## Structural Characterization of a Zinc-Coordinated Bis-Histidine Heme-Binding Site in The DUF2470 Cyanobacterial Protein

Estella F. Yee<sup>1</sup>, Kriti Chopra<sup>1</sup>, Nicolas Grosjean<sup>2</sup>, Desigan Kumaran<sup>1</sup>, Macon Abernathy<sup>3</sup>, James Byrnes<sup>1</sup>, Lin Yang<sup>1</sup>

<sup>1</sup>Brookhaven National Lab, <sup>2</sup>Joint Genome Institute, <sup>3</sup>Stanford Synchrotron Radiation Lightsource eyee@bnl.gov

A large family of domain of unknown function (DUF)-containing proteins was recently identified by phylogenomic studies to bind to heme. DUF2470 and related subfamilies of phototroph-specific homologs have diverse heme-related functions, but the structure- function link of DUF2470 itself had yet to be determined. In Synechocystis, DUF2470 forms single domain proteins and were discovered to bind heme and zinc ions, generating a unique two-fold symmetric, zinc-bound bis-histidine heme site. Structural and spectroscopic characterizations of the wild-type and variants lacking conserved histidine residues elucidate the importance of zinc-binding and histidine residues for heme-binding activity.

Results here supplement in vivo experiments and observed phenotypes that implicate DUF2470 in heme-dependent regulation of electron transport chains.