BROAD GOALS AND PERSONAL BRANDING
The author opens with a broad description of their general research interests which frames their goals for their PhD.

TRANSITIONS
The author utilizes a mix of chronological ★ and thematic ★ framework to tell their journey.

This choice helps them walk readers through the multiple different research experiences, while explaining how each experience led to the next and has prepared them for graduate school.

RESEARCH EXPERIENCE 1
Begins with meaning, why they did the project and why it was important, before going into specifics of the projects, explaining the specific goal and how they went about achieving it, name-dropping specific techniques.

Ends with a clear output ("validated the motif") as well as wet-lab skills and lessons learned from the experience.

RESEARCH EXPERIENCE 2
Author transitions into a new research experience, guiding the reader to where, when and what the experience is.

Author states clearly what was learned and what was done independently.

Concludes with specific skills gained, as well as what they learned about their own interests.

RESEARCH EXPERIENCE 3
Transition directly builds off previous experiences.

Author describes specifics of project without getting lost in the weeds.

Meaning of what they accomplished and how it will influence their future work in graduate school.

RESEARCH EXPERIENCE 4
Begins with why they joined this lab, as well as meaning of this being their most significant experience.

Describes goals of the project, how they approached the problem, and clear outputs both in science communication (presenting at a symposium) and inspiration for future work.

Author adds a transition within the experience to discuss ongoing work, with a focus on goals and plans for the project.

BROAD GOALS AND PERSONAL BRANDING
Author reiterates their research and career goals.

PROGRAM OF INTEREST
Highlighting the match of the program, noting key parts of curriculum, unique opportunities and multiple specific faculty with which they want to work.

Concluding with program match plus personal career goals.

I chose to study biological engineering at MIT because I was fascinated by the idea that while every cell in an organism has the same genetic information, differences in gene expression lead to the vast diversity of cell capabilities. Over the course of my studies, I have come to understand that the ways cells process information is far more complex than my initial understanding of gene expression. I now appreciate the beauty of the intricate organization of biology into pathways and how even subtle disruption to this precision can lead to fatal disease. Therefore, studying the networks regulating cellular processes can shed light on the mechanisms underlying such disorders. Specifically, I believe immunology provides the tools necessary to create novel therapies to treat or prevent a wide range of diseases, including infectious diseases and cancer. Through my research as a PhD candidate, I hope to uncover the intricate details of immune system regulation and explore innovative strategies in immune engineering.

★ I conducted my first research experience in the [redacted] Lab at [redacted] where I explored how sequence motifs within introns may enhance gene expression. The purpose of introns was the first unanswered question I was ever faced with in my biology education, and I was excited to begin my research career exploring a topic that was conceptually accessible to me. I began by optimizing a library assembly cloning protocol with my direct supervisor. As I became more comfortable with cloning, troubleshooting, and molecular biology techniques, I took on an independent project, which was to validate the efficacy of a sequence motif found in a previous screen to enhance gene expression. I designed and cloned eight constructs, genomically integrated the plasmids into a cell line, and quantified the fold change in gene expression with flow cytometry and qRT-PCR. The results validated that the motif of interest was enhancing gene expression. After a year in the lab, I gained valuable molecular biology and flow cytometry skills, which are two techniques that will be ★ critical in my PhD research. While I enjoyed the problem-solving needed to answer this basic science question, I felt disconnected from the research. I learned that I wanted to transition to translational research, where I could envision more clearly how my work could impact the lives of patients in the clinic.

★ Over the summer of 2022, I conducted research in the [redacted] Lab at [redacted], working on developing a lipid nanoparticle encapsulating mRNA that could be delivered to the lung to reduce inflammation in acute respiratory distress syndrome . I learned the lab's method for developing LNPs and shadowed my supervisor during mouse experiments. Independently, I built and tested three different LNP formulations in cell culture. Through learning about the ★ development of drug delivery systems and mouse models for disease, I solidified my interest in translational biology research. I would like my PhD to similarly focus on the design and implementation of targeted therapeutic interventions that have clinical applications.

In the summer of 2023, I was a computational biology intern at [redacted], a ★ biotech start-up focused on developing programmable mRNA therapies for disease. The design of mRNA was a strategy that I wanted to explore further in the [redacted] Lab the summer prior, and I was curious to see how research is approached in an industry setting. Additionally, I wanted to learn more about computational modeling of gene regulatory networks, a topic that I was first introduced to in the Analysis of Biomolecular and Cellular Systems course I took in the fall of 2022. Over the course of the internship, I modeled the dynamics of four different gene circuits using systems of ordinary differential equations. Using [redacted]'s internal live cell imaging data, I was able to fit parameters to two of the models and successfully simulate the protein concentration output of the genetic circuits over time. Additionally, I was able to extract the decay rate of the RNA in the circuits, a measurement that we could not trivially complete at the bench. I learned the value ★ of a mechanistic model as a hypothesis-generating tool and aim to incorporate modeling of gene regulatory networks into my PhD research.

★ I joined the [redacted] Lab at [redacted] in the Fall of my Junior year, as I was compelled by the Lab's simultaneous desire to understand the mechanisms regulating host-pathogen interaction and to use this knowledge to inform the development of novel therapies for tuberculosis. This has been my most significant research experience in terms of both length and contribution. I began on a project to optimize a fluorescence-based reporter for M. tuberculosis death within live macrophages. Having this technology would allow us to observe the heterogeneity of macrophage response to M. tuberculosis infection and subsequently dissect the underlying differences between the host cells. I designed and executed a cloning strategy to build five new permutations of the reporter and tested them in the model organism M. smegmatis and human monocyte-derived macrophages through flow cytometry and fluorescence microscopy. I wanted to expand my computational skills, so I developed an image analysis pipeline to analyze the results of the reporter time course fluorescence microscopy experiments. I presented a poster about my work at MIT BE's Undergraduate Research Symposium. From these projects, I've learned about ★ technology development and image processing, which inspires me to develop clever ways to report on phenomena of interest in my own PhD research.

In my Senior fall, after 12 weeks of improving my comfort with coding and data analysis at ★ [redacted], I set out to improve my image analysis pipeline, as well as adapt parts of it to be able to analyze images from immunostaining experiments of a similar design. I am currently working on a new project which aims to deliver an exogenous protein to the phagosome of macrophages. This is a challenging task, given the difficulty of expressing foreign DNA in human monocyte-derived macrophages. Moreover, the phagosome is a transient organelle that forms from the fusion of an unpredictable location on the cell membrane around extracellular material, making it difficult to target. By engineering the macrophage in this manner, we will have a new tool to dissect the nuance of host-pathogen interaction in M. tuberculosis infection.

Overall, I aspire to delve into the molecular and cellular mechanisms that govern immune responses and contribute to the development of targeted interventions for diseases. My goal is to bridge the gap between fundamental immunological understanding and practical applications, leveraging my skills in sequencing, protein engineering, synthetic biology, and computational modeling. Between the rigorous core training in biochemistry, genetics, and mechanistic biology, the customizability of curriculum, and access to top nationwide hospitals and biotech companies, I believe that the BBS program at Harvard would be the ideal place for me to conduct my PhD research in immune engineering. I would be eager to work in the lab of Dr. Roni Nowarski, given that their research on the regulation of pathways controlling immune tolerance in the gut allows for an understanding of the dysregulation leading to chronic inflammatory diseases. Additionally, I am compelled by the lab of Dr. Nir Hacohen, as I admire their genetics-based approaches to uncovering the networks regulating immunity, as well as their investigation into the role that genetic variation plays in immune responses between individuals. By the completion of Harvard's Biological and Biomedical Sciences graduate program, I will have taken a significant step towards my career goal of making tangible advancements in healthcare through research in immunology and translation of scientific knowledge.