

Personal Statement

“Almost all aspects of life are engineered at the molecular level, and without understanding molecules we can only have a very sketchy understanding of life itself.”-Francis Crick

I am applying to the graduate program in Molecular Cellular and Developmental Biology because I enjoy the stimulating academic research environment, I have found an area that I feel I can greatly contribute to, and my ultimate goal is to perform biological research and teach at the university level.

I earned my Bachelor of Science in Biochemistry and Bioinformatics from Ramapo College in 2008, and attained a Master of Science in Biomedical Informatics from Rutgers University (UMDNJ) in 2010. I completed a Master of Science in Computational Biology and Bioinformatics from Yale in 2014, and am now seeking to apply my bioinformatics skills to enhance structured noncoding RNA research in Professor Breaker’s lab in the Molecular Cellular & Developmental Biology department.

I was involved in a wide variety of research projects that helped to develop my biological research skills. In 2006, I studied the behavioral, demographic, and racial differences between seriously mentally ill (SMI) persons with and without HIV at the University of Pennsylvania. In 2007, I sped up a computational protein folder by 50% in order to better model protein evolution at Harvard. Working with Dr. Bagga at Ramapo from 2005-2008, I studied Quadruplex-forming G-rich sequences, which have been recognized for their role in RNA processing and translation, and as therapeutic targets.

In 2011, I created an automated image analysis algorithm for detecting HIV at Bristol-Myers Squibb (BMS). Under the direction of Mikhail Frenkel, I worked along with the Virology department in developing the algorithm over six weeks. In the fall of 2011, I began the graduate program in Computational Biology & Bioinformatics at Yale University. My first research project used Bayesian modeling to study the development of drug resistance in the hepatitis B viral genome with Dr. Jing Zhang. I also worked with Dr. William Jorgensen to optimize ligands for PAD4 binding, before working with Dr. Jeffrey Townsend to quantify the effects of driver genes on various cancers.

I am fascinated by the work of Dr. Ronald Breaker on structured non-coding RNAs, particularly riboswitches and ribozymes. Over the past decade, the Breaker lab has discovered more ribozymes and riboswitches than any other lab. Dr. Breaker’s lab is the undisputed leader in the field of such research. However, with the recent departure of Dr. Zasha Weinberg, it’s leading bioinformatics postdoc, and the impending graduation of Shira Stav, the primary graduate student pursuing bioinformatics methods in the lab, there is a void that must be filled. Given my background in programming and bioinformatics, I can help to fill this void. I have

already begun making sense of the Perl code that Dr. Weinberg wrote, while working with Shira on her method of discovering RNAs in long intergenic regions with high guanine and cytosine content. Besides assisting this lab with my bioinformatics expertise, I am also excited about the opportunity to improve upon the experimental lab experience I gained while pursuing a major in biochemistry and bioinformatics in college.

The training I receive in Yale's MCDB program, with the guidance of Dr. Breaker, will provide me with the skills and knowledge necessary to conduct rigorous research that I can use to effect practical biological research.

I look forward to hearing from the committee soon, and I am eagerly anticipating pursuing my PhD at Yale, while continuing research with Professor Breaker. Thank you in advance for your time and consideration of my application!