Apr 12th, 9:00 AM - 10:00 AM

Structural Implications of Fluorescent Properties of the Global Transcription Factor, FNR

Melanie Zupancic
Illinois Wesleyan University

Laura Moore, Faculty Advisor
Illinois Wesleyan University

Poster Presentation P45

STRUCTURAL IMPLICATIONS OF FLUORESCENT PROPERTIES OF THE GLOBAL TRANSCRIPTION FACTOR, FNR

Melanie Zupancic and Laura Moore*
Department of Chemistry, Illinois Wesleyan University

The FNR protein is a transcription factor that allows *Escherichia coli* to undergo anaerobic cellular respiration. It is known to positively regulate the expression of several genes required for anaerobic respiration as well as negatively regulate genes responsible for aerobic respiration. Consequently, FNR is active under anaerobic conditions and inactive under aerobic conditions. Although the tertiary structure of FNR is unknown, previous studies have indicated that FNR is inactive in the monomeric state and active in the dimeric state. Thus, it is believed that in anaerobic conditions, FNR undergoes a conformational change from the monomeric to dimeric state. The mechanism involved in going from the monomeric to dimeric state is not completely understood, but it is thought to be triggered by the acquisition of a $[4Fe\text{-}4S]^{2+}$ cluster in the N-terminal region of FNR. The acquisition of the cluster causes a conformational change to be transmitted through the allosteric domain to the dimerization helix resulting in the active dimeric species. Information regarding the environment of amino acid residues in the dimerization helix in both the active and inactive forms of FNR could be helpful in eliciting a better understanding of the dimerization mechanism. Such environmental conditions can be determined by the fluorescent properties of the amino acid, tryptophan. Surface exposed tryptophan residues are expected to have a longer λ_{max} than those buried in the hydrophobic core. In order to gain insight into the environment of the amino acids on the dimerization helix we have created tryptophan mutants that either lay on or near the helix. The mutants LW146, KW163, and KW164 all lie on the periphery of the helix while MW147 lies on the helix. Of the four mutants, MW147 and KW163 retained anaerobic activity indicating that their structure is similar to the wild type protein with the exception of the single amino acid substitution. Because MW147 lies on the helix directly it is a better candidate to yield information regarding conformational changes along the helix during the monomeric-dimeric shift than KW163. By comparing the fluorescence of the active and inactive forms of MW147 and KW163, we hope to gain a better understanding of the dimerization mechanism of FNR.