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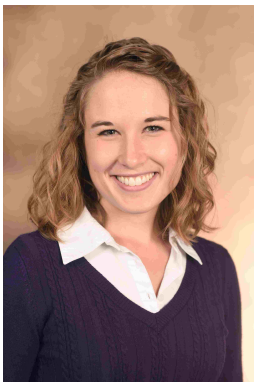

## 2018 Poster Presentation

**Membrane-targeted expression of proteins from B. burgdorferi in E. coli for structural and functional studies**

*Borrelia burgdorferi* employs unique integral-membrane proteins and lipoproteins to masterfully manipulate and evade the host immune system. Additionally, the pathogen is unable to synthesize key nutrients, and must uptake them from the host using integral membrane proteins. These membrane proteins are key to further understanding the *Borrelia* infection pathway and would make optimal drug targets. To the best of our knowledge, all membrane-associated protein structures for *B. burgdorferi* in the Protein Data Bank (PDB) have been determined by cleaving off the membrane-targeting signal sequences and folding the proteins in the cell cytoplasm. However, structures from other bacteria have shown that maintaining the signal sequence results in a completely different structure due to the influence of complex membrane protein folding pathways. Towards structure determination of membrane-integral proteins from *B. burgdorferi*, we have successfully expressed in *E. coli* several membrane-associated proteins with suspected roles in pathogenesis by maintaining the *B. burgdorferi* membrane targeting sequence, and screened two for membrane localization and detergent solubility.