

My path from environmental engineering to CRISPR technology development has not been a straightforward one, but a winding one that has allowed me to learn a lot about myself and the science I love. Growing up in San Diego, I developed a deep respect for the ocean, which evolved into a passion for the environment. During high school, I actively sought out ways to help our planet, starting a school recycling program, building a greywater system for our home, and volunteering for various stewardship projects. This interest carried into college, when I applied to MIT to study environmental or ocean engineering and completed an internship for the Navy building autonomous vehicles for collection and analysis of various indicators of ocean health.

This plan changed during my first year at MIT, when one of the closest people in my life was diagnosed with stage 4 prostate cancer. I threw myself into studying this disease and I became increasingly frustrated by the gap between published research and actual treatments offered in the clinic. I wanted to help, but this disparity was insurmountable, and I was forced to sit back as he slowly died.

I found myself drawn to the molecular biology I was reading about in my efforts to understand the current state of prostate cancer research. As I learned more, I was shocked by how little we still know about our genetic code and was captivated by the tools that have been developed to gain more insight into it. I wanted to combine this newfound interest in molecular biology with my desire to combat climate change, so I changed my major to biological engineering, which blended aspects of both fields. In order to get hands-on experience in this realm, I began an internship at the J. Craig Venter Institute working on gene editing of lipid biosynthesis pathways in the model diatom *Phaeodactylum tricornutum* to increase biofuel production. This project was very interesting but progressed slowly, because genome editing tools like CRISPR were not yet optimized in this organism. As the summer continued, I gravitated towards developing technology to improve CRISPR delivery and editing efficiency in diatoms, and asked to shift my focus towards those endeavors. This was my first real exposure to technology development of this nature, and I eventually realized that functional genomics underpinned research efforts in these two seemingly disparate fields of environmental engineering and cancer biology that I found so engaging.

I became fascinated by the broader problem of developing genetic manipulation tools to be compatible with a wide variety of model systems and biological questions. I continued in this space for the rest of college, working on projects like optimizing electroporation for bacterial species beyond *E. coli* with the ultimate goal of increasing genetic tractability for a wide range of organisms. For my senior research project I found a niche where I could apply functional genomics to my areas of interest, using genetic engineering to make plants drought resistant, with applications for locations impacted by climate change. Through these experiences, I discovered two things - I really loved lab work and I wanted to take more ownership over my projects and see them through from conception to results.

I thus sought out the opportunity to work at the Broad Institute, under John Doench on the R&D team of the Genetic Perturbation Platform (GPP). The mission of GPP is to develop and distribute functional genomics tools and expertise to a wide audience, which makes it an incredibly collaborative platform with a wealth of multidisciplinary work. This unique role has allowed me to work on a diverse range of projects, from base editing screens tiling across important DNA damage repair genes such as *BRCA1* and *CHEK2* to our recently-published work on improving on-target Cas9 sgRNA design rules based on tracrRNA identity. Through these projects, I gained hands-on experience with nearly every available

CRISPR technology. In doing so, I realized that there was no toolkit that enabled other researchers to pressure-test these systems in the way that our well-funded and well-connected lab so easily could.

I initiated a project to address this gap - developing a modular approach to CRISPR vector assembly. This technique, based on Golden Gate cloning, reduces both the time and cost associated with making new vectors and, more importantly, allows for systematic comparisons of novel CRISPR components. This flexible, easily adaptable system, now called Fragmid, along with a website supported by our software team, has enabled the creation of hundreds of custom vectors for dozens of labs across the country, even prior to publication. After many months of optimization and even more months spent meticulously organizing and future-proofing this toolkit as a distributable resource, the pipeline was recently released to all Broad affiliates. In the final step before submitting for publication, I am expanding this toolkit beyond mammalian cells into *Drosophila* and other model insects, in collaboration with the Perrimon Lab at Harvard, and working with the Sontheimer Lab at UMass Medical to expand to delivery mechanisms beyond lentivirus, such as AAV. This platform that I conceptualized, iterated on hundreds of times in the lab, and distributed is enabling researchers who I have never met to probe their diverse biological questions in a more efficient manner, pushing the edge of science forward in many different areas. The desire to close the gaping disparity between what is physically possible and what is available on the bench or in the clinic drives me to continue to work on basic technology development and distribution.

Mirroring my desire to make genomic tools available to more people is my goal to make science itself equally accessible. I deeply understand the benefit that diversity of thought brings to a workplace and actively work to improve this in every role I'm in. Specifically, I have aimed to make scientific access more equitable, both through individual mentorship for women in STEM as well as my participation in established programs, such as the inclusion, diversity, equity, and allyship (IDEA) ambassador program at the Broad. As one of twenty IDEA ambassadors, I received extensive DEI training, which enabled me to expand my capabilities for doing this type of work. I am currently leading an effort, supported by this program, to evaluate hiring and retention metrics within our group and make these processes more equitable. I will bring these tools to my graduate studies and continue to work to address the divide in access to science and higher education.

I am driven by a love for the environment and basic biology that has morphed with time and experience into a passion for developing and distributing genetic manipulation tools. My work in GPP has made it very clear that I enjoy the process of generating ideas and driving a project forward from start to finish. I want to continue developing my research and leadership skills, particularly in the space of functional genomics, and the GS program at UW provides a unique opportunity for me to do so. Specifically, I am very excited that the coursework is centered around genomics, and I am especially interested in the Grant Writing and Scientific Speaking courses, as scientific communication is important to me. Additionally, I am drawn to the tight-knit community and many department-wide activities that the small size of GS affords. I hope to continue advancing my career by working in a group such as that of Jay Shendure and Lea Starita on massively parallel functional genomics. I am also interested in the Fowler Lab and Stergachis Lab, which both leverage functional genomics to answer a variety of fundamental biological questions. I'm confident that my extensive research experience, leadership, and desire to make science more accessible have laid the foundation for a successful career, which I am excited to potentially further at UW, with the ultimate goal of leading my own lab one day.