

W0400

Crystal Structures of Nucleotide and Non-Nucleotide Bound FtsZ from *Bacillus subtilis*. Scott Lovell*, Zachary Halloran*, Kathryn Hjerrild#, Dean Sheridan#, Alex Burgin#, Lance Stewart#, deCODE Biostructures, Woodridge, IL 60517*, Bainbridge Island, WA 98110#.

The tubulin homolog FtsZ, polymerizes in a reversible GTP dependent manner at the site of cell division and disassembles once cell division is complete.¹ We have determined the crystal structures of FtsZ from *Bacillus subtilis* in both non-nucleotide and nucleotide bound states. A primitive orthorhombic crystal form was observed that contained non-crystallographic dimers in the asymmetric unit and GDP in the nucleotide binding pocket of each subunit. The GDP was acquired from the expression host and could be displaced in one subunit after soaking the crystals in the presence of a non-hydrolyzable form of GTP (GTP- γ -S). C-centered orthorhombic and primitive tetragonal forms were also observed when grown in the presence of lithium sulfate. These crystal forms contain a monomer in the asymmetric unit and no nucleotide bound. However, sulfate molecules, that apparently displaced the GDP present in the expressed protein prior to crystallization, were observed in the nucleotide-binding pocket. These sulfate ions adopt positions within the nucleotide-binding pocket that would normally be occupied by the phosphate groups of GTP or GDP and serve as mimics for nucleotide binding.

¹ Romberg, L. and Levin, P.A., Annu. Rev. Microbiol. 2003, 57, 125-154.