Department of Molecular and Cellular Biology

Graduate Seminar MCB*6500

Friday, Jan. 19, 2018 in SSC 1511 @ 12 noon

presented by:

Laura Seidel

(Advisor: C. Khursigara)

"Investigating the structure of the cell division protein $FtsK_N$ in *Escherichia coli.*"

In bacterial cells, cytokinesis is carried out by the divisome; a highly complex, multi-protein machine. It is responsible for septum formation, constriction of membranes, and subsequent synthesis of septal peptidoglycan. The divisome protein FtsK (filamentous temperature sensitive protein K), is an integral membrane protein that coordinates cell division and chromosome segregation in *Escherichia coli.* The N-terminal end of FtsK ($FtsK_N$) is the only domain implicated in cell division and is of unknown structure. This project will use covariance-guided Rosetta *ab initio* modeling to solve the structure of $FtsK_N$. Recent integrations of co-evolution derived residue-residue contact predictions into the Rosetta algorithm allowed for the prediction of large protein structures within families of unknown structures. We will test the hypothesis that intraprotein residue contacts predicted by covariance analysis can be confirmed by showing that deleterious mutations in one site can be rescued by a complementary mutation in the interacting residue. The covariance predictions are then used to produce a constrained structural prediction in Rosetta. In parallel, work to determine the x-ray crystallographic structure of $FtsK_N$ will be pursued. The approaches taken in this project should serve as a general method for validating *in silico* predictions, as well as give insight into the structure of *E. coli* $FtsK_N$.