SOLUTION STRUCTURE OF THE TOXIC *E. COLI* PEPTIDE, TISB

Beilin Li (Stephen R. Wassall, Bruce D. Ray, Philip A. Gurnev[1], and Horia I. Petrache), Department of Physics, Purdue School of Science, Indiana University–Purdue University Indianapolis, Indianapolis, Indiana 46202

Antibiotics act by interfering in bacterial metabolism. Thus, antibiotics are only effective against metabolically active bacteria while dormant cells are highly tolerant to antibiotics. Such persistent bacterial cells may be the main culprits in chronic infectious diseases resistance to antimicrobial therapy. In *Escherichia coli*, expression of a toxic peptide, TisB, sends cells into dormancy by decreasing the proton motive force thus decreasing ATP levels. TisB is a 29 amino acid residue peptide with 70% hydrophobic residues. It has a predicted alpha helical transmembrane domain spanning residues 6 - 28. In membrane channel studies, ion transport is observed with TisB and with some TisB mutants. As a preliminary to combining multi-dimensional NMR spectroscopy with circular dichroism to determine the structure of the TisB membrane ion transport complex in lipid micelles, NMR spectroscopy is used to determine the structure of TisB in ethanol.

[1]National Institute of Child Health and Human Development, Bethesda, MD 20892