Ackert Hall, Room 120
Wednesday, September 10, 2025
4:00 P.M.

Coffee and Cookies
Chalmers Hall, Room 168
3:45 P.M.

Biochemistry & Molecular Biophysics Seminar

Challenging the archetype: Exploration of a protein-protein interaction controlling *Vibrio fischeri* biofilm formation

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Bacillus subtilis anti-sigma factor antagonists SpoIIAA and RsbV are archetypes for bacterial single-domain STAS proteins. These proteins utilize a partner-switching mechanism with their cognate anti-sigma factor to regulate transcription. The *Vibrio fischeri* STAS domain protein SypA shares sequence similarity to the archetype proteins and is critical for biofilm formation. While SypA's role is unknown, we know biofilm formation is dependent on the phosphorylation state of SypA and that this is controlled by SypE, a dual functioning serine kinase/phosphatase. The kinase domain of SypE shares strong sequence similarity to the *B. subtilis* anti-sigma factors, suggesting SypA and SypE should function through a similar mechanism. We have found that despite the predicted similarities, SypA does not function as a typical anti-sigma factor antagonist. Using biochemical, biophysical, and computational approaches, we are building on years of cellular and genetic work to determine detailed molecular mechanisms of SypA and SypE. Our findings suggest protein dynamics and additional binding partners distinguish SypA as an atypical single-domain STAS protein.