
BIOGRAPHICAL SKETCH

NAME: Shataer, Shadikejiang

eRA COMMONS USER NAME: SSHATAER

POSITION TITLE: Graduate Student (Research/Teaching Assistant)

EDUCATION/TRAINING

| INSTITUTION AND LOCATION | DEGREE | Start Date | Completion Date | FIELD OF STUDY |
|--------------------------------|--------------------|------------|-----------------|--------------------------------|
| Shanghai Jiao Tong University | BA | 09/2011 | 07/2015 | Biotechnology (Bioinformatics) |
| University of Glasgow | Master of Science | 08/2016 | 07/2017 | Biotechnology |
| Birkbeck, University of London | Master of Research | 09/2018 | 06/2019 | Structural Biology |
| University of Delaware | PhD | 08/2019 | NA | Structural Biology |

A. Personal Statement

My initial fascination with structural biology was sparked during an undergraduate summer research project. I distinctly recall encountering a crystal structure of a human GPCR, and I was instantaneously captivated by the intricate insights the structure unveiled. Progressing to my master's studies, I delved deeper into X-ray crystallography, particularly focusing on membrane proteins, while engaged at the Cogdell laboratory at the University of Glasgow. Although the power of X-ray crystallography enthralled me, the challenge of obtaining well-diffracting crystals prompted me to approach the field with cautious optimism.

The advent of the 'Resolution Revolution' within Cryo-EM propelled me to explore this method further, under the guidance of Prof. Elena Orlova at Birkbeck College, University of London. Collaborating with an adept team, I achieved the atomic resolution structure of a phage portal protein within a year using Cryo-EM. This endeavor acquainted me with the theoretical underpinnings of Cryo-EM and image processing, as I employed RELION to analyze my structure, deepening my comprehension of this field.

During my doctoral studies at the University of Delaware, under the mentorship of Dr. Parashar, I gained practical expertise in integrated structural biology, along with additional biophysical techniques such as small-angle X-ray scattering (SAXS), microscale thermophoresis (MST), and analytical ultracentrifugation (AUC). Presently, my efforts are divided between two distinct projects necessitating the fusion of these aforementioned techniques. The first project centers on the comprehensive characterization of newly discovered enzyme inhibitors within the cyclic-di-AMP signaling pathway, while the second project focuses on the structural elucidation of enzymes integral to the same pathway. Overall, I am convinced that the current landscape of my research,

coupled with my proposed training plan, will furnish a robust groundwork for my enduring aspiration to establish myself as an academic researcher.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments:

2019 – Present PhD Student, College of Health Sciences, University of Delaware

Honors:

2023 **Poster Presenter**, Health Science Research Day, University of Delaware

2022 **Poster Presenter**, Health Science Research Day, University of Delaware

2014 Chinese National Merit Scholarship Program

2013 Chinese National Merit Scholarship Program

C. Contributions to Science

- 1. Masters Research Project:** While working in the Orlova lab at Birkbeck College, University of London, I was able to process a set of Cryo-EM data for a phage portal protein. Under the mentorship of Prof Orlova and Dr. Javed, I was able to quickly obtain an atomic structure¹.

Javed, A.; Villanueva, H.; **Shataer, S.**; Vasciaveo, S.; Savva, R.; Orlova, E. V. Cryo-EM Structures of Two Bacteriophage Portal Proteins Provide Insights for Antimicrobial Phage Engineering. *Viruses* **2021**, *13* (12), 2532. <https://doi.org/10.3390/v13122532>.

- 2. PhD Research:** My current doctoral research is centered around exploring the metabolic regulation of the cyclic-di-AMP signaling pathway, as well as its pivotal role within bacterial genome repair processes. My work has yielded intriguing findings, indicating that the enzyme responsible for synthesizing cyclic-di-AMP in *Mycobacterium tuberculosis* displays a distinctive structural pattern. This discovery holds promise in advancing the development of improved vaccines against this pathogen. I firmly believe that the outcomes of my research will bear substantial significance for human health. By shedding new light on the intricate mechanisms of this resilient and intricate pathogen, my findings have the potential to provide valuable insights into addressing complex health challenges.