**Statement of Purpose**

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Mesmerized by the magic power of chemistry, I chose to become a member of the Chemistry Olympiad Class when I was in high school. My hard work, dedication and love for chemistry led me to win the first place in the National Chemistry Olympiad in Henan province. At the awarding ceremony, Prof. Xi Zhang (Chair of Department of Chemistry, Tsinghua University) said something that I would never forget: ‘though humanity has made great progress in chemistry, we are still far from being able to design molecules as we wish.’ This sparked my curiosity to find the underlying molecular driving forces and made me pursue a scientific career.

I decided to major in Chemical Engineering at Tsinghua University in 2012 as an undergraduate. My strong passion for scientific research incentivized me to join the lab of Prof. Yushan Zhu when I was a sophomore, where I worked on computational design for a new enzyme that could catalyze the acylation reaction in cefataxime synthesis. I set up my own evaluating standards and a trial-and-error protocol. Finally, a new enzyme satisfying my evaluating criteria with five-residue mutations was found to bind cefataxime well *in silica*. This experience definitely provided me with a deep understanding of how to make a hypothesis and how to find an appropriate method to solve the problem based on the hypothesis in scientific research.

Due to my strong academic performance, I was awarded a scholarship to study at UW-Madison for fall semester of 2014, where I received firsthand experience of an American graduate school, as well as deepened my understanding of theories in molecular design through course study. One of my classes was *Advanced Chemical Engineering Thermodynamics* where I discussed representative papers about molecular simulation with Prof. Nicholas Abbott and other PhD students to understand the research carried out in this area. I appreciated this approach of graduate study because it made me feel more involved in research by providing us with opportunities to discuss open problems. I also joined Prof. Christos Maravelias’ Process Systems Engineering group where I learned mathematical models and algorithms of Linear Programming and Mixed Integer Linear Programming problems. I emulated the current best model for scheduling of multistage batch process under utility constraints with discrete time formulation by using continuous time formation. I built three new models and the correctness of my new models was validated by solving sample problems. This experience enhanced my capability for modeling and enriched my knowledge for numerical optimization, which are indispensable as a computational scientist in molecular engineering.

In order to be exposed to the frontiers of protein design, I undertook an internship in Prof. David Baker’s Lab at University of Washington this summer. I worked with a graduate student on de novo design of protein fiber using Rosetta, the computational tool of Baker Lab. We first docked our building blocks, someαhelical bundles, into helical structure, after which over five thousand docking structures were obtained and ranked by their second largest interacting surface area. I selectively visualized 20% of the output structures and classified the docking structures into four topologies. Among them, I selected 26 structures with “good” topologies and interacting surface areas based on previous experience of the lab. My heuristics proved to be helpful after the graduate student ran further design protocol, which would output hundreds of thousands of design structures, laborious and intimidating for manual selection. He also found excellent designs using the docking structures I selected. Moreover, after he used the 26 structures as training data to calibrate the parameters of the filter, more “good” docking structures were found and were in the process of design. I also worked with the graduate student to express and purify recombinant proteins in *E.coli*. The purified proteins were characterized using TEM and one protein sample displayed fiber-shaped structure.

I’m more passionate about protein design when I saw the amazing progress we made on building fibers. Moreover, by working in Baker Lab, I’m impressed by the advancement researchers made in protein design, from designing non-functional globular proteins to more complex functional proteins, such as enzyme, binders, and nanomaterials. I expect protein design will be one of the solutions in drug delivery, vaccine design, tissue engineering and chemical production. During my PhD, I’m eager to develop novel computational methods to improve the sampling efficiency and energy function in protein design. I will also collaborate with other researchers on designing and testing functional proteins. Finally, I’m well prepared for pursuing a PhD in computational protein design owing to my rich research experience and excellent background in mathematics and computer science. I’m always a good cooperator in my groups in China and America where I have closely collaborated and communicated with students and postdocs from different cultural and academic background.

UW MolE program has not only solid curricula on molecular design, synthesis, and characterization but also faculty working on my interested areas. I’m especially interested in Dr. David Baker’s work on computational protein design and experimental characterization. I admire Dr. Valerie Daggett, one of the leaders in using computational method to design diagnostic and therapeutic agents to target amyloid diseases. My background also pertains to Dr. Jim Pfaendtner’s work on computational enzymology and molecular simulation.

After receiving a PhD degree, I plan to be a leading scientist in academia. I am enthusiastic about making my own contributions to unmask the underlying mechanism of molecular interaction and improve the design methods. I look forward to collaborating with colleague on solving design problems, and guiding students through the excited process of scientific discovery.