

Houston Area Molecular Biophysics Program (HAMBp) Training Program

Grant No. T32 GM150582

Program Director: **Theodore Wensel**, PhD
Professor, Department of Biochemistry and Molecular Pharmacology
Baylor College of Medicine

<http://www.gulfcoastconsortia.org/home/training/molecular-biophysics-hambp/>

Meet the Trainees 2026-2027



Mussie Araya

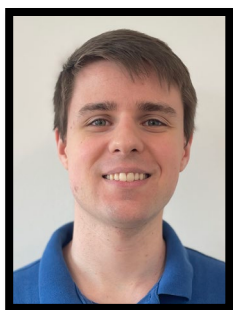
Appointed November 1, 2025 – October 31, 2026

Department of Integrative Biology and Pharmacology, University of Texas Health Science Center at Houston

Primary Mentor: Dr. Alemayehu A. Gorfe, Integrative Biology and Pharmacology (UTH)

Role of Membrane Lipid Composition in Arf1 Dynamics, Effector Engagement, and Ligand Binding

Small GTPase ADP-ribosylation factor 1 (Arf1) is a membrane-bound molecular switch of vesicle-mediated intracellular trafficking that maintains homeostasis of protein turnover in eukaryotic cells and initiates immune responses. Arf1 orchestrates the recruitment of cargo proteins and effector adapter protein type 1 (AP-1) to membranes to mediate vesicular trafficking between the Golgi and endosomes. During viral infection, viral proteins directly target the Arf1:AP-1 complex, and vesicular trafficking of defense proteins are subverted, resulting in down-regulation of the immune response. During the invasion and proliferation of many cancers, Arf1-mediated vesicle trafficking is upregulated. While membrane dynamics of many lipidated small GTPases are believed to facilitate effector engagement and cellular function as well as ligand binding, much less is known about the structural dynamics of Arf1 in its host membranes. This goal of my research is to understand and characterize the membrane dynamics of Arf1 monomer and in complex with its AP-1 in bilayers of different lipid composition, and the application of membrane dynamics to assess ligand binding properties of Arf1 monomer and in complex with effector. My approach involves development of bilayer-bound computational models of Arf1 and Arf1-AP1 complexes and conducting atomistic and coarse-grained molecular dynamics simulations to study their membrane binding, dynamics, effector interactions, and ligand binding in bilayers of complex lipid mixtures. The outcome of this proposed work will provide a basic understanding of how Arf1 functions in different membrane environments and identify small-molecule ligands that may modulate its function in specific endomembrane organelles.



Erik Bergstrom

Appointed November 1, 2025 – October 31, 2026

Chemical, Physical & Structural Biology Graduate Program, [Baylor College of Medicine](#)

Primary Mentor: Dr. Joshua Riback, Molecular and Cellular Biology (BCM)

Nucleolar Nanoscale Remodeling Tunes Ribosome Biogenesis According to Environmental Signals

Biomolecular condensates are membranous organelles formed by phase transitions driven by multivalent interactions among biomolecules. At the nanoscale, transient interactions within condensates create a dynamic meshwork, whose properties are dynamic and have the potential to influence biochemical processes. However, it is poorly understood if and how changes in the nanoscale organization of condensates relate to functional changes. My project aims to characterize how the nanoscale organization of the nucleolus, a condensate that is the site of ribosome biogenesis, is linked to nucleolar function by examining how nucleolar nanoscale organization and function are altered during stress.



Precious Castillo

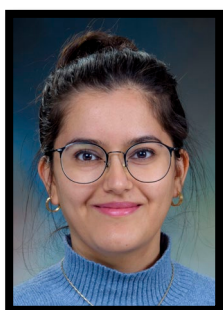
Appointed January 1, 2026 – December 31, 2026

Department of Biosciences, [Rice University](#)

Primary Mentor: Dr. Cameron Glasscock, BioSciences (Rice)

Developing a High-Throughput Binding Assay for Improving AI-Driven Design of DNA-Binding Proteins

DNA-binding proteins (DBPs) regulate essential cellular processes by controlling when and how genes are expressed. Recent advancements in artificial intelligence (AI) have enabled the design of DBPs, but these design tools are limited because they have only been trained on a small and biased set of known protein-DNA complexes. My project aims to develop a high-throughput platform capable of characterizing the binding interactions of tens of thousands of proteins against tens of thousands of DNA sequences. By combining high-throughput sequencing with automated protein purification and biophysical characterization, I will generate quantitative, reproducible maps of binding affinity and specificity. The resulting large-scale dataset will offer greater structural and sequence diversity than currently available. Training AI design models on this richer dataset will improve their accuracy in predicting protein-DNA interactions and designing candidate DBPs. The long-term goal is to enable the successful design of reliable, engineerable DBPs that selectively regulate disease-related genes. This capability would provide a foundation for new strategies in gene regulation for addressing diseases such as cancer, genetic disorders, and immune dysfunction.



Akanksha Gurtu

Appointed November 1, 2025 – October 31, 2026

Department of Pharmacology and Toxicology, [University of Texas Medical Branch Galveston](#)

Primary Mentor: Dr. Fernanda Laezza, Pharmacology and Toxicology (UTMB)

Uncovering the Non-Catalytic Signaling Role of GSK3 β in Ion Channel Regulation: A Paradigm Shift in Kinase Biology and Neuropharmacology

Protein kinases are versatile regulators of signaling and highly conserved enzymes, best known for catalyzing ATP hydrolysis and phosphorylating substrates. Beyond this canonical role, kinases also perform non-canonical functions, such as mediating protein-protein interactions (PPIs). This project characterizes the non-canonical function of glycogen synthase kinase 3 beta (GSK3 β), a kinase which drives early Alzheimer's disease-related neuronal network hyperexcitability (NH), through its interaction with the neuronal voltage-gated Na⁺ channel Nav1.6. Using surface plasmon resonance (SPR), high-

throughput automated patch-clamp electrophysiology, and cheminformatics, I will define the PPI interface of the GSK3 β /Nav1.6 complex and reveal the mechanisms underlying NH.



Kelsey Haggerty

Appointed September 1, 2026 – August 31, 2027

Chemical, Physical & Structural Biology Graduate Program, [Baylor College of Medicine](#)

Primary Mentor: Dr. Lynn Zechiedrich, Molecular Virology and Microbiology (BCM)

DNA Supercoiling and Supercoiling-Associated Structural Changes Regulate Canonical and CENP-A Variant Nucleosome Dynamics

In cells, nucleosomes must contend with the full range of DNA supercoiling—from positive to extremely negative—and with supercoiling-promoted structural alterations.

Most in vitro studies utilize linear DNA with nucleosome positioning sequences, which

are convenient for addressing many questions, but limit nucleosome dynamics and do not

reflect the genome. My work aims to uncover how DNA looping, supercoiling, and supercoiling-promoted DNA structural changes impact nucleosome assembly and positional dynamics.



Tom Hennigan

Appointed November 1, 2025 – October 31, 2026

Chemical, Physical & Structural Biology Graduate Program, [Baylor College of Medicine](#)

Primary Mentor: Dr. Joshua Riback, Molecular and Cellular Biology (BCM)

Mapping the Nanoscale Mesh of Condensates to Understand Biomolecular Transport and Selectivity

Cells rely on tightly regulated biochemical reactions to survive. Many of these occur in membrane-less organelles called condensates, which compartmentalize essential processes such as ribosome assembly and mRNA storage during stress. Initially thought to be simple

liquids, condensates display solid-like behaviors and are increasingly linked to diseases such

as cancer and neurodegeneration. Yet their complexity and the field's infancy mean we still lack reliable ways to probe how they organize and function without membranes. My work focuses on developing molecular tools that measure condensate architecture at nanometer precision in living cells, to reveal how these dynamic assemblies form, function, and go awry in disease.



Haley Johnson

Appointed November 1, 2025 – October 31, 2026

Quantitative and Computational Biosciences Graduate Program, [Baylor College of Medicine](#)

Primary Mentor: Dr. Lynn Zechiedrich, Molecular Virology and Microbiology (BCM)

BaseHunter; A New Approach to Determining DNA Sequence in CryoEM Density Maps

Existing tools cannot model DNA sequence for cryoEM maps with resolution worse than ~3

Å. The industry standard is to replace the DNA density with a generic adenine-thymine repeat, which prevents any understanding of how DNA sequence impacts protein-DNA

complexes. To fill this gap, we developed a shape-based approach that we call “BaseHunter” to distinguish shape differences between purines and pyrimidines, which is sufficient to

determine DNA sequence. I aim to make BaseHunter an automated and quantitative method for analyzing cryoEM densities of protein-DNA complexes and plan to build it into widely used cryoEM modeling software, Chimera.



Kevin Juarez

Appointed January 1, 2026 – December 31, 2026

Biochemistry and Cell Biology Graduate Program, [Rice University](#)

Primary Mentor: Dr. Yimo Han, Materials Science and NanoEngineering (Rice)

Structural Investigation of the Foreign Body Reaction at Neural Interfaces

Neural prosthetics represent next-generation technologies for treating debilitating CNS disorders, but their long-term stability is critically limited by the Foreign Body Reaction (FBR). While the FBR has been investigated using optical microscopy, advances in microfabrication have shifted this paradigm, now requiring higher-resolution techniques to identify ultrastructural hallmarks. This project aims to establish a standardized methodology using both room-temperature and cryogenic electron microscopy to characterize the probe-tissue interface. We hypothesize that novel ultrastructural FBR hallmarks, yet to be characterized, contribute to the instability at the prosthetic-tissue interface. These results will provide an updated structural understanding of the FBR, supporting the development of next-generation neuroprosthetics for rehabilitation and diagnostics.



Meghan McReynolds

Appointed September 1, 2026 – August 31, 2027

Molecular and Translational Biology Program, [University of Texas Health Science Center at Houston](#)

Primary Mentor: Dr. Irina Serysheva, Biochemistry and Molecular Biology (UTH)

Defining How Native IP₃ Receptor Organization Controls Cooperative Gating and Cellular Calcium Signaling and Dysfunction

Communication between cells in the brain depends on carefully controlled movements of calcium ions, and one of the major proteins responsible for releasing calcium inside cells is the inositol 1,4,5-trisphosphate receptor (IP₃R). These proteins assemble into groups, or clusters, that coordinate calcium release inside cells. Using advanced imaging and structural biology methods, including cryogenic electron microscopy, structure-guided mutagenesis, and planar lipid bilayer electrophysiology, I will visualize IP₃R assemblies in native cell membranes and determine how individual channels interact with one another. By revealing how groups of IP₃R channels work together, this research will provide fundamental insights into how brain cells communicate and respond to changing conditions.



Steven Mendoza

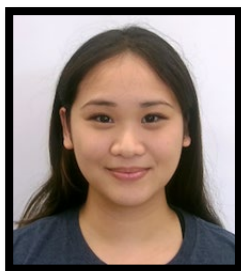
Appointed September 1, 2026 – August 31, 2027

Department Biology and Biochemistry, [University of Houston](#)

Primary Mentor: Dr. Quentin Vicens, Biology and Biochemistry (UH)

Structural Basis of Z-RNA Recognition by the ADAR1 p150 Z α -Linker-Z β Unit and Its Disruption in Aicardi-Goutières Syndrome

Steven's project investigates the structural biology of non-canonical nucleic acid structures and their recognition by specialized sensor domains involved in innate immune signaling. The work combines RNA biochemistry, fluorescence-based binding assays, and single-particle cryo-electron microscopy to characterize how these higher-order conformers are selectively engaged at the molecular level.



Leah Peralta

Appointed January 1, 2026 – December 31, 2026

Department of BioSciences, [Rice University](#)

Primary Mentor: Dr. Yang Gao, BioSciences (Rice)

Structural Insights into DNA Polymerase θ in DNA Repair and Integration

DNA polymerase θ (Pol θ) is a multifunctional eukaryotic enzyme that repairs lethal DNA double-strand breaks through the Theta/microhomology-mediated end-joining (TMEJ) pathway. Pol θ is an emergent synthetic lethal partner in homologous repair-defective tumors and is essential for Agrobacterium-mediated transformation (AMT). Pol θ consists of an N-terminal helicase and a C-terminal polymerase linked by a long, disordered central region; although studies have resolved individual helicase and polymerase structures, the ATPase-driven dynamics of the helicase, the architecture of full-length Pol θ , as well as the higher-order assemblies that promote foreign DNA integration during AMT, are not defined. This project uses cryo-EM, fluorescence spectroscopy, and biochemical methods to investigate the structure, dynamics, and mechanisms of full-length Pol θ in DNA repair and integration.



Walter Pham

Appointed September 1, 2026 – August 31, 2027

Chemical, Physical and Structural Biology Program, [Baylor College of Medicine](#)

Primary Mentor: Dr. Anthony Mustoe, Therapeutic Innovation Center (THINC) (BCM)

Role of RNA Folding Energetics in Partitioning into Processing Bodies

Beyond the classical role of encoding proteins, RNAs perform diverse cellular functions owing to the ability to fold into flexible, dynamic structures. These structures shape interactions with RNA-binding proteins that guide every stage of an RNA's lifespan. However, our understanding of the molecular determinants of protein recognition and binding of target RNAs remains incomplete. My lab applies chemical probing methods to interrogate RNA structure and dynamics. With these methods, my research focuses on how RNA folding dynamics regulate RNA-protein interactions and cellular function, with a focus on Pumilio proteins, a family of RNA-binding proteins involved in post-transcriptional regulation, and the interplay between RNA structure and biomolecular condensates.



Anya Porter

Appointed November 1, 2025 – October 31, 2026

Quantitative and Computational Biosciences Program, [Baylor College of Medicine](#)

Primary Mentor: Dr. Steven Ludtke, Biochemistry and Molecular Pharmacology (BCM)

Incorporating Microscope Effects into a Gaussian Reconstruction Method for Cryo-EM Data

Studying the structure of proteins and other biomolecules is key to understanding how the molecules function or malfunction in disease which can then be used for structure based drug design. Electron cryo-microscopy (cryoEM) is a technique used to image individual biomolecules and assemblies and study their structures and motions at an atomic level. The current methods used to convert 2D cryoEM images into high resolution structures use the weak phase approximation, which reduces the physical accuracy of how the imaging process is modeled and leads to representing atoms in the structure as a set of converging lines rather than the distinct objects they are. While these methods have been surprisingly effective, we are developing a new reconstruction method based on representing discrete objects as spherical Gaussian blobs. Preliminary results have already developed improved structures. I aim to further improve structures by extending this method to refine orientations, as well as better account for the physics of the microscope such as Ewald sphere curvature and beam tilt.



My Quan

Appointed September 1, 2026 – August 31, 2027

Department of Biochemistry & Molecular Pharmacology, Baylor College of Medicine

Primary Mentor: Dr. Allan Ferreon, Biochemistry and Molecular Pharmacology (BCM)

Single-Molecule Fluorescence Microscopy Dissection of Tau/TDP-43 Co-Condensation and Co-Pathology in Alzheimer's Disease and FTL

Mixed pathology, for example the co-occurrence of the intrinsically disordered proteins Tau and TDP-43 within the same aggregates, is common in Alzheimer's Disease (AD) and Frontotemporal Lobar Degeneration (FTLD) and is linked to more severe cognitive decline.

However, conventional structural and bulk biochemical methods cannot resolve the transient, heterogeneous protein species that are likely to drive this co-pathology. Using single-molecule and fluorescence lifetime techniques, including FRET-FLIM, smFRET, and FCS/FCCS, I will map Tau/TDP-43 co-aggregate abundance in postmortem AD and FTLD brain tissue against disease severity, then characterize how the properties of Tau/TDP-43 co-condensates are modulated in vitro and in neurons. This work will identify the molecular species that drive co-pathology and establish tissue-based measurements that link condensate biophysics to clinical outcomes.



Hayden Stegall

Appointed January 1, 2027 – December 31, 2027

Biochemistry and Cell Biology Program, Rice University

Primary Mentor: Dr. Linna An, BioSciences, Chemistry, and Bioengineering (Rice)

De Novo Reaction Sensors for Machine Learning-Guided Enzyme Evolution

Recent advances in computational protein engineering have made it possible to design small-molecule-binding proteins in silico with relatively high success. My project builds on this by designing a binder that is split in two, with each half fused to a fragment of a fluorescent protein, yielding a de novo sensor that fluoresces only in the presence of the target ligand. I will use this sensor to detect doxorubicin, a widely used chemotherapeutic, and to screen for higher-producing enzyme variants that lower drug production costs. Then, I intend to build this into a generalizable workflow that lets researchers design a sensor against the ligand of their choosing and set up high-throughput screens of their own.



Nicolette Valdez

Appointed December 1, 2025 – November 30, 2026

Department of Biochemistry and Molecular Biology, University of Texas Medical Branch Galveston

Primary Mentor: Dr. Matthieu Gagnon, Microbiology & Immunology (UTMB)

Structural Basis of Ribosome Rescue and Antibiotic Resistance

The ribosome is the molecular machinery responsible for translating mRNA into proteins through four crucial steps: initiation, elongation, termination, and recycling. During elongation, the growing polypeptide chain can interact with the ribosome and force the ribosome to stall prematurely. The ribosome is also forced to stall by ribosome-targeting antibiotics. Bacteria have evolved ways to detect and resolve ribosomal stalls by both the polypeptide chain and antibiotics. One such mechanism is the ATP-Binding Cassette subfamily F (ABC-F) proteins which can result in antibiotic resistance. This project will investigate the various ribosome rescue mechanisms employed by ABC-Fs by elucidating what ribosome features are altered, as well as what molecular interactions occur between the ribosome and ABC-F proteins. We will combine cryo-electron microscopy and biochemical methods such as protein purification and single-particle analysis to obtain high-resolution structures.



Deepika Yerva

Appointed January 1, 2027 – December 31, 2027

Biochemistry and Cell Biology Program, Rice University

Primary Mentor: Dr. Jane Tao, BioSciences (Rice)

Structural and Biochemical Characterization of DinoRNAV, a +ssRNA Virus, That Infects Key Coral Endosymbionts

Coral reefs form symbiotic relationships with photosynthetic dinoflagellates of the family Symbiodiniaceae, which reside within coral tissues and supply metabolic energy in exchange for shelter and inorganic nutrients. Stress-induced loss of these endosymbionts results in coral bleaching. Recent studies indicate heightened activity of dinoRNAV, a group of positive-sense single-stranded RNA (+ssRNA) viruses, in thermosensitive Symbiodiniaceae strains, particularly within the genus *Cladocopium*. However, a lack of structural and biochemical characterization limits our understanding of dinoRNAV replication mechanisms, host interactions, and potential contributions to bleaching events. This project will characterize the dinoRNAV RNA-dependent RNA polymerase (RdRp) and secondary uncharacterized viral proteins to elucidate their specific roles in viral replication and host pathogenesis.

Affiliates



Kieran Brown

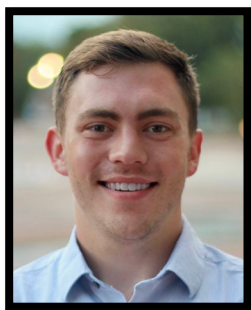
Appointed September 1, 2026 – August 31, 2027

Chemical, Physical, and Structural Biology Program, Baylor College of Medicine

Primary Mentor: Dr. Furqan Fazal, Biochemistry and Molecular Pharmacology (BCM)

Defining RNA Structural Zipcodes that Direct mRNA Localization to the Mitochondrial Surface

My project studies how RNA molecules are delivered to the correct location inside cells. Our lab identified a candidate “zipcode” RNA that may guide localization by folding into a specific structure. I will create thousands of mutated versions of this zipcode to test whether localization depends on the RNA’s exact sequence, its folded structure, or both. I will also identify proteins that bind this zipcode, revealing how cells read RNA delivery addresses to organize protein production in space and time.



Andrew J. Ensenberger

Appointed November 1, 2025 – October 31, 2026

Department of Pharmacology & Toxicology, University of Texas Medical Branch at Galveston

Primary Mentor: Dr. B. Montgomery Pettitt, Sealy Center for Structural Biology and Molecular Biophysics (UTMB)

Investigating the Role of Polarizability in Biomolecular Condensate Structure

We use large-scale molecular dynamics simulations to help understand how atomic forces and, in particular, electronic polarizability shape the structure and electrostatic environment of biomolecular condensates. By comparing traditional fixed-charge force fields with more advanced polarizable and Drude models, we quantify how properties such as peptide solubility, internal water content, and the local dielectric constant differ between dilute solutions, condensates, and folded protein environments. This work is the link between atomistic dipole correlations and phase behavior, with implications for how cells organize electrostatic signaling inside membraneless organelles. Ultimately, these insights

may help guide the design of therapeutics that selectively target proteins within condensates by exploiting their distinct dielectric environment.



Silvia Summers

Appointed November 1, 2025 – October 31, 2026

Department of Biochemistry and Molecular Pharmacology, Baylor College of Medicine

Primary Mentor: Dr. Lynn Zechiedrich, Biochemistry and Molecular Pharmacology (BCM)

Wielding DNA Looping and Supercoiling to Uncover Chromatin Structure and Dynamics

Nucleosomes, the building blocks of chromatin, regulate access to DNA. Most studies of nucleosomes are currently done with linear DNA, which lacks the structural changes associated with looping and torsional strain of DNA in cells. I utilize supercoiled minicircle DNA to model a more physiologically relevant environment. My project aims to uncover how DNA supercoiling and looping impact nucleosome structure, stability, and dynamics through single particle cryoEM and biophysical methods and to build the first polynucleosome model.

The HAMBP program is Administered by the:



www.gulfcoastconsortia.org

Questions: Contact Elizabeth Lawrence

el53@rice.edu, (713) 348-4752

The GCC is a collaboration of:

Rice University

Baylor College of Medicine

University of Houston

University of Texas Health Science Center at Houston

University of Texas Medical Branch at Galveston

University of Texas MD Anderson Cancer Center

Institute of Biosciences & Technology at Texas A&M Health Science Center

Houston Methodist Research Institute