Protein Structure Dynamics in Gram Negative Bacterial Secretion Systems
Nicholas Bragagnolo

Bacteria have evolved a variety of secretion systems that enhance their virulence. For example, type IV secretion systems allow for conjugative transmission of mobile DNA elements in bacteria, whereas type IV pili are akin to the type II secretion system and are responsible for promoting infection through host cell adhesion and twitching motility. Understanding the structure and function of all components in these systems would elucidate the mechanisms of bacterial commensalism and antagonism, and it would aid in the development of inhibitors to bacterial pathogenesis by disrupting the tools virulent species use for stable, long-term infections. The entry exclusion protein of the F-like type IV secretion system, TraG, consists of a membrane-bound N-terminal domain and a periplasmic C-terminal domain, denoted TraG*. TraG* is essential in preventing redundant DNA transfer through interaction with a cognate TraS in the inner membrane of the recipient cell to prevent conjugation when the recipient cell carries the same plasmid. Using a multitude of biophysical methods including small angle X-ray scattering and collision induced unfolding mass spectrometry, my research on the structural dynamics of TraG* provides evidence for the mechanism behind this long-distance interaction. This talk will also feature my research on the Type IV pilin of *Pseudomonas aeruginosa* strain P1, detailing how I solved the crystal structure of the protein using a processed AlphaFold model for molecular replacement.