Jaila D. Lewis, B.S.

Email: jdlewis11@uh.edu, **Website:** https://jaid06.github.io, **Phone:** 678-907-8750

Personal Statement

I am a 5th year Biochemistry Ph.D. Candidate at the University of Houston, specializing in structural bioinformatics and immunoinformatics to improve the safety and design of cancer immunotherapies and viral vaccines. My research involves developing immunoinformatics pipelines to identify novel cancer vaccine candidates, an objective centered on achieving health equity for all patients. I am proficient in Bash, Python, and R, which I used to build my pipelines. Additionally, I collaborate closely in interdisciplinary teams, to identify their safest and most efficacious candidates from wet-lab techniques and to validate my own candidates yielded by my pipelines. My ultimate career goal is to provide safe, high-quality immunotherapy options to treat different cancer types, autoimmune diseases and mitigate health disparities for everyone, especially for marginalized patients such as children and understudied patients of color.

Education

Ph.D. in Biochemistry
University of Houston, Houston, Texas
Degree expected in May 2026

B.S. in Biochemistry and Molecular Biology
Minors: Biology, Chemistry, Philosophy, and Religion
Mercer University, Macon, Georgia
Degree earned May 2021

Awards and Fellowships

Cullen Fellowship Travel Grant
University of Houston's Graduate School, October 2025, Houston, Texas
Competitive award to support the presentation of research at a national or international conference

Student Travel Award
University of Houston's Department of Biology and Biochemistry, October 2025, Houston, Texas
Departmental award to support graduate students' presentations of research findings

Excellence in Mentorship Award
University of Houston's Department of Biology and Biochemistry First Annual Gala, May 2025, Houston, Texas
Recognized for dedicated guidance and support of graduate and undergraduate mentees

Best Poster Award
SACNAS National Diversity in STEM Conference, October 2023, Portland, OR
Selected as one of the five outstanding graduate poster presentations out of thousands of participants

Best Poster Award
Sealy Center for Structural Biology Symposium, University of Texas Medical Branch, April 2023 Galveston, Texas

Best Poster Award
Center of Nuclear Receptor and Cellular Signaling Symposium, University of Houston, December 2022, Houston, Texas

Peer-Reviewed Publications

Castillo MB, Rankothgedera S, Thevasagayampillai S, Kandasamy A, **Lewis J**, Woody C, Vaz de Freitas M, Antunes DA, El-Zein R and Gunaratne PH (2025) Identification of immunogenic KIF5B-RET fusion neopeptides driving immune stimulation in tumor specific CD8+ T cells. Front. Immunol. 16:1635810. doi: 10.3389/fimmu.2025.1635810

Alves CC, Lewis J, Antunes DA, Donadi EA. The Role of Vimentin Peptide Citrullination in the Structure and Dynamics of HLA-DRB1 Rheumatoid Arthritis Risk-Associated Alleles. Int J Mol Sci. 2024 Dec 24;26(1):34. doi: 10.3390/ijms26010034. PMID: 39795892; PMCID: PMC11719467.

Selected Abstracts, Oral Presentations, and Lectures

Improving Cancer Vaccine Design for African American and Latine Patients with PIK3CA-associated Breast Cancer – *Oral Presentation*
Center for Nuclear Receptors and Cell Signaling Seminar, University of Houston, November 2025, Houston, Texas

General Biochemistry I, Glycolysis – *Lecture*
Department of Biology and Biochemistry, University of Houston, November 2025, Houston, Texas

Improving Cancer Vaccine Design for African American and Latine Patients – *Poster Presentation*
Society for Immunotherapy of Cancer (SITC) Conference, November 2025, National Harbor, MD
Abstract Publication: https://doi.org/10.1136/jitc-2025-SITC2025.1294

General Biochemistry I, Enzyme Kinetics – *Lecture*
Department of Biology and Biochemistry, University of Houston, November 2025, Houston, Texas

Improving the design of cancer vaccines targeting PIK3CA-associated antigens for underrepresented patients of color – *Poster Presentation*
SACNAS National Diversity in STEM Conference, October-November 2024, Phoenix, Arizona

Determining the Accuracy of Alternative Scoring Functions for Docking Peptides to HLA Receptors *- Poster Presentation*
SACNAS National Diversity in STEM Conference, ***Best Poster Award,*** October 2023, Portland, Arizona

Analyzing Dynamic Interactions of Drug Activators for the Pseudokinase MLKL *– Poster Presentation*
Sealy Center for Structural Biology Symposium, University of Texas Medical Branch, ***Best Poster Award,*** April 2023, Galveston, Texas

Assessing the Ranking Power of Dissimilar Peptide-HLA Scoring Functions *– Poster Presentation*
Center of Nuclear Receptor and Cellular Signaling Symposium, University of Houston, ***Best Poster Award,*** December 2022, Houston, Texas

Research Projects

Improving the Design of Immunotherapies for African American and Latine Patients: Thesis Project
Principal Investigator: Dr. Dinler Antunes, December 2022 – Present
Cancer immunotherapy leverages a patient's immune system, enabling the required immunological responses and memory to combat diseases like cancer or infections. However, this innovative treatment is not accessible for all. Due to many limitations impacting the healthcare system (e.g., lack of representation in clinical trials), understudied patients of color (UPCs) may not receive the benefits of immunotherapy. Instead, they can experience higher rates of toxicity and death when treated with some cancer immunotherapies. Therefore, it is imperative we address this health inequity with inclusive treatment design. In my thesis, I combine sequence-based algorithms and structural modeling to identify high-quality and generalized peptide cancer vaccine candidates for UPCs. I developed a new tool, PPmGen, to design highly biochemically similar, altered peptide ligands for the human leukocyte antigen (HLA) alleles restricted to UPCs. As a result, I yielded 90 peptide candidates that are safer, more efficacious, and generalized for

the UPC alleles of interest. These findings are currently being experimentally validated, and the manuscript is in progress. This project was funded under the National Institute on Minority Health and Health Disparities (NIMHD) of the National Institutes of Health (NIH) to the University of Houston under Award Number U54MD015946.

Discovery of Immunogenic Neopeptides from Actionable Chimeric RNAs to Develop Vaccines for Lung and Breast Cancer Treatment

Principal Investigators: Dr. Dinler Antunes and Dr. Preethi Gunaratne, June 2023 - Present

Somatic mutations in key genes can cause multiple diseases, including different types of cancer. One somatic mutation event is known as gene fusions, where two chromosomes can recombine, translocate, or experience deletions with each other, giving rise to multiple aggressive cancers. In collaboration with the Gunaratne Lab at UH and MD Anderson, we identified fusion neoantigens expressed by patients diagnosed with non-small-cell lung cancer and breast cancer and tested their ability to be used in a cancer vaccine. I utilized molecular docking with our tool APE-Gen2.0 to model and predict the binding of fusion neoantigens from lung and breast cancer to the human leukocyte antigen (HLA) receptors expressed by the patients. I also predicted the risk of off-target toxicity associated with T-cell cross reacting after exposure to the fusion neopeptides. Our predictions were validated by wet lab techniques like ELISpot and ImmuDex protocols. We have completed both these projects, published the work for the *KIF5B-RET* lung cancer project, and will publish our findings for the remaining breast cancer projects.

Analyzing Dynamic Interactions of Drug Activators for the Pseudokinase MLKL

Principal Investigators: Dr. Dinler Antunes and Dr. Greg Cuny, August 2022 – August 2024

Innate immunity hosts essential immune processes against cancer and viral infections. The necroptosis pathway regulates inflammatory cell death towards diseased cells. Certain tumors, however, can downregulate necroptosis. These are called *cold* tumors (i.e., tumors unresponsive to immunotherapy) and are associated with particular cancers. Therefore, identifying ligands capable of directly triggering necroptosis in *cold* tumors represents a promising avenue for treatment. Our team identified small molecule activators to target and activate mixed lineage kinase domain (MLKL) pseudokinase, a downstream executioner in the necroptosis pathway and may be a promising avenue for increasing antitumor activity against *cold* tumors. We paired *in vitro* experiments to observe the activation of necroptosis with molecular docking and molecular dynamics simulations to analyze the structure-activity relationship for ligand binding to both the open inactive and closed active conformations of MLKL. If successful, we will elucidate the interactions required for activating MLKL, guide our *in vitro* experiments, and provide direct applications for targeting *cold* tumors. This project was funded by UH's Drug Discovery Institute (DDI).

The Role of Vimentin Peptide Citrullination in the Structure and Dynamics of HLA-DRB1 Rheumatoid Arthritis Risk-Associated Alleles

Principal Investigator: Dr. Dinler Antunes and Dr. Eduardo Donadi, March 2023 – December 2024

Citrullinated peptides and other post-translational modifications are related to rheumatoid arthritis (RA) as some of these peptides trigger autoimmune responses. Moreover, some HLA-DRB1 Alleles encode molecules with a particular shared epitope sequence in the peptide binding groove of the HLA, which binds to certain citrulline-modified peptides. Therefore, our team was focused on evaluating the intermolecular interactions occurring between normal or PTM-associated vimentin peptides and HLA-DRB1 alleles that have higher risks for RA risk and the identifying the role of key binding pockets (P4) within these HLAs. Specifically, I took 251 pHLA conformations yielded from molecular dynamic (MD) trajectories and conducted the scoring of each conformation via AutoDock4. I found that the citrullinated vimentin peptides bound more strongly to the HLA-DRB1 alleles, especially HLA-DRB1*04:05, than the non-citrullinated vimentin peptides, indicating enhanced pHLA binding and stability observed for the citrullinated vimentin peptides may influence RA disease outcomes. This work was published in December 2024.

Evaluation of Scoring Functions to Rank Bound Conformations of Peptide-HLA Complexes

Principal Investigator: Dr. Dinler Antunes October 2021 – Present

Cancer immunotherapies experience limitations, especially regarding the genetic diversity of different patients and cancers. One contribution of these experienced limitations could be the use of the gold-standard human leukocyte antigen (HLA) binding algorithms. These sequence-based algorithms are trained on large datasets from databases like The Cancer Genome Atlas (TCGA), which has an

underrepresentation of non-White patients. This data bias can cause an algorithmic bias, which might yield inaccurate HLA binding predictions for HLA alleles prevalently found in understudied patients. Instead, we proposed that structure-based methods (e.g., molecular docking) can better categorize peptide binders and conformations for many diverse HLA receptors, not just the alleles most commonly studied. I used our meta-docking tool DINC (Docking INCrementally) to predict the structure of the validated crystallized peptide-HLA complexes to yield multiple conformations with ranging Root Mean Square Deviations (RMSD) values, with the lowest RMSD values representing the best structures. However, structure-based methods are limited in determining the best or biologically feasible peptide-HLA conformations. Therefore, we evaluated 11 alternate SFs in their rankings of the several peptide-HLA conformations per crystal structure. We concluded we should combine these diverse SFs in a consensus method to develop an accurate, user-friendly scoring function for protein-ligand complexes, especially for peptide-HLA complexes. We worked alongside Rice University, UH-Downtown, UH, and immunologists from the MD Anderson Cancer. We expanded this project to develop an AI and structure-based SF, which was funded by UH's Drug Discovery Institute.

Metal Sulfide Alloy Nanoparticles for Compound Semiconductor Curved Surfaces, Mercer University
Research Advisor: Dr. Dale Moore, August 2019 – May 2021
Gallium arsenide is a compound used to form nanoparticles in modern satellite technology. However, gallium arsenide is carcinogenic and can cause chronic and acute illnesses in workers who synthesize nanoparticles. So, it is imperative that safer compounds are used to synthesize nanoparticles, all while maintaining the efficiencies of communication devices. Dr. Dale Moore's lab addresses this problem by synthesizing cadmium and zinc sulfide nanoparticles. My research project was dedicated to improving the efficiency and size consistency of the cadmium-zinc sulfide nanoparticles. In the past, the lab had issues creating nanoparticles that were uniform in size, which impaired their efficiency. Dimethylformamide was used in our protocol and improved this problem, however; dimethylformamide made the nanoparticle size become small and restricted. In order to improve the size consistency problem, I proposed utilizing alcohols that pair with the solution's polarity, allowing for a wider range in nanoparticle size. My hypothesis had improved our measurements for cadmium-zinc sulfide nanoparticles, enabling optimal solvent mixes and will potentially lead to nontoxic compounds in technology. With innovative thinking, I had accomplished size consistency for nanoparticles and assisted Dr. Dale in creating two new projects to better the lab's research.

Biology and Organic Chemistry with Mathematical Modeling (BOMM Program), Mercer University
Research Advisors: Dr. David Goode and Dr. Linda Hensel – August – December 2018
Overprescribing antibiotics for bacterial infections has led to the ongoing bacterial antibiotic resistance crisis. Currently, antibiotics specifically target bacterial cells to lyse them, allowing for the remaining bacteria to mutate and continue to grow. These methods led to difficulties in targeting pathogenic bacteria medicinally. Instead, our lab proposed targeting the quorum sensing mechanism that occurs within the following strains: *Bacillus subtilis*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *and Streptococcus mutans* and the formed biofilm. We created antibiotics by coupling amino acids and carboxylic acids in a combinatorial fashion and to target with the five bacterial strains. I hypothesized to our lab that the antibiotics should have hydrocarbon-dense, polar amino acids that might interact with the peptidoglycan walls of the bacteria and ultimately block the quorum sensing. Unfortunately, our antibiotics were activators of quorum sensing. Although we do not know how antibiotics interact with the peptidoglycan walls, we believe our observation may lead to new insights on the mechanisms controlling quorum sensing.

Involvement in Funded Research Projects

NIMHD R01 Grant
Contributed as co-author, grant was based on my thesis project, May 2025. Application selected for review

University of Houston's HEALTH-RCMI, NIH and NIMHD Funded Pilot Grant Program
Contributed as co-author, grant was based on my thesis project, executed entire pilot project, and solely completed bimonthly and quarterly reports. Funding was approved in March 2024

University of Houston Drug Discovery Institute
Contributed as co-author, funding Approved April 2023, led a portion of computational execution for pilot project