My favorite fruit is strawberries. As a child, their vibrant color and sweet taste delighted me, but it was their hidden complexity that truly captured my imagination. I learned that strawberries produce flavonoids—compounds that act as natural defenses—much like our immune system's arsenal of cells and proteins working in concert to protect us from harm. This discovery was like uncovering the first piece of a puzzle—a puzzle that grew more intricate as I delved into the study of immunology. Just as I loved piecing together jigsaw puzzles to reveal the bigger picture, I became fascinated by how something so small could possess such extraordinary defenses.

The immune system is both a protector and a betrayer. At the age of ten, I was diagnosed with Mixed Connective Tissue Disease (MCTD), an autoimmune condition encompassing lupus, rheumatoid arthritis, and Raynaud's phenomenon. My body's defense system had turned against me, triggering chronic pain, severe fatigue, and a bewildering array of symptoms. Growing up as a Black and Filipino child in a medically underserved community, navigating healthcare meant not only managing my disease but also contending with systemic inequities that left my family without the resources to support my condition. These challenges shaped my early resilience and ignited my curiosity about the immune system's mysteries, motivating me to transform my experiences as a patient into a lifelong pursuit of scientific discovery.

This led me to Indiana University Indianapolis (IUI), where my undergraduate journey provided the foundation for my passion for research and innovation. Majoring in Biomedical Informatics, I sought to combine my interest in biology with the computational tools essential for unraveling the complexities of disease. Under the mentorship of Dr. Randall Roper in in the Louis Stokes Alliance for Minority Participation (LSAMP) program, I conducted RNA sequencing (RNA-seq) analysis to investigate gene expression changes in the femurs of Ts65Dn mouse models of Down syndrome. This research uncovered dysregulated pathways, including JAK/STAT and PI3K/AKT, which are crucial to skeletal development. These findings not only provided insights into the molecular basis of skeletal anomalies but also solidified my commitment to using bioinformatics to explore disease mechanisms.

Navigating the rigorous demands of my undergraduate education came with its own set of challenges. Balancing coursework with the physical toll of my disability and my responsibilities as the eldest sibling meant that my academic performance in courses like BIOL-K 101 and BIOL-K 102 reflected these competing priorities. Despite these struggles, I never let go of my passion for science. My sophomore and junior years were especially difficult, but my senior year marked a personal turning point. I developed strategies to better manage my health and time, enabling me to excel in courses like INFO-B 473: Applied Programming for Biomedical Data Analysis and INFO-B 429: Machine Learning for Bioinformatics. These experiences taught me resilience and adaptability, qualities that have strengthened my ability to navigate challenges and continue growing as a scientist. Although my transcript reflects the challenges I encountered, it also stands as a testament to my growth and determination, demonstrating my ability to persevere and thrive in the face of adversity.

Seeking to expand my scientific expertise, I joined the NIH Post-Baccalaureate Research Education Program (iPREP) at Indiana University School of Medicine (IUSM) under the

mentorship of Dr. Christopher Robinson. Tasked with predicting CD8+ T cell epitopes in Coxsackievirus B3 (CVB3)—a leading cause of viral myocarditis—I identified a gap in computational methods for immunodominant epitope prediction and took the initiative to address it. Using tools such as PSSMHCpan and the Immune Epitope Database (IEDB), I independently designed and implemented a comprehensive bioinformatics pipeline to analyze peptide-MHC binding affinities, generating a ranked list of the top 25 predicted epitopes. This pipeline, developed from scratch, serves as the foundation for subsequent in vitro and in vivo validation studies. The creation of this pipeline was transformative, allowing me to merge computational innovation with practical applications in immunology while sharpening my expertise in bioinformatics, data analysis, and computational immunology. This work has deepened my understanding of host-pathogen interactions, reaffirmed my passion for unraveling the immune system's complexities, and inspired my commitment to bridging computational predictions with experimental validation. By integrating these approaches, I aim to address the immune system's most pressing challenges and translate insights into therapies that target autoimmune and infectious diseases.

The integration of computational and experimental approaches in immunology provides a powerful avenue to uncover the complexities of immune memory, T cell differentiation, and transcriptional regulation in autoimmunity. My research interests lie in exploring how immune dysregulation shapes diseases like rheumatoid arthritis, identifying transcriptional regulators as potential therapeutic targets, and restoring immune function in conditions of chronic immunosuppression. By bridging these approaches, I aim to contribute to advancements that not only deepen our understanding of immune dynamics but also pave the way for innovative therapies.

As I continue my journey in science, I do so with a profound sense of purpose. My path has been about more than overcoming odds—it has been about redefining them. I am driven by the desire to transform challenges into opportunities, leveraging creativity and persistence to advance immunological research. My ultimate goal is to develop therapies that address autoimmune and immune-mediated diseases while ensuring scientific progress benefits all communities equitably. By uncovering the immune system's puzzles, I hope to contribute to solutions that empower those whose bodies have become both a *battleground* and a source of *resilience*.