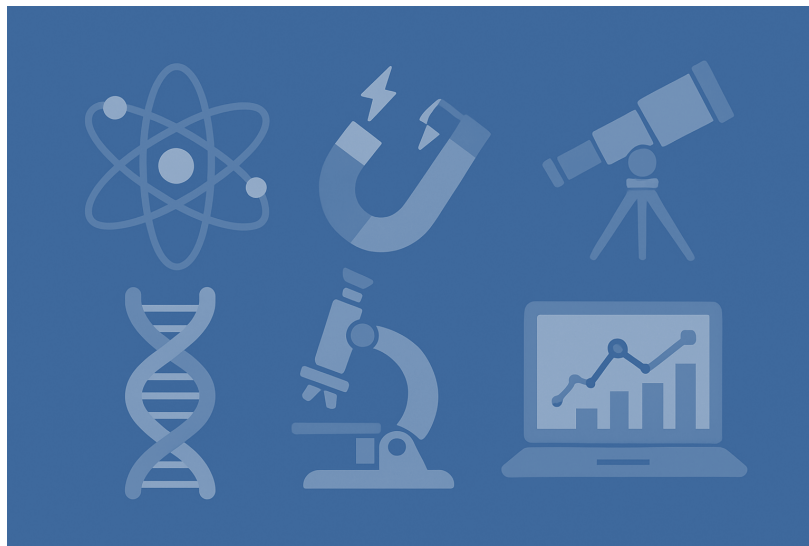


# Yale

## Science, Technology, and Research Scholars



## STARS II Annual Symposium

April 21, 2025

4:00 PM – 6:30 PM

Yale Science Building  
Marsh Auditorium  
260 Whitney Ave

# Schedule of Presentations

5:00 – 5:05	Dr. Alexia Belperron Associate Dean, Science Education Director, STEM Fellowships	Welcoming Remarks
5:05 – 5:15	Valeria Ceron Department of Neuroscience Class of 2025 PI: Ellen Hoffman, MD PhD Mentor: Marina Carlson, PhD Candidate	Characterizing Behavior and Brain Activity Phenotypes in Zebrafish Mutants of the Autism Risk Gene, <i>ADNP</i>
5:15 – 5:25	Ximena Leyva Peralta Department of Chemistry Class of 2025 PI: Tianyu Zhu	Applying Machine Learning Green's Function Method for Studying Many-Body Effects in Silicon Crystals
5:25 – 5:35	Micky Rose Biomedical Engineering Class of 2025 The Saltzman Lab Mentor: Anna Lynn, MD PhD	Design of the Nanoparticle Protein Corona and Investigation of Impact on Delivery Profile
5:35 – 5:45	Kayla Samo Department of Biomedical Engineering Class of 2025 PI: Kathryn Miller-Jensen Mentor: Erick Salvador Rocha	Characterizing Paracrine Regulatory Mechanisms through Dual Stimulation of Toll-like Receptors
5:45 – 5:55	Tori Sodeinde Molecular, Cellular, and Developmental Biology Class of 2025 Lab: The Chang Lab Mentor: Dr. Rekha Rai, Senior Research Scientist	Examining the Impact of Chromatin Status on Telomere Homologous Recombination
5:55 – 6:05	Isabelle Staco Molecular, Cellular, and Developmental Biology Class of 2025 PI: Megan King Mentor: Ece Koçak (PhD student)	Defining The Role of Persistent DNA Bridges in cGAS-STING Activation by PARP Inhibitor Treatment
6:05 – 6:30	STARS II Students	Poster Presentations

# Class of 2025 Poster Presentations

4:00 – 5:00PM

Quazi Rumman Rahman <i>Physics</i> PI: Steven Girvin Mentor: Daniel Weiss (post-doc) Department: Physics	Measurement free quantum error correction with superconducting circuits
Wade Colley <i>Physics</i> PI: Steven Konezny Department: Physics	Charge Transport Properties of the Electron Hole Material Copper-Thiocyanate (CuSCN) in Thin-Film Photovoltaic Cells (PVC)
Esteban Figueroa <i>Electrical and Computer Engineering</i> PI: Dr. Rebecca Kramer-Bottiglio, John J. Lee Associate Professor of Mechanical Engineering Mentor: Dr. Bilige “Billy” Yang, PhD Student	Untethered Shape Change in Real World Deployment
Ernestine Giahvue <i>Psychiatry</i> PI: Marina Picciotto, PhD, The Picciotto Lab Lab Mentor: Zuhair Abdulla, PhD (postdoc)	Proteomics in the Medial Prefrontal Cortex of Mice Following Learned Helplessness
Michael Gordon <i>Psychiatry, Yale School of Medicine</i> PI: Kristen Brennand (PhD), The Brennand Lab Mentor: Dr. Davide Caputo (PhD, postdoc)	Examining the Impact of Environmental Toxicants on Autism
Ignacio Ruiz-Sanchez <i>Psychiatry</i> PI: Christopher Pittenger Department: Psychiatry	Contribution of early life stress in inducing Tourette syndrome-relevant pathology
Rachel Rivera <i>Molecular Biophysics &amp; Biochemistry</i> The LusKing Lab PI: Megan King Mentor: Sandra Sandria, PhD candidate Department: Molecular, Cellular and Developmental Biology	Deciphering the Regulation of Pro-fibrotic Signaling by Mechanotransduction through Sun2-containing-LINC Complexes
Cailin Hoang <i>Molecular Biophysics and Biochemistry</i> PI: Dr. Caitlin Davis Mentor: Brahmami Patel	Studying the Effect of Steric and Non-Steric Interactions on fPGK and VlsE in Live Zebrafish
Faith Lozano <i>Molecular Biophysics and Biochemistry</i> The Xiong Lab Mentor: Dr. Matt Cook, Recent Ph.D. graduate	Investigation of NonO Interactions with HIV-2 Capsid
Joanna Chen <i>Molecular, Cellular, and Developmental Biology</i> PI: Jun Lu, PhD Mentor: Vadim Kurbatov, MD, PhD	Functional Effects of HOX Gene Overexpression in Leukemia Cells

<p>Kayleigh Hackett  <i>Molecular, Cellular, and Developmental Biology</i>  PI: Scott Holley</p>	<p>Elucidating the Independent Roles of <i>tbx16</i> and <i>msgn1</i> in Presomitic Mesoderm Differentiation</p>
<p>Eric Wang  <i>Molecular, Cellular, and Developmental Biology</i>  PI: Jing Yan, PhD, The Yan Lab  Mentor: Jing Yan, PhD</p>	<p>Characterizing the Function of <i>V. cholerae</i> Biofilm Matrix Components in Protozoan Grazing Resistance</p>
<p>Nicole Ahsan  <i>Genetics</i>  PI: Kaelyn Sumigray, Ph.D.  Department: Genetics</p>	<p>Investigating the Roles of ECM in Small Intestinal Crypt Morphogenesis</p>
<p>David Gaetano  <i>Mechanical Engineering &amp; Materials Science</i>  PI: Udo Schwarz, Ph.D.; Yale Nanoprobe Group  Advisor: Amit Datye, Ph.D.</p>	<p>Toward defect density characterization of single-crystal Ni-based superalloys CMSX-4 &amp; PWA-1480</p>
<p>Carla Becerra Sabrera  <i>Molecular, Cellular, and Developmental Biology</i>  PI: Lilian Kabeche, The Kabeche Lab  Lab Mentor's name: Carlos Ramirez, Postdoc  Department: Molecular Biophysics and Biochemistry</p>	<p>Investigating the Role of ATR in Chromatin Compaction and Genome Stability</p>
<p>Madeline Pitre  <i>Molecular Biophysics &amp; Biochemistry</i>  PI: Steven K. Reilly, PhD; The Reilly Lab  Graduate Mentor: Jared Akers, PhD. Student  Department: Genetics, Yale School of Medicine</p>	<p>Characterizing Immune-Related Regulatory Variation in Positively-Selected Loci Across Diverse Populations</p>
<p>Kaiden Brown  <i>Electrical Engineering and Computer Science</i>  PI: Rajit Manohar, Ph.D.  The Computer Systems Lab  Mentor: Raghav Pothukuchi, Ph.D.  Department: Electrical &amp; Computer Engineering</p>	<p>Testing HALO Brain-Computer Interface Chip</p>
<p>Patricia Joseph  <i>Molecular, Cellular, &amp; Developmental Biology</i>  PI: Michael O'Donnell  Department: Molecular, Cellular, &amp; Developmental Biology</p>	<p>Exploring the Antagonistic Role of the SER-7 Receptor in Microbial Modulation of <i>C. elegans</i> Feeding Behavior</p>
<p>Jayson Wright  <i>Molecular, Cellular, and Developmental Biology</i>  PI: Thomas Murray MD, Ph.D.; Murray Lab  Department: Pediatrics, Section of Infectious Diseases; Infection Prevention</p>	<p>Assessing Methicillin-Susceptible <i>Staphylococcus aureus</i> Transmission in the NNICU using Whole Genome Sequencing and Environmental Surveillance</p>
<p>Elon Atlaw  <i>Molecular, Cellular &amp; Developmental Biology</i>  PI: Dr. Amy Bei; The Bei Lab  Mentor: Dr. Cyrienne Keutcha  Department: Epidemiology of Microbial Diseases, Yale School of Public Health</p>	<p>Investigating How Genetic Variation in Malaria Vaccine Candidate PfRh5 Alters Immune Evasion</p>

<p>Sean Lewis  <i>Astrophysics &amp; Engineering Science - Electrical</i>  PI: Meg Urry, Phd.  Department: Astronomy and Astrophysics</p>	<p>AGGeN: Diffusion Modeling of Astronomical Data for Improving Image Search Algorithms</p>
<p>Kidus Abebe  <i>Mechanical Engineering &amp; Astrophysics</i>  PI: Udo Schwarz, Ph.D.; Yale Nanoprobe Group  Advisor: Amit Datye, Ph.D.  Department: Mechanical Engineering &amp; Materials Science</p>	<p>Towards Uncovering the Fundamental Deformation Mechanisms of High Temperature Alloys</p>
<p>Angela Morka  <i>Molecular, Cellular, and Developmental Biology</i>  PI: Carrie Lucas, Ph.D.; The Lucas Lab  Postdoc Mentor: Dinesh Babu Uthaya Kumar, M.S. Ph.D.  Department: Immunobiology</p>	<p>Deciphering Roles of ELF4 in the Regulation of Systemic Inflammation via Macrophages</p>
<p>Merat Semma  <i>Molecular Biophysics and Biochemistry</i>  PI: Professor Wendy Gilbert,  Mentor's name: Danni Jin, Postdoctoral Researcher  Department: Molecular Biophysics and Biochemistry</p>	<p>Differential Repression of Human 5'UTR isoforms by SARS-CoV-2 Nsp1 Protein</p>
<p>Siham Busera  <i>Molecular, Cellular, and Developmental Biology</i>  PI: Erol Fikrig, MD; The Fikrig Lab  Postdoc Mentors: Vaishnavi Sridhar, Ph.D. ;  Alejandro Marín López, Ph.D. Department:  Infectious Disease</p>	<p>Investigating the Binding of Mosquito Saliva Protein AAEL002693 to Human Interleukin-18</p>
<p>Joseph Elsayyid  <i>Electrical Engineering and Computer Science</i>  PI: Priyadarshini Panda, Ph.D.; The Intelligent Computing Lab  Graduate Mentor: Abhishek Moitra, Ph.D. Student  Department: Electrical &amp; Computer Engineering</p>	<p>Hardware-Aware Optimization of NanoGPT for Edge AI Deployment</p>
<p>Jordan Miller  <i>Computer Science</i>  PI: Lin Zhong  Graduate Mentor: In Gim, Ph.D.  Department: Computer Science</p>	<p>Evaluating Large Language Models on Spatial Reasoning via Rush Hour Puzzles</p>
<p>Demilade Omolade  <i>Neuroscience</i>  PI: Kathleen Martin, Ph.D.  Department: Cardiovascular Medicine and Pharmacology</p>	<p>Characterizing Novel Genes in Human Smooth Muscle Cells Responsible for Cardiac Allograft Vasculopathy</p>
<p>Angela Noumedem  <i>Molecular, Cellular, &amp; Developmental Biology</i>  PI: Maria Fernanda Forni  Department: Molecular, Cellular and Developmental Biology</p>	<p>Investigating the Role of Adipocyte-Derived Fatty Acids on Macrophage Driven Inflammation</p>

# Class of 2025 Abstracts

## Characterizing Behavior and Brain Activity Phenotypes in Zebrafish Mutants of the Autism Risk Gene, *ADNP*

Valeria Ceron<sup>1,2</sup>, Marina Carlson<sup>3,4</sup>, Vaishnavi Balaji<sup>5</sup>, William Theune<sup>5</sup>, Carter Takacs<sup>6</sup>, Priyanka Jamadagni<sup>4</sup>, Ellen J Hoffman<sup>2,4</sup>

<sup>1</sup>Science Technology and Research Scholar; Department of Neuroscience, Yale College, New Haven, CT <sup>2</sup>Department of Neuroscience, Yale University, New Haven, CT

<sup>3</sup>Interdepartmental Neuroscience Program, Yale University, New Haven, CT 06511

<sup>4</sup>Child Study Center, Yale University, New Haven, CT 06511

<sup>5</sup>University of New Haven, New Haven, CT

<sup>6</sup>Frank H. Netter MD School of Medicine, Quinnipiac University, North Haven, CT 06473

Autism spectrum disorder (ASD) affects 1 in 31 children in the United States. ASD is a developmental disorder characterized by deficits in communication and social interactions, as well as restrictive and repetitive behaviors. One of the most common genetic causes of ASD is an *ADNP* mutation, accounting for 0.17% of all ASD cases. *ADNP* Syndrome affects various bodily systems and results from heterozygous loss-of-function in the *ADNP* gene. The mechanism by which *ADNP* affects neural development is not well described. To investigate this, the project aims to identify the behavior and brain activity phenotypes in zebrafish mutants null for the function of *adnp*. We performed three assays, which generated a behavioral fingerprint for the mutants based on 24 parameters. We find that *adnp* mutants show daytime hypoactivity and an increased visual startle response to a lights-on stimulus compared to wild-type fish. We then conducted immunostaining experiments to label pERK, an indicator of active neurons within approximately 5 minutes before fixation, and tERK for total neurons. Whole mount confocal microscopy and the Brain Registration and Evaluation for Zebrafish (BREEZE) pipeline were used to quantify changes in activity and volume in the *adnp* mutants. The brain activity analysis revealed that *adnpab*<sup>+/-</sup> mutants have increased activity in the optic tectum, and *adnpab*<sup>-/-</sup> mutants have decreased activity in the habenula, compared to wild-type fish. The brain volume analysis showed a decrease in volume of the hypothalamus and hindbrain in *adnpab*<sup>+/-</sup> mutants versus wild-type fish. In summary, this study will provide insight into the circuit-level functions of *ADNP*, illuminating its contributions to neural activity and behavior.

# Applying Machine Learning Green's Function Method for Studying Many-Body Effects in Silicon Crystals

Ximena Leyva Peralta<sup>1,2</sup>, Christian Venturella<sup>2</sup>, Tianyu Zhu<sup>2</sup>

<sup>1</sup>Science Technology and Research Scholar, Yale College, New Haven, CT 06520, United States

<sup>2</sup>Department of Chemistry, Yale University, New Haven, CT 06520, United States

Computational methods have become essential in chemistry and materials science by facilitating the rapid discovery of novel structures and elucidating their properties. Accurately describing systems with multiple interacting particles and their associated many-body effects is essential for calculating the density of states (DOS), which provides key insights into the electronic and optical characteristics of materials. Despite their accuracy, the high computational scaling of many-body methods limits their large-scale application in computational discovery. In this work, we develop a deep learning framework (MBFG-Net) targeting the many-body Green's function that bypasses computationally expensive GW calculations. We demonstrate MBFG-Net's good capabilities in simulations of large-scale nanomaterials, where theoretical results are mostly restricted to DFT-based methods. An MBFG-Net model was trained on 160 hydrogenated silicon nanocrystal structures with up to 36 Si atoms to predict the photoemission and optical spectra of nanocrystals up to 147 Si atoms in size. MBGF-Net achieves highly accurate predictions of band and optical gaps, with errors under 25 meV for nanoclusters within the size of the training set and around 200 meV for nanoclusters up to four times larger. Only 11 out of 160 training samples have more than 20 Si atoms, demonstrating MBGF-Net's high data efficiency and transferability. These results underscore the potential of MBGF-Net to enable simulations of large-scale materials beyond the reach of traditional methods.

After graduation, I'm excited to start a two-year, EU-funded Master's program called "*Materials for Energy Storage and Conversion*." Each semester will take me to a new country, starting with Poland!

# Design of the Nanoparticle Protein Corona and Investigation of Impact on Delivery Profile

Micky Rose<sup>1,2</sup>, Anna Y. Lynn<sup>2</sup>, W.M. Saltzman<sup>2,3,4,5</sup>

<sup>1</sup>Science, Technology, and Research Scholar, Yale College, New Haven, CT 06520 <sup>2</sup>Department of Biomedical Engineering, Yale University, New Haven, CT 06511, USA <sup>3</sup>Department of Chemical & Environmental Engineering, Yale University, New Haven, CT, 06510, USA <sup>4</sup>Department of Cellular & Molecular Physiology, Yale University, New Haven, CT, 06510, USA <sup>5</sup>Department of Dermatology, Yale School of Medicine, New Haven, CT, 06510, USA

Nanomedicine is a rapidly growing field of research concerned with the theranostic application of nanoscale, often particulate, materials to a range of pathologies from genetic conditions to vaccines to cancer. Polymer based nanoparticles (NPs) are a popular class of nanomaterial for drug delivery because of their tunability and biocompatible nature. A significant challenge to successful drug delivery via NPs is the rapid protein adsorption that occurs at the NP surface—the formation of a protein corona (PC) – which changes the properties and biological fate of the delivery vehicle and its cargo. However, other work has shown that purposeful incorporation of specific proteins at the NP surface has a favorable effect on NP uptake and targeting. In this work, we formulated NPs from poly(lactic-co-glycolic) acid (PLGA) and adsorbed single proteins to form a single protein-protein corona (SPPC). To confirm the successful and robust adsorption of our desired proteins to the NP surface, we used protein electrophoresis, concentration assays, and mass spectrometry to confirm the presence, quantity, and identity of protein in SPPC-NPs. We evaluated the stability of the NPs and SPPC-NPs in water, culture media, and human serum, finding that SPPC-NPs matched the stability of unmodified NPs in general, and outperformed them in serum. We then evaluated the uptake of our NPs *in vitro*, finding that the identity of the SPPC protein had a significant effect on the uptake in A549 cells. Our study demonstrates the important role of adsorbed proteins in NP behavior, and the potential to take advantage of this natural process through purposeful incorporation of SPPC formation, standing in contrast to previous methods which aim to reduce/eliminate the PC.

# Characterizing Paracrine Regulatory Mechanisms through Dual Stimulation of Toll-like Receptors

Kayla Samo<sup>1</sup>, Erick Salvador Rocha<sup>1</sup>, Kathryn Miller-Jensen<sup>1,2</sup>

<sup>1</sup>Department of Biomedical Engineering, Yale University, New Haven, CT 06511 <sup>2</sup>Science Technology and Research Scholar, Yale College, New Haven, CT

The innate immune system is the primary defense mechanism for humans against infection. It produces an inflammatory response and initiates the adaptive immune response. Innate immune cells initiate inflammatory processes through the activation and signaling of Pattern recognition receptors (PRRs) which identify pathogen associated molecular patterns; repeated structures commonly associated with pathogenic organisms that are perceived as foreign molecules. One important group of PRRs are Toll-like receptors (TLRs). When simulated, TLRs transmit signals through either the MyD88 and/or TRIF pathway. These signals produce an inflammatory response by forming proinflammatory cytokines. Previous research has shown that TLR signaling pathways that are activated simultaneously can result in a synergistic or an antagonistic cytokine response. Specifically, it has been observed that the dual stimulation of TLR2 (MyD88) and TLR3 (TRIF) results in a synergistic response of key proinflammatory cytokines. To further characterize TLR-mediated synergy, we used other combinations of TLRs, which included TLR2 (MyD88) with TLR7 (MyD88) and TLR3 (TRIF) with TLR7 (MyD88). We hypothesized that the dual stimulation of TLRs that activate two different signaling pathways will result in synergistic cytokine responses. To test this hypothesis, we cultured bone marrow-derived macrophages and conducted dual simulations using immunostimulants R848, PolyIC, and Pam3CSK. Cell supernatant was collected at time points 2, 4, 8, 12, and 24 hours after stimulation. We conducted enzyme-linked immunosorbent assays (ELISA) to measure the production of cytokines TNF, IL-6, CXCL10, IFN $\beta$  and determine if dual stimulation elicited synergetic responses in comparison to the respective single stimulations and their expected additive response. The results showed that synergistic cytokine production occurred after stimulation with R848 and PolyIC, suggesting that signal transmission occurring through both the MyD88 and TRIF pathways result in synergistic responses. These results inform how infections, which activate multiple signaling pathways, affect inflammatory responses. It also demonstrates how drugs that activate the necessary signaling pathways can potentially have a therapeutic effect.

# Examining the Impact of Chromatin Status on Telomere Homologous Recombination

Tori Sodeinde<sup>1,2</sup>, Rekha Rai<sup>2</sup>, Sandy Chang<sup>2,3</sup>

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<sup>3</sup>Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT 06511

Telomeres are nucleoprotein structures at the ends of eukaryotic chromosomes. They are composed of DNA tandem repeats and an associated protein complex termed shelterin, which forms a protective coating on telomere DNA. Without shelterin's protection, cellular DNA damage-sensing machinery would recognize telomere ends as broken DNA, resulting in aberrant DNA repair and chromosome fusions. Previous research in our lab has shown that two shelterin proteins, telomeric repeat-binding factor 2 (TRF2) and repressor-activator protein 1 (RAP1), cooperate to prevent chromosome fusions mediated by homology-directed repair (HDR). When TRF2's basic domain (TRF2<sup>b</sup>) and RAP1 are both deleted, telomeres aberrantly engage in HDR, leading to clustering of multiple telomeres into structures termed ultrabright telomeres (UTs). We aimed to understand the mechanism of TRF2<sup>b</sup> and RAP1's protective roles against telomere HDR. We found that when TRF2<sup>b</sup> is genetically deleted, the heterochromatin-promoting chromatin modifier ATRX is recruited to telomeres, and no HDR occurs. However, when RAP1 is deleted in combination with TRF2<sup>b</sup>, ATRX is no longer recruited to telomeres and high levels of HDR occur. Thus, we hypothesized that RAP1 promotes recruitment of ATRX to telomeres to protect against aberrant telomere HDR. Using immunofluorescence microscopy and ATAC-seq, we found that ATRX knockout increases telomere HDR and chromatin accessibility. However, we also found that RAP1 and ATRX do not interact directly, so the mechanism by which RAP1 modulates ATRX recruitment to telomeres remains to be elucidated. To date, no chromatin-modifying role has been discovered for mammalian shelterin proteins, so our findings imply a novel mechanism of telomere-mediated genome protection and advance our understanding of the many ways in which shelterin safeguards telomeres and genome stability.

# Defining The Role of Persistent DNA Bridges in cGAS-STING Activation by PARP Inhibitor Treatment

Isabelle Staco<sup>1,2</sup>, Ece Koçak<sup>2</sup>, Megan King<sup>2,3</sup>

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<sup>2</sup>Department of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, CT 06511 <sup>3</sup>Department of Cell Biology, Yale University, New Haven, CT 06511

Breast and ovarian cancer are the second and fifth leading cause of cancer death for women in the United States, with individuals who are BRCA1 or BRCA2 mutation germline carriers having an increased risk. Deficiencies in homologous recombination (HR) caused by pathogenic BRCA1 and BRCA2 mutations generate genomic instability contributing to tumorigenesis and breast and ovarian cancers. As these mutations also confer an HR defect, they also generate hypersensitivity to Poly(ADP-ribose) polymerase (PARP) inhibitors (PARPi). PARPi, small molecules that bind and inhibit the activity of PARP enzymes, have been demonstrated in the clinic to be a promising treatment to target tumor cells in HR-deficient cancers. However, the mechanism by which PARPi induces cytotoxicity is poorly understood. Preliminary studies from our group suggest that surveillance of mitotic errors by the cGAS-STING innate immune sensing pathway plays a role in the PARPi response. We use BRCA1-deficient and BRCA1-complemented ovarian cancer cells to analyze how cGAS-STING activation is achieved at PARPi-induced persistent DNA bridges in BRCA1-deficient cells. Immunofluorescence of IRF3, a downstream target of cGAS-STING, showed that PARPi treatment modulates IRF3 translocation in a BRCA1-dependent manner. Furthermore, RT-qPCR analysis of interferon-stimulated cytokines revealed that PARPi treatment elevates cytokine expression and depletes with BRCA1 complementation. Surprisingly, inhibition of cGAS and STING activity reduces micronuclei and bridge formation in BRCA1-deficient and complemented cells. Future directions include further investigation of cGAS-STING activation through RNA-FISH to measure change in cytokine mRNA expression and fluorescent STING-IRF3 biosensors. The findings of this project will contribute to designing robust diagnostic tools used in the clinic to help better match PARPi treatment to patients and could help provide a rationale for ongoing attempts in the clinic to combine PARPi with immunotherapies.

Upon graduating in May 2025 with a Bachelor of Science in Molecular, Cellular, and Developmental Biology, Isabelle plans to pursue a two-year post-baccalaureate fellowship at the National Institute of Arthritis and Musculoskeletal and Skin Diseases within the NIH as she prepares for MD-PhD applications.

## **Measurement free quantum error correction with superconducting circuits**

Q. Rumman Rahman<sup>1,2</sup>, S.M. Girvin<sup>2</sup>, D.K. Weiss<sup>2</sup>

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The realization of a large-scale quantum computer necessitates error correction mechanisms in the physical medium. Traditional quantum error correction (QEC) protocols rely on measurements followed by feed-forward control. However, these face challenges such as measurement-induced errors and the overhead imposed by real-time classical feedback. Recently, Krastanov and coauthors proposed an all unitary, measurement-free QEC protocol for photonic qubits. Here, we present a modified version of their strategy in a circuit quantum electrodynamics (cQED) architecture. Our system consists of three microwave cavities coupled via Josephson-junction-based nonlinear elements, with auxiliary transmons enabling control and readout. Through numerical simulations, we demonstrate that our protocol can correct single-photon loss in a binomially encoded logical qubit with a fidelity exceeding 0.99. Furthermore, we show that by choosing an optimal waiting time between repeated applications of the protocol, the lifetime of the logical encoding can be extended to twice that of the cavity, surpassing the break-even point for QEC. Our work highlights the potential of gate-based, measurement-free QEC for fault-tolerant quantum computing.

Postgraduation plan: I am very excited to join the quantum science and engineering department at Princeton University for a PhD. My interests are in quantum computing hardware with superconducting circuits.

# Untethered Shape Change in Real World Deployment

Esteban Figueroa <sup>1,2</sup>, Jiefeng Sun <sup>3</sup>, Luis Ramirez <sup>4</sup>, Billy Yang <sup>4</sup>, Brandon Lin <sup>4</sup>, Rebecca Kramer Bottiglio <sup>4</sup>

<sup>1</sup>Science, Technology, and Research Scholar, Yale University

<sup>2</sup>Department of Electrical and Computer Engineering, Yale University

<sup>3</sup>School for Engineering of Matter, Transport and Energy, Arizona State University <sup>4</sup>Department of Mechanical Engineering and Materials Science, Yale University

Pneumatic-enabled shape-changing robots have demonstrated efficient locomotion in real world environments. Field-deployable robots require robust, low energy, and adaptable hardware in order to be viable; however, previous shape changing or locomoting systems are often tethered to air compressors and valves for actuation. Here we present an untethered solution for pneumatic-based shape-change systems which address the requirements for deployable robots, a Pneumatic Control Unit (PCU). The PCU employs the use of a single miniature pump and four valves to allow for a variety of configurations corresponding to positive and negative pressure actuation and stiffness change. Quantifying the effectiveness of the system involved measuring the power consumption, actuation time, and positive and negative pressure values achieved by our PCU. This has allowed us to measure the cost of morphing and time taken to perform various functions such as inflation, deflation, jamming, and unjamming. We found that the PCU is a viable untethered solution for pneumatically actuated systems, despite morphing sequences taking more time than tethered solutions, the PCU still performs as well in terms of actuation pressure. We are able to eliminate external air compressors for pouch-based pneumatic actuation, which all consume more energy than the PCU. This system opens the door to untethered solutions for field

# Elucidating the Independent Roles of *tbx16* and *msgn1* in Presomitic Mesoderm Differentiation

Kayleigh Hackett<sup>1,2</sup>, Guoyu Zhu<sup>2</sup>, Miriam Genuth<sup>2</sup>, Scott Holley<sup>2</sup>

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<sup>2</sup>Department of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, CT 06511

Throughout development, the same gene regulatory networks (GRNs) can produce a wide range of phenotypes using only a small set of genes, achieving a variety of outcomes in different contexts. Although GRN function is key to understanding development, it is challenging to investigate exactly how they work, due to issues of pleiotropy and redundancy amongst genes.

Vertebrate body axis elongation involves a series of complex pathways incorporating tissue patterning, cellular differentiation, and tissue morphogenesis, tightly regulated by GRNs. The early embryonic tailbud contains bipotential neuromesodermal progenitor cells, which migrate within the tailbud and differentiate into mesodermal cells. These then move into the presomitic mesoderm and give rise to the somites that build the spine.

*Msgn1* and *tbx16* are two well-characterized transcription factors that are critical for the differentiation of mesodermal progenitors. The phenotype produced in *tbx16;msgn1* double and single mutants, the latter of which are less severe, is well documented; however, the mechanisms driving their activities in spinal column development have remained largely unclear due to their semi-redundant activity. This genetic system allows us to study how specific transcription factors differentially regulate downstream GRNs and dynamic morphogenetic processes. We use the heat-shock promoter to drive overexpression of *tbx16* and *msgn1* to investigate how they control mesodermal differentiation and tissue migration during spinal column development. More broadly, this will give insight into how GRNs are regulated throughout development, as well as a better understanding of the dynamics of spinal column development, with far-reaching implications for human health and medicine.

# Functional Effects of HOX Gene Overexpression in Leukemia Cells

Joanna Chen<sup>1</sup>, Vadim Kurbatov<sup>2,3,4</sup>, Xujun Wang<sup>3</sup>, Jun Lu<sup>3,4,5</sup>

<sup>1</sup>Science, Technology, and Research Scholar, Yale College, New Haven, CT 06520, USA <sup>2</sup>Department of Surgery, Yale University School of Medicine, New Haven, CT, USA <sup>3</sup>Department of Genetics and Yale Stem Cell Center, Yale University School of Medicine, New Haven, CT 06520, USA

<sup>4</sup>Yale Cancer Center, Yale University, New Haven, Connecticut 06520, USA <sup>5</sup>Yale Cooperative Center of Excellence in Hematology, New Haven, CT, USA.

HOX transcription factors play crucial roles in embryonic development by establishing cellular identity and positioning along the anterior-posterior body axis. Accumulating evidence supports that the dysregulated expression of HOX transcription factors is involved in cancer biology; however, it is unclear whether there could be a unifying model on how the expression patterns of HOX genes impact human cancers. Preliminary data from the Lu Lab observed that solid tumors frequently adopt a HOX expression pattern associated with posterior normal tissues, with higher-grade malignancies showing stronger posterior HOX signatures. Interestingly, acute myeloid leukemia (AML) represents an exception to this pattern, displaying HOX expressions more analogous to mid-body tissues. This observation prompted an interrogation on the different functionality of HOX genes within solid-state tumors and liquid tumors.

To uncover this relationship, my project aims to functionally assess the consequences of HOX gene dysregulation in leukemia cells through CRISPRa-mediated gain-of-function experiments. Using the cell lines of MOLM 13, HL-60, and K562, all myeloid leukemia cell lines, I systematically overexpress posterior HOX genes to test the hypothesis that improper expression of posterior HOX patterns increases malignant tendencies in solid-state tumors but is deadly to leukemia cells. Information on cell viability and proliferation rates is obtained through a competition assay and analyzed through next-generation sequencing. Resulting findings will help advance the understanding of why leukemia cells represent an anomaly to the common posterior HOX patterning observed in malignant solid-state tumor cells and reveal new insights into cancer development and potential prognostic and therapeutic approaches.

## **Contribution of early life stress in inducing Tourette syndrome-relevant pathology**

Ignacio Ruiz-Sanchez<sup>1,2,3</sup>, Cheng Jiang<sup>2,3</sup>, Christopher Pittenger<sup>2,3</sup>

<sup>1</sup>Science Technology and Research Scholar Class of 2025, Yale College, New Haven, CT <sup>2</sup>Department of Psychiatry, Yale School of Medicine, Yale University, New Haven, CT 06511 <sup>3</sup>Connecticut Mental Health Center, Yale University, New Haven, CT 06511

Tourette's syndrome (TS) and other tic-like disorders are a group of neurodevelopmental disorders characterized by motor and vocal tics with a characteristic developmental trajectory. TS symptoms usually arise through interactions of genetic and environmental influences over the course of development and markedly occur more prevalently in males. Clinical studies have identified early psychological and physical stress, which can be modeled in preclinical research using an early life stress (ELS) paradigm, as significant risk factors for the onset of TS and other tic disorders. We applied this ELS paradigm to mice, and hypothesized that ELS can induce behavioral, cellular, and molecular phenotypes relevant to TS. We have observed that ELS increases grooming time and tic-like head-body twitching in adolescent male mice, but not in adolescent females, and adult mice of either sex, reminiscent of the male preponderance and developmental trajectory in human TS. Stressed mice also show a reduction in the number of critical interneurons involved in regulating acetylcholine in the striatum, a structure involved in higher neurological processing and motor control. Similarly, we find significant male-specific neuroinflammation in the dorsal striatum of adolescent mice and increased activity in cortical neurons that project to the dorsal striatum in stressed mice, again replicating what have been reported in human TS. Under this framework, our future studies will further examine the neurobiological mechanisms underlying sexual dimorphism of ELS-induced onset of TS-relevant phenotypes, potentially benefiting the development of sex-specific intervention and prevention strategies.

## Deciphering the Regulation of Pro-fibrotic Signaling by Mechanotransduction through Sun2-containing-LINC Complexes

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Cellular communication relies extensively on mechanical signaling pathways, with the Linker of Nucleoskeleton and Cytoskeleton (LINC) complex—spanning the nuclear envelope—serving as a direct conduit for transmitting mechanical cues into the nucleus. SUN2, a core component of the LINC complex, has emerged as a key player in mediating fibrosis. Deletion of *Sun2* in murine models has demonstrated protection against bleomycin induced lung fibrosis, including decreased expression of TGF- $\beta$  target genes. TGF- $\beta$  signaling is a central driver of fibrosis, promoting fibroblast activation and extracellular matrix deposition. Surprisingly, our preliminary data suggest that the TGF- $\beta$  signaling pathway remains activated in *Sun2*-null cells, indicating that SUN2 may regulate TGF- $\beta$ -dependent gene expression downstream of canonical signaling events. To elucidate the transcriptional mechanisms through which SUN2 influences TGF- $\beta$  responses, we aim to dissect stiffness- and TGF- $\beta$ -dependent transcriptional responses in SUN2-deficient and wild-type murine lung fibroblasts using RNA and ATAC-sequencing. By modeling healthy and fibrotic lung, and in the presence or absence of exogenous TGF- $\beta$ , we will examine how substrate mechanics and TGF- $\beta$  exposure synergistically or independently modulate transcriptional programs in the context of SUN2 loss. This approach will allow us to determine whether SUN2 is required for the chromatin accessibility and transcriptional activation of TGF- $\beta$  target genes under fibrotic conditions. RNA-sequencing of wild-type murine lung fibroblasts identified *Vgll4*, *Rnd3*, and *Fgf18* as stiffness- and TGF- $\beta$ -independent genes. To determine whether SUN2 regulates these genes at the chromatin level, we performed ATAC-seq on matched conditions and have submitted samples for sequencing. We expect ATAC-seq to reveal more sensitive and upstream changes in chromatin accessibility, as chromatin remodeling often precedes transcriptional activation. These data will clarify whether SUN2 facilitates accessibility at mechanoresponsive, pro-fibrotic loci. Future studies will extend these findings to assess nuclear organization of SUN2-regulated genes via fluorescence in situ hybridization. This integrated analysis of mechanical and biochemical cues in fibrosis will deepen our understanding of LINC complex-mediated nuclear mechanotransduction and reveal novel regulatory nodes in the fibrotic gene program.

I will be working as a post-graduate researcher at the Stanford Cardiovascular Institute for two years in preparation for a career as a physician-scientist. During this time, I'll focus on research at the intersection of genomics and cardiovascular disease.

# Studying the Effect of Steric and Non-Steric Interactions on fPGK and VlsE in Live Zebrafish

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In the cellular environment, biomolecules bounce, stick, crowd, and chemically interact with one another. The stability, dynamics, and function of biomolecules are modulated by the tug of war between these steric crowding and non-steric chemical interactions. Variations in the balance of these interactions regulate biomolecular activity in different cell types, as different cell types contain different extents of crowding and different chemical compositions. This informs a need for studying biomolecules in their native cell environments. Two main proteins have been used in the literature to study the interaction between steric and non-steric interactions. The protein phosphoglycerate kinase (PGK) has been shown in *in-vitro* and in *in-vivo* cell studies, to be stabilized by increasingly crowded cellular environments. In contrast, the protein variable major protein-like sequence, expressed (VlsE) shows destabilization in cells. *In-vitro* studies using both inert molecular crowding mimics and reagents that mimic non-specific chemical interactions show that VlsE's stability cannot simply be modeled with steric or non-steric interactions individually. Understanding the native stability of proteins thus necessitates an understanding of the balance between steric and non-steric interactions. Various methods have been utilized to study the stability and dynamics of proteins in different local environments. Among them, FReI (fast relaxation imaging) permits measurements of stability and folding kinetics with temporal and spatial resolution in living cells. One current method of studying biomolecules in different differentiated tissue of live zebrafish employs meganuclease-mediated transformation coupled to FReI microscopy. Better understanding of how interactions vary across differentiated cell types is necessary for more accurate study of the native stability and dynamics of biomolecules.

# Proteomics in the Medial Prefrontal Cortex of Mice Following Learned Helplessness

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Major depressive disorder (MDD) affects around 8.4% of the US population. While most pharmacotherapies work by modulating monoaminergic or glutamatergic systems, none are effective for all patients, suggesting MDD has multiple etiologies. It is therefore necessary to investigate alternative systems contributing to MDD, such as the acetylcholine (ACh) system. ACh levels in the medial prefrontal cortex (mPFC) of mice increase in response to inescapable shock in the learned helplessness model. To discover the mechanisms involved in these cholinergic increases, we conducted proteomics on the mPFC of mice that went through learned helplessness to determine how inescapable shock alters the ACh-related proteome. Our analysis revealed differences in the concentration of 4 ACh receptors, with notable sex differences also apparent. We also identified alterations to the ACh Receptor and Synaptogenesis Signaling Pathways. Overall, this study further implicates mPFC ACh signaling and synaptic alterations in learned helplessness. This research may unveil potential biomarkers for MDD or targets for new pharmacotherapies. Future studies will assess the proteomes of mice resilient or susceptible to the stress of inescapable shock, which will increase our understanding of the individual differences that lead some to develop MDD following stressful life experiences.

# Characterizing the Function of *V. cholerae* Biofilm Matrix Components in Protozoan Grazing Resistance

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In its natural environment, *Vibrio cholerae*, the causative agent in the diarrheal disease cholera, persists often in biofilm form. Biofilm structures arise in response to environmental stressors, strengthening resistance to chemical and physical disturbances. In particular, biofilms deter grazing by protozoa, allowing *V. cholerae* colonies to resist predation and survive during inter-epidemic periods. While the protective nature of fully-formed biofilms is apparent, the role of its constituent elements in generating this mechanism of defense remains largely unknown. Therefore, characterizing the function of biofilm matrix components in the context of predation resistance will elucidate further functionalities of this lifestyle employed by numerous bacterial species. To this end, we break down the *V. cholerae* biofilm into its main structural components, namely the matrix proteins RbmA, RbmC, and Bap1, as well as the exopolysaccharide VPS to investigate the necessity of each matrix component in forming a robust deterrence to predation. Through coinubation experiments of the protist *Tetrahymena pyriformis* with *V. cholerae* mutants with various knockouts of biofilm-matrix components, we measured protist growth rates as a proxy for the efficacy of predation resistance. We found that the presence of matrix protein RbmA limits the efficacy of protozoan grazing. Furthermore, our data suggest that the distribution of matrix components and the quality of the matrix play an important role in determining the defensive capabilities of a biofilm. For rugose strains, the medium-density biofilm provided the greatest degree of protection against protozoan predation, indicating an optimal biofilm growth pattern that maximizes predation defense.

## **Investigation of NonO Interactions with HIV-2 Capsid**

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Human immunodeficiency virus type 2 (HIV-2) is a retrovirus that, if left untreated, proceeds to acquired immunodeficiency syndrome (AIDS) and death. HIV-2 affects millions of people worldwide, yet it has been understudied compared to HIV-1. While HIV-2 is less transmissible and progresses slower than HIV-1, the viruses share important characteristics like their viral life cycle. A key part of HIV's successful infection is the viral capsid (CA) protein's interactions with cofactors and restriction factors that promote or inhibit HIV infection, respectively. NonO is a known restriction factor of HIV-2 that is thought to interact with HIV-2 CA in the nucleus. NonO reduces infectivity of HIV-2, but it does not well restrict HIV-1. Current data indicates this may be due to differential binding between NonO and HIV CA proteins. Our objective is to gain a mechanistic understanding of NonO's interactions with HIV-2 CA lattice by elucidating the structure via cryo-electron microscopy (cryo-EM) and biochemical assays. We have purified to homogeneity a NonO construct (35-312) containing relevant domains that interact with HIV-2 CA. We aim to validate that NonO binds preferentially to HIV-2 CA compared to HIV-1 CA. We have identified biophysical characteristics of the interaction. Initial negative stain and cryo-EM imaging of the complex revealed that the capsid lattice is maintained in presence of NonO. Optimization of freezing conditions will be performed to obtain a high-resolution structure. We intend to generate an atomic model of the interaction, which would reveal details of HIV-2 biology and provide information about HIV-1 restriction escape.

# Examining the Impact of Environmental Toxicants on Autism Spectrum Disorder

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Autism Spectrum Disorder (ASD) is an early-onset neurodevelopmental disorder characterized by impairments in social interaction, communication, and repetitive patterns of behavior. ASD affects approximately 1% of the global population, with a 4:1 male-to-female ratio, and its prevalence has markedly increased. While changes in diagnostic criteria account for much of this increase, a significant proportion remains unexplained. ASD is a highly heterogeneous and multifactorial disorder influenced by a complex interplay of genetic, epigenetic, and environmental factors. Although over 100 genes are associated with ASD risk, genetic mutations alone do not guarantee its onset. Environmental factors influence ASD risk and severity, yet the precise mechanisms underlying gene-environment interactions are poorly defined. Environmental toxicants such as lead, bisphenol A (BPA), and phthalates (DEHP) have been implicated in neurodevelopmental disorders. To investigate the effect of these toxicants on biological pathways in a relevant disorder cell type, we exposed human induced pluripotent stem cell (iPSC)-derived neural progenitor cells (NPCs) to various concentrations of lead, BPA, and DEHP for 5 days and performed bulk RNA sequencing. Lead exhibited the highest number of Differentially Expressed Genes (DEGs), many linked to reactive oxygen species (ROS) response and ASD. To validate our transcriptomic findings, we conducted a time-course experiment on NPCs, measuring ROS levels after different concentrations of lead exposure. A dose-dependent effect emerged after 5 days of treatment, reflecting the dose-dependent effect on ROS response observed in bulk RNA-seq. Parallel assessments of apoptosis events and cell counts revealed a dose-dependent increase in apoptosis at 72 hours, which became more pronounced after 5 days, aligning with decreased cell proliferation. These findings reveal shared altered pathways between lead exposure and ASD. In follow-up experiments, we will test lead exposure in combination with ASD-associated genetic variants using CRISPR and Massively Parallel Reporter Assays (MPRA) to further investigate gene-environment interactions in ASD.

# **Charge Transport Properties of the Electron Hole Material Copper-Thiocyanate (CuSCN) in Thin-Film Photovoltaic Cells (PVC)**

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Among renewable energy sources, photovoltaic solar cells have been one of the most promising alternatives to fossil fuels for their relatively cheap manufacturing cost and high power conversion efficiency. However, there remains energy inefficiencies within certain device components. The HTL is one of the main bottlenecks in improving device performance, meaning improvement of these materials is crucial for increasing PVC efficiency. Emergent thin-film photovoltaics, such as perovskite solar cells, have garnered significant attention in energy research due to rapid and significant advancements in power conversion efficiency. A particular material of interest for the HTL of these devices has been Copper-Thiocyanate (CuSCN). Research on CuSCN has indicated massive potential for its use as the HTL, as it is relatively low-cost and highly stable. In this work, we optimize the energy efficiency of CuSCN via research into its charge transport mechanism. Our results demonstrate a thorough understanding of the underlying material properties and its potential as a HTL.

# Class of 2026 Abstracts

## **Investigating the Roles of ECM in Small Intestinal Crypt Morphogenesis**

Nicole Ahsan<sup>1,2</sup>, Jessie Wang<sup>2</sup>, Kaelyn Sumigray<sup>2</sup>

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The epithelium of the mammalian small intestine has a rapid turnover rate that is regulated by intestinal stem cells (ISCs). ISCs are located at the bottom of crypts which are glandular invaginations found on the luminal surface of the small intestine. Crypts are located around the base of villi, the finger-like projections that maximize absorptive area of the gut. While villi form embryonically in mice, the intervillous regions begin to invaginate postnatally from postnatal day 0 (P0), leading to the development of crypts. This process is followed by the formation of hinges at the crypt-villus boundary at P5, which contributes to the maturation of the crypt structure and the compartmentalization of crypts from villi. Within the crypts, ISCs reside in a niche composed of various mesenchymal cells and extracellular matrix (ECM), which helps with self-renewal and differentiation of the stem cells. These two processes are regulated by niche signaling pathways including Wnt, BMP, and Notch. While there are many studies that highlight how the niche supports ISCs in adult small intestine, there is minimal information on how it supports and regulates crypt morphogenesis during early postnatal development of the small intestine. The ECM provides structural support and external stimuli to regulate stem cell behavior and fate, potentially influencing the mechanisms controlling crypt invagination. Our lab's preliminary data has shown defects in crypt invagination after ablating fibroblasts postnatally. I hypothesize that ECM remodeling is essential to crypt morphogenesis during postnatal development. The objective of this project is to study how the ECM functions physically and cellularly across developmental timepoints to support the stem cell niche. Developing an understanding of the ECM can provide basis for studying role of ECM proteins in regulating signaling events which could be helpful in treating diseases where the ECM is disrupted such as cancer and many genetic disorders including Marfan syndrome.

# **Toward defect density characterization of single-crystal Ni-based superalloys CMSX-4 & PWA-1480**

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Single-crystal superalloys like CMSX-4 and PWA-1480 are of particular interest in specialized fields like aerospace and jet engine manufacturing because they exhibit heightened material properties that are ideal for high-precision, extreme environments, in part because of the uniformity in their crystal structures and composition. Because of this, we are interested in understanding and characterizing the defect density of these materials. Understanding the defect condition during the manufacturing of these alloys is essential for tailoring their mechanical properties to meet specific performance requirements, while also preserving certain properties like ductility in the material. Traditional methods of characterizing defect density, such as transmission electron microscopy, are typically slow and costly, so we seek to improve upon these established methods. The methodology developed in this project utilizes nanoindentation and dynamic mechanical analysis techniques to statistically quantify the local condition of defects present to optimize the mechanical properties of the superalloys during processing. Nanoindentation tests have been run with a variety of spherical tip sizes for CMSX-4 and PWA 1480, revealing consistent trends in pop-in behavior that correlate with underlying defect distributions. Dynamic mechanical analysis tests in torsion and in bending are also underway with the goal of bolstering defect density calculations with bulk mechanical insight, which will be used in conjunction with the data from the nanoindentors to provide concrete density values.

# Investigating the Role of ATR in Chromatin Compaction and Genome Stability

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Concerns about chromosomal instability (CIN) in cancer have highlighted the need to understand molecular mechanisms that maintain genome stability. ATR (Ataxia telangiectasia and Rad3-related) kinase is a key regulator of genome integrity, primarily known for its role in the DNA damage response. However, recent findings suggest ATR also plays a role in mitotic chromosome segregation. In this study, we investigated ATR's function in chromatin compaction by examining its relationship with Topoisomerase II $\alpha$  (TOP2A), an enzyme essential for chromosome organization. Phosphoproteomic analysis of ATR-inhibited mitotic cells revealed changes in TOP2A phosphorylation, leading us to hypothesize that ATR regulates chromosome compaction via modulation of TOP2A activity.

To test our hypothesis, we examined chromosome compaction and ATR-TOP2A interactions in U2OS cells treated with ATR and/or TOP2A inhibitors. Chromosome spreads were used to quantify changes in compaction, and western blotting was performed to analyze Aurora B activity, a known downstream substrate of ATR. Our analysis revealed that inhibition of ATR, TOP2A, or both led to decreased chromosome compaction.

Our results indicate ATR regulates chromatin compaction in addition to its known function in chromosome segregation and further research is needed to elucidate the precise mechanisms by which ATR maintains mitotic genome stability, with potential implications for developing targeted cancer treatments.

# Characterizing Immune-Related Regulatory Variation in Positively-Selected Loci Across Diverse Populations

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Natural selection and environment-specific selection pressures across ancient human populations have contributed to present-day ancestry-specific variation in disease risk, a process known as local adaptation. The increasing availability of ancient genomes enables the identification of regions of the genome previously under selection by performing genome-wide scans to directly analyze changes in allele frequency. However, distinguishing functional alleles from non-functional ones at these loci remains challenging, especially since adaptive loci are enriched in regulatory elements and often act distally or through transcription factors. Using existing epigenomic annotations, I can filter derived alleles from ancient European populations to find the single-nucleotide polymorphisms (SNPs) most likely to be responsible for the adaptive phenotype. I will then utilize CRISPR-Cas9 HDR editing for allelic replacement in the T-cell-derived Jurkat cell line, and conduct functional assays such as qPCR and antibody probes to investigate how these variants affect gene expression and signaling pathways in immune cells. By identifying the mechanisms by which these candidate causal alleles act, I will generate empirical data to test the long-standing evolutionary hypothesis that ancient selection against pathogens is associated with hyper-immune activation and modern autoimmune diseases.

## Testing HALO Brain-Computer Interface Chip

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Brain-computer interfaces (BCIs) offer the potential to transform medicine and neurotechnology by establishing direct communication between the brain and external devices. However, BCI systems face challenges in achieving high-speed, low-power performance suitable for implantation. This project investigates the HALO (Hardware-Software Architecture for Low-Power BCIs) chip, a novel BCI accelerator designed for energy-efficient neural signal processing. We focused on verifying HALO's hardware functionality by integrating it with the Ibex RISC-V processor and testing data flow between modules using a cyny-p2p handshake protocol. Testbench files were developed to ensure timing and output correctness. The interface enables seamless integration between HALO and general-purpose processors, maintaining data reliability. Timing diagram analyses confirmed correct handshaking and data transfer operations. Future directions include quantifying energy use and processing latency for neural signals, as well as taping out a second chip revision with enhanced functionality and efficiency. This work supports the goal of developing implantable, real-time BCI systems optimized for clinical and research applications.

# Investigating the Antagonistic Role of the Serotonin Receptor SER-7 in Microbial Modulation of *C. elegans* Feeding Behavior

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Feeding behavior in *Caenorhabditis elegans* is regulated by a conserved serotonergic pathway, providing a powerful system to study gut-brain interactions. Serotonin, synthesized by *tph-1* and *pah-1*, modulates pharyngeal pumping through multiple receptors, including SER-7, a 5-HT7 orthologue. Surprisingly, our lab found that in serotonin-deficient mutants (*tph-1*; *pah-1*), removal of *ser-7* restores normal pharyngeal pumping. This suggests that in the absence of serotonin, SER-7 may exert basal inhibitory activity, potentially influenced by host or microbial-derived inverse agonists. To explore this, we are employing genetic crosses with fluorescent PharaGlow worms to recover marked single, double, and triple mutants for genotype-specific behavioral assays. We are currently validating these strains by PCR and visually confirming fluorescent integration. In parallel, we are conducting molecular docking analyses comparing serotonin and known inverse agonists (e.g., methiothepin, SB-269970) at the SER-7 binding site. To further understand receptor modulation, we are developing a high-throughput assay using PharaGlow to quantify feeding across strains exposed to microbial candidates. These experiments will allow us to identify compounds or microbes that modulate SER-7 signaling and clarify its antagonistic role in the absence of serotonin. Overall, this work aims to dissect how microbial signals shape neuromodulation and feeding behavior through the gut-brain axis.

# Investigating the Roles of ECM in Small Intestinal Crypt Morphogenesis

Nicole Ahsan<sup>1,2</sup>, Jessie Wang<sup>2</sup>, Kaelyn Sumigray<sup>2</sup>

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The epithelium of the mammalian small intestine has a rapid turnover rate that is regulated by intestinal stem cells (ISCs). ISCs are located at the bottom of crypts which are glandular invaginations found on the luminal surface of the small intestine. Crypts are located around the base of villi, the finger-like projections that maximize absorptive area of the gut. While villi form embryonically in mice, the intervillous regions begin to invaginate postnatally from postnatal day 0 (P0), leading to the development of crypts. This process is followed by the formation of hinges at the crypt-villus boundary at P5, which contributes to the maturation of the crypt structure and the compartmentalization of crypts from villi. Within the crypts, ISCs reside in a niche composed of various mesenchymal cells and extracellular matrix (ECM), which helps with self-renewal and differentiation of the stem cells. These two processes are regulated by niche signaling pathways including Wnt, BMP, and Notch. While there are many studies that highlight how the niche supports ISCs in adult small intestine, there is minimal information on how it supports and regulates crypt morphogenesis during early postnatal development of the small intestine. The ECM provides structural support and external stimuli to regulate stem cell behavior and fate, potentially influencing the mechanisms controlling crypt invagination. Our lab's preliminary data has shown defects in crypt invagination after ablating fibroblasts postnatally. I hypothesize that ECM remodeling is essential to crypt morphogenesis during postnatal development. The objective of this project is to study how the ECM functions physically and cellularly across developmental timepoints to support the stem cell niche. Developing an understanding of the ECM can provide basis for studying role of ECM proteins in regulating signaling events which could be helpful in treating diseases where the ECM is disrupted such as cancer and many genetic disorders including Marfan syndrome.

# Assessing Methicillin-Susceptible *Staphylococcus aureus* Transmission in the NNICU using Whole Genome Sequencing and Environmental Surveillance

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*Staphylococcus aureus* (*S. aureus*) is a bacteria that commonly colonizes the human nasal cavity, skin, and gastrointestinal tract, representing a leading cause of infection in premature neonates due to their immunologic immaturity and compromised skin barriers. Methicillin Susceptible *S. aureus* (MSSA) infection remains a significant cause of increased morbidity, mortality, and prolonged hospital stays for neonates. While hospital screening programs typically focus on Methicillin-resistant *S. aureus* (MRSA), they often omit MSSA. Despite quality improvement interventions at Yale's Neonatal Intensive Care Unit (NICU), MSSA rates have remained a persistent phenomenon. This study aimed to assess MSSA acquisition pathways among neonatal patients and evaluate how MSSA surveillance and environmental culturing coupled with whole genome sequencing (WGS) can inform targeted interventions to reduce MSSA colonization and infection rates. This study employed a multi-modal surveillance approach in a 64-bed level IV NICU from July 2020 to December 2024, including weekly MSSA screening of all infants, hand hygiene and environmental cleaning monitoring, environmental cultures of high-touch surfaces, and whole genome sequencing (WGS) of clinical and environmental MSSA isolates. Results demonstrated no significant correlation between new MSSA colonization rates and invasive infection rates or process measures. However, WGS analysis revealed both endemic MSSA strains and multiple independent strain introductions. Patient transfers were identified as a likely contributor to MSSA spread throughout the unit and between floors. Environmental sampling identified contamination of high-touch surfaces in patient rooms and nursing stations. This study highlights the value of combining environmental surveillance with WGS for understanding MSSA transmission patterns and informing targeted interventions in the NICU setting, despite limitations in sampling and sequencing comprehensiveness.

# Investigating How Genetic Variation in Malaria Vaccine Candidate PfRh5 Alters Immune Evasion

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Malaria is a leading cause of death globally, particularly affecting children and pregnant women in sub-Saharan Africa. Although treated with antimalarial drugs and prevented by insecticide-treated nets (ITNs), drug resistance has stalled malaria control efforts. Vaccine development offers another strategy, with sporozoite-stage vaccines like RTS,S and R21 showing promise, but their efficacy is challenged by the parasite's complex life cycle and genetic diversity, highlighting the need for a next-generation vaccine. The Rh5 protein in *P. falciparum* (PfRh5) is a promising target for a blood-stage vaccine due to its conservation, essential role, and antibody susceptibility. A recent phase 2b trial showed that the Rh5.1 vaccine had the highest efficacy of any blood-stage vaccine, but the impact of genetic variations in Rh5 on immune evasion is unclear. We propose to study the effect of three prevalent single-nucleotide polymorphisms (SNPs) in PfRh5—D243N, D249G, and F505Y—found in endemic regions of Senegal, on immune response, invasion, and antibody binding. To this end, I first aim to assess the functional roles of PfRh5 variants on immune neutralization using CRISPR-Cas9 gene editing of parasites. My second aim is to biochemically characterize the interaction of PfRh5 variants with host receptor, BSG using surface plasmon resonance. Our objective is to investigate the role of selected PfRh5 genetic variants in immune evasion both through a cellular and biochemical angle to guide the design of the next-generation malaria vaccine.

# AGGeN: Diffusion Modeling of Astronomical Data for Improving Image Search Algorithms

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Active Galactic Nuclei (AGN) are supermassive black holes surrounded by bright matter at galaxy centers. One way AGNs and their host galaxies may grow is through mergers. Star formation and other galactic properties are also thought to be triggered by these mergers. We previously developed the DRAGON tool (Data Reduced AGN and Galaxy Optical Network), a convolutional neural network (CNN) to identify these mergers at different stages allowing us to understand the rate at which they happen. However, the model's ability to identify mergers was hampered by the lack of available training data. Galaxy mergers require computationally intensive simulation to model that still may not be similar enough to real telescope data to be usable. To address this, we developed AGGeN (Astronomical Graphical Generative Network), a diffusion model for generating realistic telescope images of galaxy mergers. AGGeN is a LoRA (Low-Rank Adaptation) model built on Stable Diffusion 1.5—a general-purpose image generator already capable of producing galaxy-like images. LoRAs are lightweight models that fine-tune features within larger models like Stable Diffusion. We trained AGGeN on 11,009 g-band merger images from Galaxy Zoo imaged by the Hyper-Suprime Cam instrument on the Subaru telescope, enabling Stable Diffusion to generate realistic merger data. These synthetic images will be useful for understanding and improving the training of our DRAGON model. The method AGGeN establishes could prove to be a new and viable way to generate artificial data of rare objects, whether they're a merging galaxy or a type of cell.

# **Towards Uncovering the Fundamental Deformation Mechanisms of High Temperature Alloys**

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To reenter Earth's atmosphere, spacecraft must have materials that can withstand temperatures as high as 3000 °C and high aerodynamic stresses. To select materials for these applications, it's vital to characterize and understand the thermo-mechanical properties of aerospace-grade materials. The state-of-the-art thermal shock test system is the Arc Jet Complex operated by the NASA Ames Research Center. This facility is capable of testing large samples and simulating various flight conditions (high altitude flight, reentry, etc.), playing a key role in the design & qualification of cutting-edge materials. However, large power requirements (up to 150 MW) and long test setup times (2-3 samples/day) make the Arc Jet a costly test mechanism. The facility also cannot apply mechanical stress as experienced by aircraft due to high reentry velocities (up to 25 Mach) on the test samples while they undergo thermal shock. Accurate material characterization under faithful application conditions is essential to the design and manufacture of aerospace alloys and structures. To this end, we plan to design & build a thermo-mechanical tester to characterize the high-strain rate response of materials under thermal shock. This new system builds on the thermal shock heater built by previous Yale senior design students in the Yale Nanoprobe group, in collaboration with the NASA Ames Research Center.

# Deciphering Roles of ELF4 in the Regulation of Systemic Inflammation via Macrophages

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The immune system protects the body from both pathogens outside the body and disease-causing changes that occur within the body by distinguishing “self” from “nonself” via specialized inflammatory cells. However, it is not fully known how these inflammatory cells establish balance of the immune system. Recently, the Lucas Lab identified loss-of-function variants in the X-linked transcription factor gene ELF4 among pediatric male patients, a disorder named DEX Deficiency in ELF4, X-linked. Clinically, these patients presented symptoms including severe recurrent fevers, oral ulcers, and mucosal inflammation. Using inflammatory cells from patients and mouse models, the lab found that ELF4-mutant macrophages exhibited hyperinflammatory response in response to innate stimuli. Additionally, the lab discovered that ELF4 both sustained the expression of anti-inflammatory genes and limited the upregulation of inflammation amplifiers in mouse macrophages. Thus, ELF4 regulates the immune response and represses pathological inflammation. However, the precise molecular mechanism by which ELF4 acts in macrophages to regulate the immune response is still unknown. As I investigate the molecular interactions of ELF4, I aim to (i) optimize biochemical conditions to molecularly label ELF4 binding partners using TurboID and (ii) elucidate the role of ELF4 in the regulation of interferon signaling pathway. My findings of the mechanistic and functional characteristics of how ELF4 protects against inflammation and disease may translate more broadly for human inflammatory disorders, such as inflammatory bowel disease.

# Differential Repression of Human 5'UTR isoforms by SARS-CoV-2 Nsp1 Protein

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SARS-CoV-2's non-structural protein 1 (Nsp1) selectively inhibits host mRNA translation, but the role of 5' untranslated region (5' UTR) variation in mediating this repression remains poorly understood. This project investigates whether alternative 5' UTR isoforms confer differential sensitivity to Nsp1. We combined a high-throughput biochemical assay named direct analysis of ribosome targeting (DART) with in vitro translation assays with reporter mRNAs to test translational output in the presence and absence of Nsp1. Our findings in this specific case indicate that longer 5' UTR isoforms generally exhibit greater resistance to Nsp1-mediated translational repression compared to shorter ones, highlighting the role of UTR length and structural elements in modulating sensitivity. However, the variation in repression across isoforms also suggests that features beyond the 5' UTR—such as elements within the coding sequence—may contribute to Nsp1's inhibitory effects on translation initiation. Understanding these layered mechanisms of Nsp1 sensitivity can inform future strategies to protect host translation during viral infection.

# Investigating the Binding of Mosquito Saliva Protein AAEL002693 to Human Interleukin-18

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Blood-feeding arthropods, like mosquitos, can act as vectors by transmitting disease-causing pathogens to humans. When a mosquito takes a blood meal from a host, it injects saliva, which contains salivary factors and potential pathogens. In this scenario, multiple interactions between pathogen and host, host and vector, and vector and pathogen take place. This triangular-like system sets a basic framework from which we can investigate factors that influence disease transmission, invoke host or vector response, contribute to susceptibility or resistance, etc. By using REAP (Rapid Extracellular Antigen Profiling), we have identified mosquito salivary proteins that target human proteins; for example, binding between *Aedes aegypti* salivary factor AAEL002693 and human IL-18. Using recombinant yeast colonies that express AAEL002693, we confirmed this binding by flow cytometry. Now, we are expressing AAEL002693 in mammalian and insect cell lines to further validate this interaction by ELISA. To understand the biological relevance of this interaction, we will study the effect of the mosquito salivary 2693 factor in immune cells that are regulated by IL-18, like peripheral blood mononuclear cells (PBMCs). These potential immune response alterations may change the course of the arbovirus infections after the mosquito bite.

# Hardware-Aware Optimization of NanoGPT for Edge AI Deployment

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Transformer models like NanoGPT offer powerful language modeling capabilities, but their resource demands pose challenges for deployment on low-power, real-time systems like FPGAs. This project investigates how hardware-aware strategies can bridge that gap. We simplify the NanoGPT model architecture, identify compute bottlenecks using PyTorch profiling, and apply post-training quantization techniques to reduce memory and computational cost. Our optimized model reduced parameters by over 70% while maintaining near-baseline validation loss (~1.68 to ~1.81). This demonstrates the feasibility of deploying large language models in edge environments such as IoT and embedded NLP systems, without significant performance degradation. These findings contribute to the broader goal of enabling transformer-based AI in real-time, resource-constrained applications.

# Evaluating Large Language Models on Spatial Reasoning via Rush Hour Puzzles

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Large Language Models (LLMs) like GPT-4 have demonstrated impressive linguistic capabilities but often struggle with spatial reasoning tasks. This project evaluates LLM spatial reasoning by presenting Rush Hour puzzles, a sliding block game requiring path planning and obstacle recognition. We designed a custom text-based Rush Hour interface to minimize visual noise and assessed model performance across simple and complex board configurations. Early findings show that GPT-4 frequently failed to solve even trivial puzzles, often repeating invalid moves or stalling. We observed modest improvements through prompt engineering and moving history feedback. Future work will extend evaluation to open-source LLMs (e.g., Claude, LLaMA) and refine prompting strategies to better align LLM reasoning with spatial task demands. This work contributes to understanding the limits of current LLMs in physical reasoning environments.

# Cardiac allograft vasculopathy (CAV)

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**Background:** Cardiac allograft vasculopathy (CAV) is characterized by the formation of occlusive lesions in the arteries of a transplanted heart. These lesions are caused by arterial smooth muscle cells (SMCs) that dedifferentiate after exposure to the cytokine interferon- $\gamma$  (IFN- $\gamma$ ). Several candidate genes of interest were determined to be upregulated in a cluster of mouse SMCs that may initiate the process of allograft vasculopathy: *Nav3*, *Mast4*, *Mecom*, *Ktn1*, and *Nav2*. These novel genes have never been characterized in human coronary artery SMCs (hCASMCs). **Methods:** hCASMCs were cultured in Fetal Bovine Serum and treated with IFN- $\gamma$  for 24 hours and 48 hours. Additionally, an siRNA mediated knockdown of *Nav2* was conducted. The expression of these novel genes was then quantified using qPCR and western blotting. **Results:** The qPCR showed that *Mast4*, *Ktn1*, and *Nav2* were significantly upregulated following IFN- $\gamma$  treatment, consistent with potential roles in SMC dedifferentiation. The western blot also showed that the relative protein expression of *Ktn1* increased following IFN- $\gamma$  treatment. The *Nav2* knockdown showed inhibition of *Acta2* and *Nav2*, suggesting *Nav2* may modulate SMC phenotype. **Conclusions:** Further characterization, these genes may be targets for drug therapies to prevent CAV or serve as diagnostic markers for the progression of CAV.

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