Thesis Defense Announcement
To: The George Mason University Community

Candidate: Sarah Parron
Program: MS in Biology

Date: October 29, 2021

Time: 10:30 AM Eastern Time
Zoom Link: https://gmu.zoom.us/j/95483638035?pwd=NUJZbjFOVW5KS0hTQ0JJS0dsa1dWZz09

Title*: Computational Modeling of Francisella novicida Target Protein OppA with LL-37 Antimicrobial Peptide*

Committee Chair: Dr. Monique van Hoek
Committee Members: Dr. Iosif Vaisman, Dr. Amy K. Smith
All are invited to attend the defense.

ABSTRACT:
As a potential biological threat agent, the virulent bacterium Francisella tularensis remains an important topic of research. Understanding the mechanisms of action of antimicrobial peptides on F. tularensis is crucial to developing alternative treatments in the event of engineered or natural antibiotic resistance. The antimicrobial peptide LL-37 produces bactericidal effects in Francisella species and has demonstrated interaction with the membrane as well as periplasmic and intracellular proteins. One Francisella protein identified as an LL-37-binding protein is the periplasmic oligopeptide permease (Opp) complex protein, OppA.

To perform computational structural modeling of the Francisella's oligopeptide substrate-binding protein, crystal structure templates of homologs from several species were used to create models of F. novicida's OppA sequence. To characterize the interaction of OppA and LL-37, computational docking was performed on the LL-37 fragment, KR-12 and then on the longer fragment LL-20. These studies revealed the favorable binding of KR-12 and LL-20 within the cavity of the OppA protein. This computational modeling supports the experimental data. These studies also revealed significant insight on the effect of open or closed protein conformations on the computational docking process. This approach illustrates the power of computational docking to reveal information about potential bacterial protein targets of antimicrobial peptides.