) of the mitochondria are critical to maintaining healthy RGCs. We are interested in examining how vulnerable and resilient RGC types utilize mitochondrial components of the ETC and determining if/how metabolic strategies differ across RGC types. We hypothesize that RGC types have varying levels of mitochondria density and expression of integral ETC components. To explore cell-to-cell metabolic heterogeneity among RGCs, we stain retinal tissues with antibodies against representative proteins of ETC complexes I-V, quantify mitochondria density among RGCs costained with type markers, and analyze mitochondrial morphology between RGC types. Preliminary data show that there is variability of ETC complex expression among RGCs, which may indicate differences across RGC types. Results from this study can elucidate catabolic strategies and mitochondrial traits that underlie resilient RGC types and reveal metabolic targets for interventions against neurodegenerative conditions, such as glaucoma.

Presenter(s): Jizhi Yan
School: University of Chicago
Session: Poster: P3.19
Title: Glutamine Metabolism is Altered in Myeloproliferative Neoplasms and Represents a Potential Novel Therapeutic Target
Advisor(s): Shannon E. Elf, The Ben May Department for Cancer Research, University of Chicago
Co-Author(s): Chad Coen, Hunter Blaylock, Katarzyna Zawieracz, Nicole S. Arellano, Mirielle Nauman, Daniele Vanni, Caner Saygin, Silvia Catricala, Ilaria Carola Casetti, Oscar Borsani, Elisa Rumi, Daniela Pietra
Abstract: Cancer cells exhibit metabolic reprogramming to facilitate growth and proliferation. Previous studies in various cancers show cancer cells rely significantly on elevated glutamine metabolism for macromolecule biosynthesis and redox homeostasis. However, very few studies have investigated the role of glutamine metabolism in myeloproliferative neoplasms (MPNs). Glutamine catabolism begins via glutaminase (GLS1) catalyzing the rate limiting conversion of glutamine into glutamate. Many studies in different cancers have found GLS1 to be a dependency and can be therapeutically targeted. To more comprehensively decipher the role of glutamine metabolism in MPNs, we performed RNA-sequencing on MPN patient samples and found that genes involved in glutamine metabolism are significantly altered. Our data demonstrated that GLS1 levels are not significantly up-regulated and that GLS1 is not

sensitive to pharmacological inhibition. Rather, we characterized another key enzyme in glutamine metabolism, glutamine synthetase (GS), as a dependency. GS converts glutamate into glutamine and serves to satisfy the metabolic demand for increased glutamine. We found that GS mRNA is significantly up-regulated and inhibition of GS decreases cell proliferation. In summary, we have demonstrated that GLS1 may not be an effective therapeutic target for MPNs, and instead characterize GS as a novel dependency and potential point of therapeutic intervention.

Presenter(s): Amanda Yang
School: Washington University
Session: Poster: P3.1
Title: Cell-Cell Communication Analysis Using Single-Cell RNA Sequencing of Wildtype and CCR7 Knockout Human Trophoblast Organoids
Advisor(s): Sabine Dietmann, Developmental Biology, Washington University in St. Louis
Co-Author(s): Eun-Ja Yoon, Lilianna Solnica-Krezel
Abstract: The human placenta is an essential organ that delivers oxygen and nutrients to the fetus. Placental abnormalities in the first trimester can lead to pregnancy complications such as preeclampsia, miscarriage, and fetal growth restriction. Human trophoblast stem-cells (hTSCs) have been developed to self-organize into 3D trophoblast organoids that can successfully model first-trimester placenta in-vitro. These stem-cell derived trophoblast organoids (SC-TOs) contain cytotrophoblasts (CTBs) that can proliferate into syncytiotrophoblasts (STBs) or extravillous trophoblasts (EVTs). Cell-cell communication is essential for differentiation in placental development.
We investigate the influence of C-C chemokine receptor type 7 (CCR7), a G-protein coupled receptor, on WNT and VEGF signaling pathways. WNT and VEGF signaling are imperative for implantation and angiogenesis, respectively, and were analyzed in four wildtype and CCR7 knockout scRNA-seq samples. We employed CellChat, an open-source R package, to identify over-expressed ligand-receptor pairs and global communication patterns to analyze how CTB, STB, and EVT cell groups coordinated with WNT and VEGF pathways.
The results were summarized in dot, alluvial, and information flow plots. We found that CCR7 is prominently involved in EVT and STB differentiation within SC-TOs. In conclusion, CCR7 protein plays a prominent role in cell-cell communication within the EVT matrix during early placental development.

Presenter(s): Caleb Yuan
School: Lawrence University
Session: Poster: P2.15
Title: The Mindfulness-based Kindness Project: Resilience & Growth During the Pandemic
Advisor(s): Beth Haines & Kathy Phillippi-Immel, Psychology, Lawrence University & University of Wisconsin Oshkosh
Co-Author(s): Sophia Schultz
Abstract: Previous research demonstrates that mindfulness-based programming promotes young children's self-regulation, prosocial skills, and academic achievement. The Kindness Project brings mindfulness training to preschool and 4K classrooms by training teachers to implement the Mindfulness-based Kindness Curriculum (KC). Teachers receive 26 hours of training focused on personal mindfulness practices and teaching the KC, which includes 24 lessons taught over 12 weeks.
Following positive results from an initial randomized control study, we expanded our outreach to serve more preschool children in the community from 2020 to 2022. Prior to and following KC implementation, children were assessed on social competence, behavioral strengths and difficulties, development skills, and empathy skills.
Even with the ongoing challenges of the COVID-19 pandemic, we saw significant improvements in social-emotional skills, some behavioral skills, and cognitive and academic skills in the 2020-21 school year. However, there were declines in the percentage of children who improved in prosocial skills and behavioral difficulties compared to pre-pandemic years, In the 2021-22 school year, we saw patterns of recovery and improvement, especially in prosocial skills and behavioral difficulties. Our results show

young children can positively benefit from learning mindfulness-skills through the KC, and that some children may need additional support focused on self-regulation, peer relationships, and conduct problems.

Presenter(s): Elizabeth Zeng
School: Washington University
Session: Poster: P2.13
Title: How Tardigrade CAHS2 Protein forms Condensates to protect Cells from Reactive Oxygen Species induced Stress
Advisor(s): Pamela Silver, Systems Biology, Harvard Medical School
Co-Author(s): Samuel Lim
Abstract: Most living things cannot survive in extreme events. However, extremotolerant organisms such as tardigrades have developed unique molecular strategies to protect themselves against these harsh conditions. As a response to stressors, tardigrades upregulate unique intrinsically disordered proteins like CAHS2 that form condensates within the cells. However, the precise mechanism of condensate formation and stressor protection of CAHS2 remain unknown. I examine how CAHS2 promotes condensate formation in both bacterial and mammalian cells, and how the protein protects cells against stress caused by reactive oxygen species (ROS). First, I treated HeLa cells with and without CAHS2 with arsenite, a known ROS-inducing toxin, to see if CAHS2 increase cell viability. Next, to examine how CAHS2 promotes condensates, I added domains that allow for CAHS2 oligomerization to observe if condensates form without the presence of ROS-induced stress. Results show that within the range of 0.01 to 0.1mM, cells expressing CAHS2 had the best percentage of survival. Additionally, CAHS2 with oligomerization domains formed brighter condensates in E. Coli compared to CAHS2 without oligomerization domains. In conclusion, this project furthers understandings of how cells can be protected under stressful conditions, which may mean better therapeutics and stronger plants to combat food shortages.

Presenter(s): Sophia Zhang
School: Washington University
Session: Poster: P3.13
Title: Characterizing Engineered *Saccharomyces* boulardii: Interplay of Secretion Signals and Anti-infectious Protein Expression
Advisor(s): Gautam Dantas, Pathology & Immunology, Pediatrics, Biomedical Engineering, Molecular Microbiology, and The Edison Family Center for Genome Sciences, Washington University in St. Louis
Co-Author(s): Miranda J. Wallace, Rehan Mehta, Jie Ning
Abstract: Clostridioid*es difficile* (CD) infections present a formidable health challenge; antibiotics, their primary therapy, often disrupt the gut microbiota and elevate risk of recurrence. This study aims to leverage *Saccharomyces cerevisiae* var. *boulardii* (Sb) as a chassis for protein-based anti-CD therapies, given its advantages in safety and rapid transit time. We assessed and transformed 4 secretion signals (SSs) and 2 therapeutic proteins, *Gaussia* luciferase (GLuc) and an anti-CD therapy, in Sb. We assayed cultures over 72 hours via ELISA, normalizing data to growth (OD600). Significant secretion levels were observed for all constructs above baseline, and we found that secretion-maximizing SS varied across payload proteins. SS1 tripled anti-CD therapy secretion compared to other SSs at 24 hours, while SS4 maximized GLuc secretion. Different SSs also led to secretion peaks at varying timepoints: for the anti-CD therapy, SS2 and SS3 peaked at 2 and 4 hours. Despite their lower maximal secretion, their earlier peak times render them potentially more compatible with Sb's rapid transit time. These results reveal the intricacy between SSs and payload proteins, highlighting the need for nuanced evaluations in probiotic engineering. Future directions include assessing tolerance in mouse models and the correlations in 16s rRNA microbiome data derived from stools.

All Students Presenting at MCMS Undergraduate Research Symposium in Biological Sciences and Psychology at Washington University in St. Louis

Beloit College

Ama Ameyaw, Edgar Caracoza, Kendri Duran, Jayitha Gaggenapally, Kevin Kyaw, Vu-Anh Le, Takeshi Matsuda, Alexandra Murphy, Satirtha Saha Protya, Tianlong Wang

Carthage College

Juan Alberto Gómez-Solis, Mackenzie Horutz, Maverick Leer, Jessica Schultz

Colorado College

Raymond Fleming, Phoebe Gordon, Erin Kim, Kaila Luell, Sydney Morris, Lane Nelson, Mai Tien Nguyen, Tia Peterson, Julia Raddue, Aidan Wells

Grinnell College

Nancy Garcia, Feven Getachew, Genxuan Lian, Arya Murthy

Gustavus Adolphus College

Akwasi Amoah, Madeline Chaplin, Kathryn Lillemon, Kaia Meyer, Blake Rose, Ella Sontowski, Emma Stock

Hope College

Davi Zola de Araujo, Ella Bozzi, Connor Bricco, Matthew Czmer, Jacquelin D'Lamater, Anna Koppin, Taylor Laurin, Frederick Melges, Natalie Olander, Lexus Putt, Sofia Rosenberger, Elianna Sandman, Ashley Trainor

Knox College

Alexandra Marcoullier, Thy Le, Avery Leigh, Ngoc Nguyen, Goichi Suganuma

Lawrence University

Sharon Abraham, Madisyn Eyman, Nathan Finegold, Finneas Frawley, Laken Hairston, Charlotte Ho, Nicole Lagman, Arlet Montalvo-Mosso, Ryan Saladin, Caleb Yuan

Macalester College

Jo-Hsuan Chen, Alyson Hayashi, Anna Jonaus, Kody Kobayashi, Oliver Lagasse, Eunice Lim, Joe Ntayagabiri, Michelle Osiro, Moura Saad, Xenia Sofianou

St. Olaf College

Ella Homan, Blanca Torres Lopez, Nancy Nabahire Ngutete, Yalda Pourshaban, Rahaf Qarabsa, Sean Rogers, Chloe Traeder

University of Chicago

Sara Hoggatt, Phoebe Holz, Sophie Hu, Joseph Kaczor, Mayher Kaur, Hoi Wan Lee, Liam Leeming, Marco Lopez G, Morgan Ramirez, Zyva Sheikh, Sumana Turimella, Trisha Vinay, Megan Woelkers, Jizhi Yan

Washington University in St. Louis

Rose Abarbanel, Victoria Afe, Cynthia Chang, Yifei Chen, Sophia Coco, Cara Conforti, Hannah Davis, Lowell Finster, John Georgiades, Daleep Grewal, Mackenzie Joe, Levi Kaster, Kollin Kolb, Hrishi Kousik, Kira Jones, Paul Kang, Eric Kwon, Sophie Laye, Amelia Li, Joshua Liu, Saumith Menon, Arjun Nair, Neil Panwalker, Sai Prem, Divya Purswani,, Rajiv Swarup, Sean Teng, Emma Uder, Allan Wang, Wendy Wang, Andrew Wong, Shelly Xu, Amanda Yang, Elizabeth Zeng, Sophia Zhang

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Eric Cole, St. Olaf College

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Kristina Blanke, Beloit College

Anthony Bull, Colorado College

Devavani Chatterjea, Macalester College

Tom Clayton, Knox College

Wenhao Dai, Lawrence University

Shaun Davis, Lawrence University

Travis Hattery, Grinnell College

Shane Heschel, Colorado College

Vince Eckhart, Grinnell College

Pamela Kittelson, Gustavus Adolphus

Caleb Muefong (graduate student), University of Chicago

Anthony Smith, Washington University in St. Louis

Elena Tonc, Macalester College

Erin Weber, Carthage College

Yang Yu, Hope College