# HOPKINS SUMMER RESEARCH SYMPOSIUM

August 5, 2026

Mudd Atrium

## About the Conference

The Hopkins Summer Research Symposium features posters by undergraduate students who have spent the summer conducting STEM research in labs across Johns Hopkins University and Medicine. Presenters include visiting undergraduates who participated in the Amgen Scholars and BioREU programs, as well as Johns Hopkins students who have engaged in independent, faculty-mentored summer research.

## Conference Format

The conference poster session runs from 10:00 am to 12:00 pm in the Mudd Hall Atrium. Student presenters will be available at their posters to discuss their research throughout the entire session. Posters will be arranged in numerical order by student's last name, as listed in this program. Use the **Presentations at a Glance** section (pages 2-5) to navigate the symposium. The at-a-glance list is followed by **Abstracts** for each poster (beginning on page 6).

HOPKINS SUMMER RESEARCH SYMPOSIUM

# Presentations at a Glance

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2. **Katherine Aina** (Erin Jimenez), *Generation of CRISPR sgRNA and Phenotypic Screening of Hearing Regeneration Enhancers In Vivo*

3. **Hyunjoo Cho** (Ethan Yarberry, Gira Bhabha, Damian Ekiert), *Elucidating the Role of the MCE-Associated Membrane Protein Mam4A in Mycobacterial Lipid Transport*

4. **Cyrus Choudry** (Pilar O'Neal, Jamie Spangler), *Novel delivery platform for temporally - controlled drug release to enhance cancer immunotherapy*

5. **Jett DeMattia (**Vijay Kumar, Jonathan Ling), *Uncoupling TDP-43 Cytoplasmic Aggregation from Nuclear Loss of Function Using a Chimeric Splicing Repressor*

6. **Laya Devulapalli** (Ainsley McCollum, Christopher Ross), *Evaluating Modulator Ligand Toxicity Mitigation in Neuro-2A Cell Model of Huntington's Disease*

7. **Layna Do** (Drishti Soneja, Tomomi Karigo), *Hypothalamic Circuits Underlying Aggression and Care*

8. **Thanglamsang Dopmul** (Emaya Moss, Diane Peters), *Establishing a Mouse Model for Radiation-Induced Brain Injury (RIBI) for Therapeutics Evaluation*

9. **Anna Furdui** (Daniel Liu, John P. Toscano), *Structure Based Design and Synthesis of Organelle Targeted Hydropersulfide Donors*

10. **Ivy Garrity** (Raniki Kumari, Rejji Kuruvilla), *Effects of bortezomib, a chemotherapeutic agent, on sympathetic versus sensory nervous systems*

11. **Tess Halpern** (Sarah Woodson, Elise White), *An RNA mystery: Exploring riboswitch folding in psychrophilic bacteria*

12. **Jaden Harris** (Isabel Garcia, Andrew Gordus), *Investigating* C. Elegans *Foraging Behavior through Reorientations*

13. **Olivia Holman** (Sneha Agrawal, Nichole Broderick), *Investigating changes to the acidity-governed effects of* Drosophila melanogaster *microbiome shaped by carbon source in the diet*

14. **Rina Jeong** (Hey-Kyoung Lee), *Evaluating Sound Localization and Sound Discrimination Learning in Freely Moving C57BL/6J mice*

15. **Olivia Jonathan** (Amanda Shaver, Erik Andersen), *Genetic variation shapes anthelmintic responses across wild Caenorhabditis briggsae strains*

16. **Justin Kirkendall** (Natalie Lewis, Yumi Kim), *Dissecting synaptonemal complex proteostasis in* C. elegans

17. **Huy Lam** (Jaskamaljot Kaur Banwait, Damian Ekiert, Gira Bhabha), *Optimizing Fluorescent Protein Tags for studying the localization of the* E. Coli *Pqi lipid transport system in vivo*

18. **Ava Li** (Cristina Santarossa, Gira Bhabha, Damian Ekiert), *Probing the function of* E. coli *envelope spanning lipid transport systems using a suppressor mutant screen*

19. **Weili Lu** (Jotham Suez), *Sucralose Directly Impacts the Gut Microbiome to Modulate Host Metabolic Health*

20. **Anastasiia Malykhina** (Kimberly R. Smith), *Portion-Size-Dependent Anxiety-to-Eat High-Energy-Dense Foods in Anorexia Nervosa: Heterogeneous Response to Inpatient Treatment*

21. **Tommaso Marena** (Josh Beale, Stephen Fried), *Region-Specific Protein Conformational Remodeling in Schizophrenia Using LiP-MS Data*

22. **Daniel Martinez II** (Angela Xu, William Ludington), *The Colonizers of Catan: Fruit Flies. The Colonization Efficiency of Mutated and Wild Type Acetobacter cerevisiae*

23. **Arman Momeni** (Amir Manbachi, Melissa Caughey), *Quantitative Ultrasonic Evaluation of Stored Blood Quality*

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25. **Aaditya Nair** (Evan O'Brien), *Testing 6TM/7TM Mu Opioid Receptor Heterodimerization by Fluorescence Size-Exclusion Chromatography*

26. **Martin Nunes** (Sara Lumbreras Sancho)*, Automated MRI Atrophy Grading: From Visual Rating Scales to a GPU-Accelerated OASIS-2 Pipeline*

27. **Jimena Onton Cueva** (Roland J. Thorpe, Jr.), *Association Between Vascular Risk Factors and Incident Mild Cognitive Impairment Among Non-Hispanic Community-Dwelling Older Adults*

28. **Ellie Paximadas** (Zehra Husaini, Gregory V. Carr), *The impact of social isolation during adolescence and sex on oral operant self-administration of fentanyl.*

29. **Hue (Lily) Pham** (Benjamin Thomson, Yongbo Ding, Gira Bhabha, Damian Ekiert), *Engineering Fusion Proteins to Discover Outer Membrane Interactors of the Mce4 Nutrient Transporter in Tuberculosis*

30. **Ava Schaafsma** (Eric Rouviere, Kim Reynolds), *Building Enzyme Activity-Abundance Fitness Contours in* Escherichia coli

31. **Lakshith Senthil** (Erin Jimenez), *Construction of multiplexed sgRNA library for functional analysis of regeneration-responsive elements*

32. **Mahi Shah** (Spoorthy Reddy, Fenan Rassu), *Cognitive Pretesting of a Discrete Choice Experiment on Mental Health Treatment Preferences Among Adults with Chronic Pain*

33. **Meenal Srivastava** (Kellie Tamashiro), *Influence of apolipoprotein E (APOE) E4 variant on cognitive function in middle aged male and female mice*

34. **Caden Tan** (Jenn Kim, Kelsey Montgomery, Kristen Maynard), *Exploratory Molecular Profiling of VTA Fos Recruitment Following Adolescent Social Conditioned Place Preference*

35. **Hitarthee Tank** (Deeptashree Nandi, Dipali Sharma), *Bacteroides Fragilis Toxin-mediated Regulation of Polyamine Transporters in HPV-Positive Cervical Cancer*

36. **Katie Truong** (Mehmet Keles), *Drosophila visual system shows early-life intrinsic, spontaneous activity modified by visual experience*

37. **Dana Lauren Caroline Villamin** (Joshua Seewald, Janice Chen), *Investigating emotion dynamics using naturalistic conversations*

38. **Tommy Vo** (Alban Latremoliere), *Objective Assessment of Cold Avoidance in Mice*

39. **Kyle Vogtman** (Dianna Kitt, Shilva Shrestha), *Monitoring Community Dynamics in Synthetic Consortia Using Flow Cytometry*

40. **Carolyn Zhou** (Nisha Shah, Eric Raabe), *Combining a novel alkylating agent with PARP inhibition in atypical teratoid rhabdoid tumor*

# Abstracts

1. **SiLENSE: Exploring Phoneme Decoding of Silent Speech Using In-Ear and Cheek Electromyography**

   Gaurish Agrawal (Amgen Scholars Program), Maman Bhatt, Nitish Thakor

   Loss of usable speech due to stroke, laryngeal cancer, or procedures such as laryngectomy can severely restrict independent communication. We investigate whether anatomically motivated in-ear and cheek electrodes can capture articulation-related biosignals for phoneme-level decoding. The mandibular condyle of the temporomandibular joint lies immediately anterior to the external auditory canal. During articulation, nearby muscles of mastication generate electrical signals that travel through surrounding tissue, while jaw movement can deform the canal wall and alter contact between the electrode and canal skin. To test this relationship, in-ear and cheek EMG are recorded alongside synchronized audio, video, and timing signals while participants produce TIMIT-derived sentences under spoken, whispered, and minimal-motion silent conditions. In the current spoken/whispered dataset, 586 of 600 segments (97.7%) passed review across 170 unique sentences and were organized for model development and evaluation. A framework mapping two-channel EMG to phoneme sequences yielded a preliminary 16.2% reduction in phoneme edit error relative to a blank-only baseline on 87 held-out recordings. This work does not yet claim transcription has been achieved, but establishes an experimental protocol with a synchronized multimodal recording setup and a reproducible pipeline for continued phoneme-sequence modeling. Future studies will expand data collection across participants, prioritize minimal-motion silent-speech trials, and advance the development of an assistive speech prosthesis designed to restore spoken expression through a synthesized voice when natural speech is no longer possible.

2. **Generation of CRISPR sgRNA and Phenotypic Screening of Hearing Regeneration Enhancers In Vivo**

   Katherine Aina, Erin Jimenez

   Hair cells of the inner ear are sensory receptors responsible for hearing and balance in vertebrates. In mammals, these cells are permanently lost following damage, resulting

in irreversible hearing loss. Contrastingly, zebrafish regenerate hair cells through activation of injury-induced gene regulatory networks. Our laboratory previously identified regeneration-responsive enhancer elements that become accessible during hair cell regeneration in adult zebrafish inner ears. Here, we established a high-throughput CRISPR-based platform to evaluate the function of these enhancers during regeneration. 48 DNA templates for single guide RNA (sgRNA) synthesis were generated by PCR amplification, followed by in vitro transcription with T7 RNA polymerase, producing sgRNAs for CRISPR genome editing. A pooled CRISPR screen targeting candidate enhancer loci was performed in zebrafish embryos. Following microinjection, embryos were assessed for viability, swim bladder inflation, and other developmental phenotypes. Together, this work established and validated a CRISPR screening pipeline for the functional interrogation of regeneration-responsive enhancers.

3. **Elucidating the Role of the MCE-Associated Membrane Protein Mam4A in Mycobacterial Lipid Transport**

Hyunjoo Cho, Ethan Yarberry, Gira Bhabha, Damian Ekiert

Mycobacterium tuberculosis (Mtb), a global pathogen causing tuberculosis, encodes Mammalian Cell Entry (MCE) systems as key virulence factors essential for lipid uptake and bacterial survival, forming tunnel-like structures across the periplasm to transport lipids. MCE operons encode core transporter components and MCE-associated membrane (Mam) proteins, whose exact roles and structural interfaces with the core complex remain unknown. Here, we investigate Mam4A from the cholesterol-transporting Mce4 system using Mycobacterium smegmatis as a model. A key prerequisite for Deep Mutational Scanning (DMS) is a robust functional phenotype. For Mam4A, required for cholesterol uptake, our functional assay relies on cell growth using cholesterol as the sole carbon source. For preliminary validation, we performed cholesterol growth assays using a Δmam4AB strain with rescue constructs to confirm complementation, while working to generate a Δmam4A single-knockout strain using ORBIT/homologous recombination. To determine how Mam proteins influence core transporter stability, we performed Western blot analyses on Mce4 components. This optimized system will enable high-throughput DMS to map critical functional residues of Mam4A, providing structural insights into mycobacterial lipid transport.

4. **Novel delivery platform for temporally - controlled drug release to enhance cancer immunotherapy**

   Cyrus Choudry (Amgen Scholars Program), Pilar O'Neal, Jamie Spangler

   Interleukin-2 (IL-)2 is a multifunctional cytokine that stimulates the growth, activation, and survival of various types of immune cells, including effector T cells, which play a critical role in tumor clearance. As such, IL-2 has been used as a cancer therapy for over 30 years, but its performance is hindered by its short serum half-life, severe off-target effects, and concurrent activation of immunosuppressive regulatory T cells. To overcome these shortcomings, the Spangler Lab developed a fusion protein consisting of IL-2 and an anti-human IL-2 antibody (denoted F5111 immunocytokine, IC), which preferentially stimulates activated over naive effector T cells. This IC was found to synergize with immune checkpoint inhibitors (ICIs) in cancer treatment, although the timing of IC versus ICI treatment was critical to therapeutic response. Here, we aimed to further understand the role of time in treatment outcomes through the development of a polymer-based nanoparticle delivery platform for administering both the IC and ICI treatments, which will finely control the temporal delivery of these molecules in the bloodstream. The IC & ICI were encapsulated in nanoparticles composed of polyethylene glycol (PEG) and polylactic-co-glycolic acid (PLGA) nanoparticles via flash nanocomplexation/nanoprecipitation (FNC/FNP). Dynamic Light Scattering (DLS) was used to characterize nanoparticle size, revealing that a sufficient size of ~100nm was achieved. Micro bicinchoninic acid (BCA) Assay was then used to measure encapsulation efficiency, showing that ~80% efficiency was achieved. An in vitro sustained release profile showed 30-40% of nanoparticle content was released by day 57. Future steps involve further polymer optimization to achieve 80-90% nanoparticle content release, establishing an in vivo release profile, and hydrogel formulation to ensure localized release at the tumor site.

5. **Uncoupling TDP-43 Cytoplasmic Aggregation from Nuclear Loss of Function Using a Chimeric Splicing Repressor**

   Jett DeMattia (Summer Internship Program), Vijay Kumar, Jonathan Ling

   Nuclear clearance and cytoplasmic aggregation of Tar-DNA binding protein 43 (TDP-43) are the hallmark pathology of Amyotrophic Lateral Sclerosis (ALS) and occur in ~97% of

cases. However, it remains difficult to identify the transcriptome-wide effects of TDP-43 aggregation independently of nuclear loss of function because TDP-43 nuclear depletion causes cryptic exons. In this study, we used a new therapeutic chimeric TDP-43 splicing repressor (CTR), which restores RNA integrity. We used purified TDP-43 fibrils to induce TDP-43 aggregation and pathology in HEK-293, SH-SY5Y, and i3Neuron cell lines. We then used CTR treatment to suppress cryptic exon expression while preserving cytoplasmic aggregates. CTR treatment effectively suppressed cryptic exon inclusions while preserving TDP-43 aggregate pathology. Thus, this model separates nuclear loss of function from cytoplasmic gain of function in TDP-43 pathology. RNA sequencing data will be used to compare differential gene expression and identify new therapeutic targets.

6. **Evaluating Modulator Ligand Toxicity Mitigation in Neuro-2A Cell Model of Huntington's Disease**

Laya Devulapalli, Ainsley McCollum, Christopher Ross

Huntington's Disease (HD) is a neurodegenerative disorder caused by excessive CAG repeats in the Htt gene leading to mutant Huntington (mHtt) protein production. These misfolded proteins interfere with various cell functions driving neuronal loss, and are known to form insoluble inclusion bodies, or aggregates. The Cure Huntington's Disease Initiative Foundation has developed three ligands with affinity for mHtt aggregates. However, it remains unclear if this binding has any ablative effect, which may present due to the act of binding initiating degradation or inhibition of a signal cascade. As such, treating mHtt transfected cells with various CHDI ligands allows for assessing the ligands' ability to create an ablative or inhibitory effect towards the aggregates. BDNF reliably decreases HD specific toxicity, and as such serves as a positive control in this instance. Binding effects were studied in a N2A cell model. Cells were differentiated to a neuronal morphology via all trans retinoic acid treated DMEM, a process validated via preliminary NeuN and MAP2 antibody staining. These differentiated cells were transfected with Htt plasmid Exon 1 (N90)-19Q (non-expanded CAG repetition) and 91Q (expanded CAG repetition, expressing the first 91 amino acids of the Htt protein). The N90-91Q plasmid is used to demonstrate aggregations considering many mutated proteins can be created rapidly after transfection due to the truncated protein size. These transfected cells were treated with BDNF and CHDI ligands (05, 37, 42, 47, 95 and 98), fixed in 4% PFA, and stained with Anti-Htt Neo Epitope p90 and Neuronal Nuclei

specific antibodies. GFP+ cells were analyzed through visual microscopy, aggregation quantification and nuclear condensation toxicity analysis to evaluate whether CHDI ligand-treated mitigated aggregation presence in HD cell models.

7. **Hypothalamic Circuits Underlying Aggression and Care**

   Layna Do (Amgen Scholars Program), Drishti Soneja, Tomomi Karigo

   Females naturally exhibit enhanced aggression towards threatening conspecifics and enhanced case towards offspring during motherhood. However, the direct relationship between these different maternal behaviors is not understood. Previous research has established the role of VMHvl Npy2r+ neurons for aggressive behavior, including maternal aggression in lactating dams. Current work from the Karigo lab has demonstrated a novel role of this population in enhancing pup directed care behaviors. This study utilizes inhibitory DREADDs to silence VMHvl Npy2r+ neurons, assessing how this population influences aggressive behaviors toward adult male mice and caregiving behaviors toward newborn pups across different female reproductive states. DREADD inhibition in VMHvl Npy2r+ neurons in virgin females show a trend towards decreased pup directed care. In contrast, lactating dams do not show a decrease in pup care, but do show a reduction in aggression towards adult male. These findings support the role VMHvl in caretaking behaviors in virgin females in addition to maternal aggression.

8. **Establishing a Mouse Model for Radiation-Induced Brain Injury (RIBI) for Therapeutics Evaluation**

   Thanglamsang Dopmul (Amgen Scholars Program), Emaya Moss, Diane Peters

   Radiation-induced brain injury (RIBI) can produce neurocognitive deficits, particularly in pediatric patients, yet preclinical models for therapeutic screening remain limited. We evaluated fractionated whole-brain irradiation (WBI) in adolescent male C57BL/6J mice using 20 Gy and 10 Gy regimens. Mice underwent pre- and post-irradiation MRI and behavioral testing 7–8 weeks after WBI, including open field, object location, novel object recognition, and fear conditioning assays. The 20 Gy regimen caused 50% mortality and significantly reduced center activity, indicating anxiety-like behavior, while surviving mice showed trends toward impaired contextual and altered cued fear memory without significant object-location or recognition deficits. In contrast, 10 Gy

was fully tolerated but produced inconsistent behavioral changes, with no clear spatial, recognition, or contextual memory impairment. Thus, neither dose provided an optimal RIBI model for therapeutic evaluation. A 15 Gy regimen may better balance survival with reproducible neurocognitive impairment and support future rigorous preclinical testing of neuroprotective interventions.

9. **Structure Based Design and Synthesis of Organelle Targeted Hydropersulfide Donors**

Anna Furdui (Amgen Scholars Program), Daniel Liu, John P. Toscano

Ferroptosis is an iron-dependent form of regulated cell death driven by reactive oxygen species (ROS)-mediated lipid peroxidation and is implicated in cardiovascular disease, ischemia/reperfusion injury, and other oxidative stress–related pathologies. Hydropersulfides (RSSH) are potent antioxidant sulfur species that can inhibit ferroptosis by scavenging lipid radicals, suppressing lipid peroxidation chain propagation, and enhancing cellular antioxidant defenses. Because RSSH are highly unstable, effective intracellular delivery requires donor molecules capable of releasing RSSH at sites of oxidative stress. This project focuses on the structure-based design and synthesis of organelle-targeted, esterase-activated RSSH donor prodrugs directed to the endoplasmic reticulum and lysosomes, key organelles involved in the initiation and propagation of ferroptotic damage. Fluorophore-conjugated and non-fluorescent donor molecules were synthesized and evaluated. HPLC studies demonstrated that donor activation occurs through esterase-mediated cleavage. These targeted RSSH donors provide a promising novel way of studying ferroptosis and advancing therapeutic strategies for oxidative stress–related diseases.

10. **Effects of bortezomib, a chemotherapeutic agent, on sympathetic versus sensory nervous systems**

Ivy Garrity (BioREU), Raniki Kumari, Rejji Kuruvilla

Chemotherapy-induced peripheral neuropathy (CIPN) affects up to 80% of cancer patients and induces pain and numbness. Bortezomib (BTZ), a proteasome inhibitor and chemotherapy drug, is known to cause sensory, but not autonomic neuropathy, suggesting that sympathetic neurons are spared from BTZ-induced neurotoxicity. To study BTZ effects on sympathetic versus sensory neurons, I administered

ethanol/Tween80/saline as vehicle and BTZ injections over 4 weeks in mice. I performed immunostaining on the superior cervical ganglia (SCG), dorsal root ganglia (DRG), footpad, and heart tissue to visualize axonal projections, as well as immune and glial cells in ganglia. I found that sensory axons innervating the footpad tissue degenerate after BTZ injection. In contrast, sympathetic axon innervation of the heart was unaffected. Further, I observed that CD68-positive cells increased in both SCG and DRG after BTZ injection. Expression of fatty acid-binding protein 7 (Fabp7), a marker for satellite glial cells, decreased in ganglia following BTZ injection. These outcomes suggest that although BTZ treatment results in changes in CD68-positive cells and satellite glial cells in the ganglia, only sensory axons are vulnerable to BTZ-induced damage.

11. **An RNA mystery: Exploring riboswitch folding in psychrophilic bacteria**

Tess Halpern (Amgen Scholars Program), Sarah Woodson, Elise White

The folding of noncoding RNAs is essential for their diverse roles in genetic information transfer, especially in ancient bacteria. A classic example of a folding regulatory RNA is the riboswitch, found in the 5' untranslated regions of many bacterial mRNAs. Riboswitches act as receptors for their specific small-molecule ligand; when ligand-bound, the riboswitch's two domains fold to directly regulate downstream gene expression. In bacteria, these RNAs perform regulatory functions usually reserved for proteins in eukaryotes.
Recent work by Rissone et al. shows that RNA stem-loop structures, fundamental structural elements of all riboswitches, misfold under 20°C, a phenomenon hypothesized to result from the formation of a water-ribose clathrate cage. Yet, psychrophilic bacteria such as Pseudoalteromonas SM9913, Pseudoalteromonas S1727, and Vibrio cholerae thrive at low temperatures while relying on riboswitch function for their survival. In this project, I explore the folding landscape of cyclic di-GMP riboswitches in psychrophilic bacteria. Understanding how these fundamental regulatory RNAs fold will inform future questions about the history of genetic information and the "RNA world" hypothesis.

12. **Investigating *C. Elegans* Foraging Behavior through Reorientations**

Jaden Harris (BioREU), Isabel Garcia, Andrew Gordus

Animal foraging provides a decision-making model for linking observable foraging behavior to neural mechanisms. In *Caenorhabditis elegans* (*C. elegans*), their 302-neuron nervous system provides a simplified system to study complex foraging mechanisms, such as neurotransmission. During foraging, when *C. elegans* are on food, they exhibit slowed movements with high reorientation rates, and conversely, when they are removed from food, they have reduced reorientations as they travel further to find another food patch. We previously found that while foraging, *C. elegans* reorientation rates decay stochastically relative to their last food encounter. The pharyngeal neurosecretory, motor, sensory neuron (NSM) releases serotonin in the presence of food, causing *C. elegans* to slow down. Although NSM's role in *C. elegans* foraging is not fully understood, there is a potential interaction between NSM and serotonergic activity and reorientation rate during foraging. Here we present our system that quantifies *C. elegans* reorientation during optogenetic activation of NSM. Using SWF117 mutants where the NSM neuron expresses a channel rhodopsin that responds to red light, we performed 45-minute recordings with red light (to optogenetically depolarize NSM) and without red light (for our control to compare to baseline). Preliminary results validate our approach and demonstrate that NSM activation reduces reorientation rate, supporting a potential role for NSM and serotonin in modulating reorientations during foraging.

13. **Investigating changes to the acidity-governed effects of *Drosophila melanogaster* microbiome shaped by carbon source in the diet**

Olivia Holman (BioREU), Sneha Agrawal, Nichole Broderick

The *Drosophila melanogaster* microbiome is dominated by acidifying bacteria. Acidity in the microbiome plays a key role in host defense, creating a barrier against invading pathogens. Nutrition plays a pivotal role in shaping microbiome composition and affects interactions between microbiota and the host. Despite this, Drosophila research labs use a wide variety of "standard" diets. Differences in sugar source between diets have an unknown effect on the acidifying properties of native Drosophila gut microbes, making research results difficult to contextualize. This project investigates changes to

the acidity-governed effects of the *Drosophila melanogaster* microbiome shaped by carbon source in the diet. Results show that carbon source affects acidity produced by Drosophila gut microbes. Acidity-mediated protection by the microbiome against pathogen colonization depends on dietary sugar source. Additionally, microbiome members' effect on diet acidification is shaped by the carbon source being metabolized. Variation in the acidifying properties of the Drosophila microbiome based on dietary carbon source emphasizes the importance of disclosing dietary contents and contextualizing research results based on the carbon source.

14. **Evaluating Sound Localization and Sound Discrimination Learning in Freely Moving C57BL/6J mice**

    Rina Jeong, Lukas Mesik, Hey-Kyoung Lee

    Cross-modal plasticity is a form of neuroplasticity in which loss of one sensory modality leads to adaptation in the spared senses. Due to insufficient evidence for 'recruitment' of blind visual cortex by remaining senses, we hypothesize that this cross-modal recruitment might only happen with sufficient challenge following the sensory loss. Thus, to investigate whether recruitment occurs in the auditory cortex following visual deprivation, reliable behavioral assessment paradigms are necessary. Therefore, this pilot study assessed sound localization and auditory discrimination abilities of C57BL/6J mice in a T-maze. Mice underwent operant conditioning with auditory stimuli that initially varied in sound-source location and later frequency. Behavioral performance showed no significant improvement in the sound localization task, whereas performance in the sound discrimination task improved significantly for most mice. In future studies, we aim to compare blind and control mice for both tasks to determine whether blindness rescues sound localization and further improves sound discrimination.

15. **Genetic variation shapes anthelmintic responses across wild Caenorhabditis briggsae strains**

    Olivia Jonathan (BioREU), Amanda Shaver, Erik Andersen

    Parasitic nematodes are treated with anthelmintic drugs. However, anthelmintic resistance (AR) is rising, and the underlying causes must be identified. We used the free-

living nematode Caenorhabditis briggsae as a tractable model to study AR mechanisms. Six genetically diverse C. briggsae strains were exposed to nine anthelmintic drugs, and dose-response curves were created to quantify effective concentrations, slope estimates, and heritability. Findings reveal significant strain-level variation in anthelmintic responses within and across drug classes, demonstrating the importance of incorporating genetic diversity into AR studies. Heritable drug responses prioritize conditions for future genome-wide association studies to discover AR genes.

16. **Dissecting synaptonemal complex proteostasis in *C. elegans***

Justin Kirkendall (BioREU), Natalie Lewis, Yumi Kim

Accurate and stable synapsis during meiosis relies largely on the synaptonemal complex (SC), a tripartite, zipper-like protein complex that assembles between homologous chromosomes. However, the mechanisms that regulate assembly and disassembly of the SC remain unclear. Recently, Skp1-related proteins SKR-1/2, well-known adapters of the Skp1-Cul1-F-box (SCF) ubiquitin ligase, were found to moonlight as structural components of the SC in *C. elegans*. Additionally, mass spectrometry on recombinant SC proteins identified several highly ubiquitinated sites on SC protein SYP-4. To dissect the role of ubiquitination in regulating SC dynamics, four putative ubiquitination sites on SYP-4 were disrupted by CRISPR/Cas9. While *v5::syp-4*$^{K2R}$ mutants still achieved complete synapsis in pachytene, mutants showed a mild reduction in egg viability and increase in univalent chromosomes. Additionally, western blotting reveals that *v5::syp-4*$^{K2R}$ mutants have decreased SYP-4 protein levels, suggesting that loss of SYP-4 ubiquitination decreases SYP-4 stability. This work will contribute to understanding how disruptions to SC proteostasis contribute to meiotic errors that drive aneuploidy and infertility.

17. **Optimizing Fluorescent Protein Tags for studying the localization of the *E. Coli* Pqi lipid transport system in vivo**

Huy Lam, Jaskamoljot Kaur Banwait, Damian Ekiert, Gira Bhabha

In double-membraned bacteria, transport between the two membranes is essential for nutrient import, outer-membrane biogenesis, and maintenance. The Mammalian Cell Entry (MCE)-domain-containing proteins, of which the Paraquat Inducible (Pqi) system is

a member, are believed to be involved in lipid transport. The system comprises three components: PqiA, a putative monomeric transmembrane protein; PqiB, a homohexameric tunnel-like architecture with the length to span the periplasm; and PqiC, an octomeric lipoprotein anchored to the outer membrane. We do not know how these proteins localize in the cell, whether they change localization during the cell cycle, or how they colocalize. The aim of my project is to bridge this gap by using fusion protein tags on individual Pqi components and time-lapse fluorescence microscopy. I have conducted a comparative analysis of various bright monomeric fluorescent proteins and found that mLemon is optimal for the localization study due to its brightness and photostability. We anticipate that this proposed work will advance our understanding of bacterial cell envelope integrity, potentially informing future therapeutic strategies.

18. **Probing the function of *E.coli* envelope spanning lipid transport systems using a suppressor mutant screen**

Ava Li, Cristina Santarossa, Gira Bhabha, Damian Ekiert

Gram-negative bacteria are surrounded by a cell envelope consisting of an inner membrane (IM) and an outer membrane (OM), separated by an aqueous space containing the cell wall. The OM is a formidable barrier to outside stressors and toxic compounds, thereby contributing to antibiotic resistance. LetAB and PqiAB are homologous protein systems that have been proposed to maintain the cell envelope by transporting phospholipids, a key membrane component. However, their specific physiological roles in bacterial cell envelope maintenance have yet to be functionally probed. Therefore, we performed a suppressor mutant screen to identify genes related to pqiAB and letAB, which would yield insights into their cellular functions. We show that in a ΔpqiAB ΔletAB background, suppressor mutations arise in the yhdP gene, which has been implicated in phospholipid transport to the OM. Complementation of the WT genes into the suppressor mutants suggested that the yhdP mutations are likely loss-of-function. This suggests that deleting yhdP in a ΔpqiAB ΔletAB background improves cell envelope barrier function, indicating that these three transporters may act together to maintain lipid composition by transporting lipids in different directions or transporting different lipid substrates. Future mechanistic studies will reveal how these transporters coordinate to maintain the cell envelope.

19. **Sucralose Directly Impacts the Gut Microbiome to Modulate Host Metabolic Health**

Weili Lu (University Undergraduate Research Fellowship), Jotham Suez

Non-nutritive sweeteners (NNS) have become popular alternatives to caloric sweeteners, yet rates of metabolic disease have continued to rise. In fact, consumption of NNS like sucralose has been linked to increased weight gain and diabetes risk, with the gut microbiome implicated in the metabolic response to NNS. However, the underlying mechanisms remain unclear, so this project aims to characterize the direct effects of sucralose on the microbiome and how those changes impact host metabolism. My findings demonstrate that exposure to sucralose remodels the composition and function of microbiome communities in a host-independent manner. Further analysis suggests that Gram-negative bacteria utilizing the methylerythritol phosphate (MEP) pathway are particularly susceptible. In vivo, sucralose-induced changes in the microbiome have immunomodulatory effects that worsen host glycemic response, but the specific microbe-derived metabolites driving the immunometabolic phenotype are still under investigation. This work uncovers a causative mechanism for how a sucralose-perturbed microbiome negatively alters host metabolic health and can ultimately be used to predict personalized responses to NNS based on individuals' gut microbiomes.

20. **Portion-Size-Dependent Anxiety-to-Eat High-Energy-Dense Foods in Anorexia Nervosa: Heterogeneous Response to Inpatient Treatment**

Anastasiia Malykhina (Dean's ASPIRE Grant), Kimberly R. Smith

Individuals with an eating disorder diagnosis of anorexia nervosa (AN) often experience marked anxiety to consume high energy-dense (HED) foods. We previously showed that this anxiety-to-eat is portion size-dependent and improves with meal-based weight restoration treatment. Whether nutritional rehabilitation shifts this dose-response curve uniformly across patients remains unknown. Here we constructed anxiety-to-eat response curves to five portion sizes (0.25, 0.5, 1, 2, 4) of HED foods collected at hospital admission and prior to discharge in inpatients with AN and atypical AN (N=22). Changes in anxiety-to-eat with treatment were calculated and K-means clustering was used to identify treatment response subgroups from the patient curves. Two subgroups representing a treatment responsive cluster ("responsive", n=11; mean reduction in anxiety-to-eat = 13.0 points + 5.1 points) and a "non-responsive" cluster (n=11; mean

reduction in anxiety-to-eat = 0.9 points + 3.2 points) were identified. Groups did not differ at baseline in degree of eating, shape, or weight concern or eating restraint. However, the “responsive” group had greater anxiety-to-eat than the “non-responsive” group at baseline, with no differences between the groups after treatment. No other clinical or diagnostic variable predicted cluster membership or correlated with changes in anxiety-to-eat. These findings demonstrate differential responses to nutritional rehabilitation in anxiety-to-eat HED foods. This heterogeneity is not captured by current diagnostic or clinical measures. Anxiety-to-eat may represent a distinct clinical construct not reflected in standard admission assessments and may warrant incorporation into treatment monitoring.

21. **Region-Specific Protein Conformational Remodeling in Schizophrenia Using LiP-MS Data**

Tommaso Marena (BioREU), Josh Beale, Stephen Fried

Schizophrenia proteomics has focused almost exclusively on protein abundance, yet the disorder's most reproducible molecular phenotype is altered protein solubility, which is a state abundance measurements cannot resolve. We applied limited-proteolysis mass spectrometry (LiP-MS), paired with a matched trypsin-only abundance control, to post-mortem DLPFC and striatum from 13 control and 15 schizophrenia donors, decomposing every peptide-level hit into abundance and residual conformational components. Of 124 significant peptides, 54 were structural-dominant, with structural residuals markedly exceeding background across both regions. The two regions ran largely independent programs (2 shared FDR genes; peptide fold-changes uncorrelated), with only PPP1R1B and ACADM replicating across regions. The striatum showed a MAP2 cytoskeletal/medium-spiny-neuron phospho-structural program (14 of 62 peptides) that was absent in DLPFC, which instead carried a mitochondrial fatty-acid-oxidation signature. Eight peptides, ranked by structural fraction rather than fold-change, are nominated for PRM validation. These findings establish schizophrenia's protein-structure phenotype as regional, not global, and separable from abundance change.

22. **The Colonizers of Catan: Fruit Flies. The Colonization Efficiency of Mutated and Wild Type Acetobacter cerevisiae**

Daniel Martinez II (BioREU), Angela Xu, William Ludington

The digestive tracts of animals commonly contain a gut microbiome, which is a community of symbiotic microbes. The composition of these microbiomes changes with age, leading to changes in host health, but how and why this selection occurs is largely unknown. Acetobacter cerevisiae (Ac) is a commensal bacteria naturally found in the gut of *Drosophila melanogaster*, the fruit fly. A recurrent mutant Ac has been isolated from the aging fly microbiome. This mutation overproliferates in the aged fly microbiome and decreases the host lifespan. With competition colonization assays, we quantified how well wild type Ac and mutant Ac colonize axenic fruit flies over time. We hypothesize that mutant Ac colonizes older flies better and will be present in older flies at a higher amount than wild type Ac. Variations of these competition colonization experiments using different bacterial species indicate that mutant Ac is present in higher amounts in older flies.

23. **Quantitative Ultrasonic Evaluation of Stored Blood Quality**

Arman Momeni, Amir Manbachi, Melissa Caughey

More than 85 million red blood cell (RBC) units are transfused worldwide each year. Although RBC units stored in additive solution have a regulatory shelf life of 42 days, current evidence suggests that deterioration occurs at variable rates depending on donor and storage factors, highlighting the limitations of a universal expiration date. We propose amplitude-mode (A-mode) ultrasound as a noninvasive method for quantitatively assessing stored RBC quality. This preliminary study aims to establish the feasibility and reproducibility of serial A-mode ultrasound measurements in stored RBC units under standardized imaging conditions. By evaluating measurement consistency over time, this work provides the methodological foundation for our future proposed study to investigate correlations in ultrasound-derived metrics with established biomarkers of RBC storage lesions and clinical outcomes. While diagnostic variables are yet to be established, demonstrating reliable and repeatable ultrasound measurements is a critical step toward individualized assessment of RBC quality prior to transfusion.

24. **TurboID Proximity Labeling Reveals DHRS4 Interactome: Associations with Transcription Factor Networks and Redox Mechanisms**

Sareen Muthyala (Ethan M. Posner Fellowship), D. Brian Foster

Dehydrogenase/reductase 4 (DHRS4) is a short-chain dehydrogenase/reductase involved in redox and metabolic processes, but its cardiac protein networks remain poorly defined. We integrated three proteomic approaches to identify candidate DHRS4-associated proteins: TurboID proximity labeling in neonatal rat ventricular cardiomyocytes, DHRS4 coimmunoprecipitation mass spectrometry in mouse heart lysates, and size exclusion chromatography mass spectrometry (SEC-MS) in mouse heart samples. TurboID-MS identified proteins near DHRS4, Co-IP-MS detected proteins enriched in native DHRS4-containing complexes, and SEC-MS compared candidate elution profiles with DHRS4 to prioritize potential co-complex associations. Candidates were linked to RNA regulation, redox metabolism, mitochondrial function, organelle trafficking, and cardiomyocyte structure. HNRNPA1, HNRNPA2B1, HNRNPA3, PDHA1, DECR1, and HSD17B8 showed DHRS4-like SEC-MS profiles and support across multiple methods. These findings suggest that DHRS4 participates in a broader cardiac network connecting metabolism, RNA regulation, mitochondrial function, and protein-complex organization.

25. **Testing 6TM/7TM Mu Opioid Receptor Heterodimerization by Fluorescence Size-Exclusion Chromatography**

Aaditya Nair (Albstein Research Scholarship), Evan O'Brien

The mu opioid receptor (MOR) gene generates truncated six-transmembrane (6TM) splice variants in addition to full-length 7TM MORs. Zhang et al. (2020) reported that 6TM MOR-1G heterodimerizes with 7TM MOR-1 using co-immunoprecipitation, though the interaction did not survive SDS-PAGE. We used fluorescence size-exclusion chromatography (FSEC) to test whether this interaction persists as a stable, detergent-solubilized complex. 6TM-GFP alone eluted largely as aggregate regardless of an ER-targeting signal peptide, indicating an intrinsic folding defect. Coexpression with untagged 7TM did not rescue clean 6TM-GFP expression, and untagged 6TM produced no shift in the 7TM-GFP peak. Screening two detergents and two ionic strengths revealed a shift (~0.345 mL, ~43% apparent mass increase) at 100 mM NaCl that

collapsed to near baseline (4–12% mass increase) at 500 mM, suggesting nonspecific aggregation rather than a proper interface. These results do not suggest a stable, purifiable heterodimer, but do not contradict a transient 6TM/7TM interaction.

26. **Automated MRI Atrophy Grading: From Visual Rating Scales to a GPU-Accelerated OASIS-2 Pipeline**

    Martin Nunes, Sara Lumbreras Sancho

    Structural brain atrophy is assessed using visual rating scales, but manual grading is time-consuming and may vary between raters. This project investigated whether an automated pipeline could generate consistent medial temporal atrophy (MTA) and global cortical atrophy (GCA) ratings from MRI scans. Initial work focused on understanding the clinical problem, reviewing scale definitions and examples, reading relevant literature, and examining the AVRA implementation. A subset of scans was manually graded to develop familiarity with the scales and provide a human comparison. The program then indexed 1,368 OASIS-2 acquisitions from 150 subjects, performed GPU-accelerated inference, preserved scan-level identifiers and returned final results. Additional spot checks were completed after batch processing to identify obvious inconsistencies. The resulting workflow demonstrates a reproducible approach for large-scale MRI grading while recognizing limitations, including a small single-rater comparison sample and the absence of independent human labels for the locked test set.

27. **Association Between Vascular Risk Factors and Incident Mild Cognitive Impairment Among Non-Hispanic Community-Dwelling Older Adults**

    Jimena Onton Cueva, Roland J. Thorpe, Jr.

    Vascular risk factors (VRFs) are linked to mild cognitive impairment (MCI), yet the impact of cumulative vascular risk remains understudied. Objective: To examine the association between cumulative vascular risk burden and incident MCI among non-Hispanic community-dwelling adults aged 65 years and older. Methods: Data were analyzed from 4,399 Medicare beneficiaries enrolled in the National Health and Aging Trends Study (2011–2023). VRFs were self-reported at baseline, and incident MCI was assessed annually using cognitive testing. Cox proportional hazards models examined

associations of cumulative VRF burden (≥2 VRFs and VRF count) and individual VRFs with incident MCI. Results: Adults with ≥2 VRFs had a 19% higher risk of incident MCI (HR=1.19, 95% CI:1.03–1.38). Each additional VRF increased MCI risk by 7% (HR=1.07, 95% CI:1.02–1.12). Diabetes and heart attack were the strongest independent risk factors. Conclusions: Greater vascular risk burden is associated with an increased risk of incident MCI.

28. **The impact of social isolation during adolescence and sex on oral operant self-administration of fentanyl.**

Ellie Paximadas (Amgen Scholars Program), Zehra Husaini, Gregory V. Carr

Social isolation (SI) has been implicated in the development of several neuropsychiatric conditions, including depression, ADHD, schizophrenia, and substance use disorder (SUD). While isolation at any age could be harmful, isolation during adolescence can impair cognitive development and increase the risk of developing psychiatric illness later in life. Investigations from our lab have identified that mice exposed to transient SI during adolescence increase both the willingness to work for and the total consumption of high-sugar-high-fat (HSHF) rewards. This study aims to identify whether this phenomenon extends to non-food reinforcers, such as drugs of abuse. To do so, we developed a short-access oral fentanyl self-administration model to assess differences in stable consumption and reinforcing effects based on housing conditions. Our findings indicate that there appears to be a disconnect in how SI affects reward processing for food and non-food reinforcers, as social isolation did not significantly increase the consumption of fentanyl across sexes.

29. **Engineering Fusion Proteins to Discover Outer Membrane Interactors of the Mce4 Nutrient Transporter in Tuberculosis**

Hue (Lily) Pham (Amgen Scholars Program), Benjamin Thomson, Yongbo Ding, Gira Bhabha, Damian Ekiert

Yearly, approximately 1.2 million people die of tuberculosis, a major infectious disease caused by drug-resistant Mycobacterium tuberculosis (Mtb). Previous research identified the Mammalian Cell Entry (MCE) system, an important virulence factor in Mtb, as a nutrient transporter required for host persistence. Studies in our laboratory

characterized the Mce4 transport system in the nonpathogenic model Mycobacterium smegmatis (M. smeg). This work identified the core Mce system complex, including six periplasmic Mce proteins and associated inner membrane proteins. However, putative outer membrane protein partners of Mce4 remain largely unknown because transient protein-protein interactions and membrane complex instability hinder their identification. We propose a mass spectrometry-based proximity labeling approach to identify these interactors. Here, we designed several Mce4-APEX2m fusion constructs to tag regions of the Mce4 system proximal to the outer membrane for proximity labeling of neighboring proteins. We successfully generated several constructs and are testing their function using a cholesterol growth assay.

30. **Building Enzyme Activity-Abundance Fitness Contours in *Escherichia coli***

Ava Schaafsma (BioREU), Eric Rouviere, Kim Reynolds

The growth of bacterial cells is enabled by their enzymes catalyzing reactions. The contribution of a single enzyme to the organism's fitness depends on its catalytic activity and cellular abundance. There is potentially a large set of abundance–activity combinations that lead to the same flux (the rate at which substrate gets catalyzed into product) and, consequently, the same fitness. This degenerate set of activity–abundance combinations is what we call a fitness contour because, when fitness is plotted as a function of enzyme activity and abundance, these combinations lie along a curve. Although we have a guess as to what these contours might look like in theory, their true shape remains an open question. To aid in constructing these contours directly, I perturbed activity and abundance for the conditionally essential metabolic enzyme orotidine 5'-phosphate decarboxylase (encoded by the *pyrF* gene) in *E. coli* using a plasmid system in which (i) the abundance was tuned with an inducer molecule and (ii) the activity was tuned by making mutations in the protein..

31. **Construction of multiplexed sgRNA library for functional analysis of regeneration-responsive elements**

Lakshith Senthil, Erin Jimenez

Hair cell regeneration in zebrafish is controlled by dynamic changes in chromatin accessibility, including activation of regeneration-specific enhancer elements. While

genomic approaches have identified numerous candidate enhancer regions associated with regeneration, the functional significance of most of these regulatory elements remains unknown. The long-term goal of this project is to establish a high-throughput platform to systematically test the roles of regeneration-responsive enhancers during zebrafish hair cell regeneration. As the initial step toward this goal, candidate enhancer regions identified from previous single-cell genomic studies were prioritized for functional testing. Single guide RNAs (sgRNAs) targeting these candidate enhancers were designed using the UCSC Genome Browser CRISPRscan track. Following computational design, pooled oligonucleotide libraries were synthesized and cloned into Twist TOPO pooled vectors using the CLUE Wet Lab platform to generate multiplexed CRISPR sgRNA libraries. To date, 600 sgRNAs targeting 600 candidate enhancer regions have been designed and a pooled library consisting of 48 enhancer targets represented by four independent sgRNAs per enhancer has been successfully constructed. The cloned library is currently being amplified to generate sgRNA templates for in vitro transcription, producing the reagents required for future pooled CRISPR mutagenesis experiments. These reagents will enable high-throughput in vivo screening of enhancer function during zebrafish hair cell regeneration.

32. **Cognitive Pretesting of a Discrete Choice Experiment on Mental Health Treatment Preferences Among Adults with Chronic Pain**

Mahi Shah, Spoorthy Reddy, Fenan Rassu

Chronic pain is a leading cause of disability in the United States, yet little is known about which mental health treatment features adults with chronic pain value. We built a discrete choice experiment (DCE), in which respondents choose between hypothetical treatments that vary across features, and cognitively pretested it with 11 adults with chronic pain. Think-aloud interviews assessed four pretesting domains: content, presentation, comprehension, and elicitation. The DCE was revised after successive interviews until no new major issues arose. Feedback led to renaming a widely misunderstood attribute ("mode of delivery" became "session format"), a simpler display of the chance of symptom improvement, and correction of a common belief that mental health treatment means a provider dismisses physical pain. Cost was consistently a top concern and, for some, a near deal-breaker, though most weighed it against benefit and wait time. Pretesting produced a clearer, more interpretable instrument for full-sample administration.

33. **Influence of apolipoprotein E (APOE) E4 variant on cognitive function in middle-aged male and female mice**

Meenal Srivastava (Albstein Research Scholarship), Kellie Tamashiro

The ε4 ("E4") isoform of apolipoprotein E (APOE) is the most significant genetic risk factor for Alzheimer's Disease, increasing risk 15-fold. However, the specific effects APOE4 has on cognition in the context of spatial navigation tasks remain incompletely understood. We assessed spatial learning, memory, and cognitive flexibility in middle-aged E3 and E4 female and male mice using the Barnes maze. We found that E4 females showed delayed acquisition compared to sex-matched E3 mice. Thus, E4 may have contributed to deficits in hippocampal-dependent spatial learning in only the females. We observed cognitive inflexibility in E4 male mice during the reversal trials, suggesting that E4 may impact the orbitofrontal cortex (OFC) and the prefrontal cortex (PFC) in males. By improving our understanding of how E4 affects the specific neural circuitry involved in spatial learning and memory, this research can inform future preventative therapies for middle-aged APOE carriers with heightened risk of AD.

34. **Exploratory Molecular Profiling of VTA Fos Recruitment Following Adolescent Social Conditioned Place Preference**

Caden Tan (Lieber Institute for Brain Development Summer Internship), Jenn Kim, Kelsey Montgomery, Kristen Maynard

The ventral tegmental area (VTA) contains molecularly distinct glutamatergic, GABAergic, dopaminergic, and combinatorial cell populations that have different roles in reward behaviors. We used multiplex RNAscope to characterize Fos expression across VTA molecular identities following adolescent social conditioned place preference (sCPP) in mice. Whole-VTA sections were imaged on an Akoya PhenoImager Fusion and quantified in HALO software using DAPI-seeded segmentation and transcript-copy thresholds for Fos, Slc17a6 (Vglut2), Slc32a1 (Vgat), and Th. Across 18 sections and 67,543 segmented cells, Vglut2+ identities showed the highest Fos expression, which was preserved across multiple transcript-copy thresholds and leave-one-out analyses. This pilot study establishes an analysis workflow for quantifying Fos expression within multiple neuronal classes across the VTA anterior-posterior axis.

35. **Bacteroides Fragilis Toxin-mediated Regulation of Polyamine Transporters in HPV-Positive Cervical Cancer**

Hitarthee Tank, Deeptashree Nandi, Dipali Sharma

Polyamine transport plays a critical role in maintaining intracellular polyamine levels that support cancer cell proliferation, survival, and tumor progression. This study investigates the role of polyamine transporters in HPV-positive cervical cancer and examines the effect of Bacteroides fragilis toxin (BFT) on their expression. Cervical cancer cells were treated with BFT, and the expression of seven transporter genes, ATP13A1, ATP13A2, ATP13A3, ATP13A4, ATP13A5, SLC18B1, and SLC18A2, was analyzed using RT-PCR, gradient PCR, agarose gel electrophoresis, and western blotting, with GAPDH serving as the housekeeping gene. Immunohistochemistry (IHC) was performed to evaluate protein expression in cervical cancer tissues. In addition, MTT assay was used to assess cell viability, and migration and invasion assays were used to determine the biological significance of altered transporter expression. This study aims to better understand the role of polyamine transporters in cervical cancer progression and identify potential therapeutic targets by understanding how microbial toxins regulate tumor behavior.

36. **Drosophila visual system shows early-life intrinsic, spontaneous activity modified by visual experience**

Katie Truong (Jeffrey Ma Shiu and Emily Liu Endowed Award), Mehmet Keles

Spontaneous activity is critical for the early establishment of neural circuits. In mammalian sensory systems, it is required for precise topographic wiring during periods of heightened plasticity and declines as circuits mature. In contrast, the invertebrate brain after metamorphosis is considered hard-wired, and the extent of plasticity, particularly in stable sensory circuits, remains unknown. Despite this, we observed high levels of spontaneous neural activity in the optic lobe of recently eclosed *Drosophila melanogaster*. Juvenile flies exhibited heightened spontaneous activity with spatiotemporal patterns distinct from those of older flies. Interestingly, depriving flies of visual experience by raising them in complete darkness altered these stereotyped activity patterns, suggesting that extrinsic sensory experience interacts with intrinsic

processes to support the full development of both lower- and higher-order visual function. This work provides a foundation for future studies investigating conserved mechanisms underlying sensory plasticity and the development of complex sensory-driven behaviors.

37. **Investigating emotion dynamics using naturalistic conversations**

Dana Lauren Caroline Villamin (Amgen Scholars Program), Joshua Seewald, Janice Chen

Naturalistic conversations provide a unique framework for studying emotion by isolating dynamic social interactions while minimizing audiovisual confounds and causal structure characteristic of traditional narrative stimuli. Previous research has linked fluctuations in emotion during narratives to activity in emotion-related brain regions and demonstrated that inter-subject synchrony (ISC) captures shared neural responses across individuals exposed to the same stimulus. Using an existing fMRI dataset originally collected to investigate episodic memory, we examined how continuous ratings of emotional arousal and valence relate to brain activity and ISC during naturalistic conversations. Distinct conversations elicited varied emotional dynamics, enabling comparison between emotion ratings and neural activity. Relationships between emotional ratings and region-of-interest activity varied across brain regions and conversations, while ISC revealed widespread synchronized neural responses across participants. These findings demonstrate the feasibility of using naturalistic conversations as a complementary naturalistic stimulus for investigating the neural dynamics of emotion, extending beyond traditional narrative paradigms.

38. **Objective Assessment of Cold Avoidance in Mice**

Tommy Vo, Alban Latremoliere

Classical techniques to assess cold pain have major limitations: they are reflexive (i.e the pain response is defined by a brisk movement upon cold exposure), and use temperatures rarely encountered by patients (i.e. 0 to 4C, while patients often complain about 10-20C temperatures), thus narrowing clinical relevance. Furthermore, drug treatments developed from current assays have mostly failed in clinical trials, reflecting poor translational value. To study cold pain-related symptoms, we therefore require novel assays not based on reflexes or extreme temperatures. Here, I developed a

protocol where two dynamic thermal plates alternate cold (14C) and neutral (30C) temperatures to prompt place aversion 4 times per session (total time 30 min). Exposure to multiple cooling ramps during each trial provided repeated intra-individual measurements that I used to calculate a 50% avoidance threshold using MATLAB. This technique provides an objective and stable determination for cold aversion in freely moving mice.

39. **Monitoring Community Dynamics in Synthetic Consortia Using Flow Cytometry**

    Kyle Vogtman (Amgen Scholars Program), Dianna Kitt, Shilva Shrestha

    There is increasing interest in microbial-based technologies for sustainable production of value-added products. Synthetic consortia, composed of well-characterized microorganisms, enable improved process control and product formation but are less stable due to their lack of functional redundancy when compared to conventional undefined cultures. Developing stable synthetic consortia requires characterization of its resiliency and ability to recover to environmental disruptions. As such, a method to monitor the composition of synthetic community members after exposure to environmental disruptions is needed. We are designing a high-throughput flow cytometry-based assay for characterizing the composition of synthetic communities by utilizing species specific fluorescent probes and live-dead staining. To accomplish this, high temperature species specific fluorescent probes were designed for five species and evaluated for specificity using an open-source primer design software. We hope to utilize these probes in a quantitative flow cytometry assay and to use a fixable live dead stain for single preparation analysis of the samples.

40. **Combining a novel alkylating agent with PARP inhibition in atypical teratoid rhabdoid tumor**

    Carolyn Zhou (Alex's Lemonade Stand Foundation POST Program), Nisha Shah, Eric Raabe

    Atypical teratoid rhabdoid tumor (ATRT) is a rare, highly aggressive pediatric central nervous system cancer and the most common malignant brain tumor in infants under one year of age. LP-184 is a novel alkylating agent that damages DNA and is particularly effective in tumors with DNA repair pathway defects. Pamiparib (BGB-290) is a next-

generation poly(ADP-ribose) polymerase inhibitor (PARPi) with improved brain penetration and potency compared with earlier PARP inhibitors. We hypothesized that combining LP-184 with BGB-290 would produce synergistic anti-tumor activity in ATRT. To evaluate this, we determined the minimum effective combination dose and assessed treatment response using cell viability and apoptosis assays. Combination treatment reduced ATRT cell viability and increased apoptosis compared with control and BGB-290 treatment alone. These findings provide preliminary insight into BGB-290's effect in multiple ATRT cell lines and warrant further investigation of this combination strategy.

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