Project Name: Cryo-EM studies of protein allostery, motion, and evolution

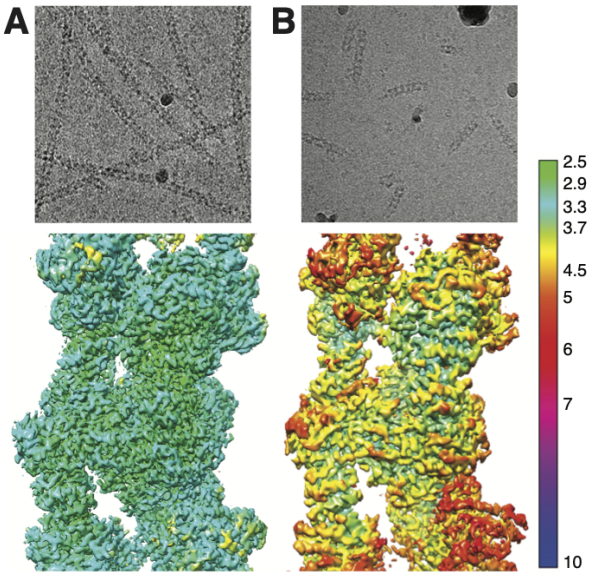

Figure 1. The emergence of a major clade of the RNR family found in many bacterial pathogens led to the loss of a conserved regulatory sequence. We previously found that a new form of allostery had evolved in a member of this clade involving filament formation [Thomas et al, Nature Comm 2019]. Here, we show a closely related RNR with 83% sequence identity. Interestingly, the filament stability depends on the identity of the allosteric inhibitor (panels A and B). These unpublished data were collected at NCCAT and set the stage for a comprehensive study of how allosteric mechanisms evolve within an enzyme family.

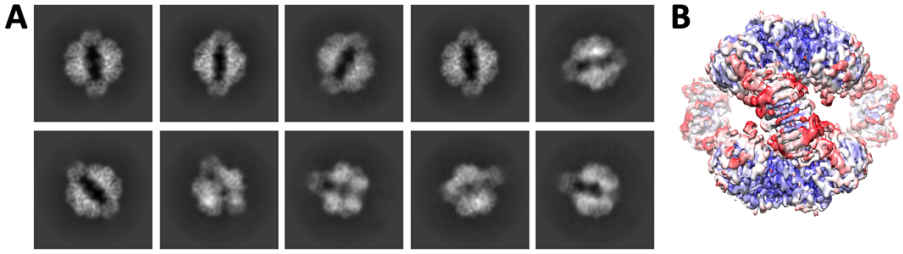

Figure 2. (A) Clear secondary structure is evident in representative 2D classes of *E. coli* ATCase under conditions optimized by SAXS. (B) Preliminary refinements led to a ~3.5 Å map.

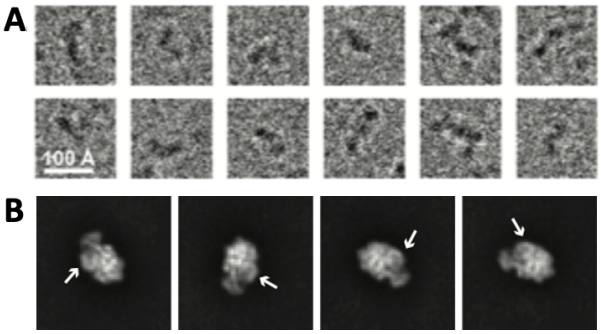

Figure 3. (A) Representative individual particles depicting the flexibility of methionine synthase. (B) Representative 2D classes depicting selective binding of flavodoxin (arrow) to the C-terminal domains of methionine synthase. The details of this interaction have been investigated by other methods, but not structurally. High-resolution structures of this system will reveal how a flexible enzyme controls specificity.