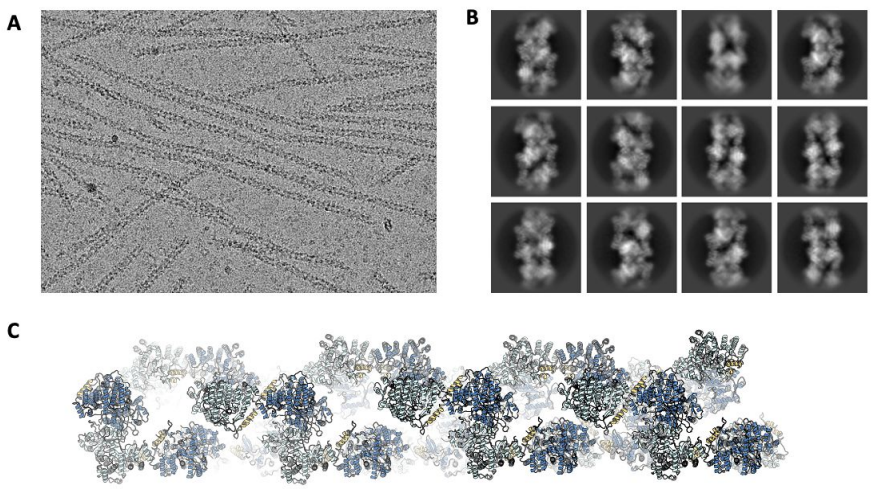

Figure 1: Representative micrograph (A) and 2D class averages (B) from *B. clausii* ribonucleotide reductase filament. We expect the resulting structure to be reminiscent of our previously published *B. subtilis* inhibited filament (C), but the allosteric effectors differ. Resolving the identities of the bound ligands and details within the binding sites is integral to understanding the evolution of allostery in RNRs.

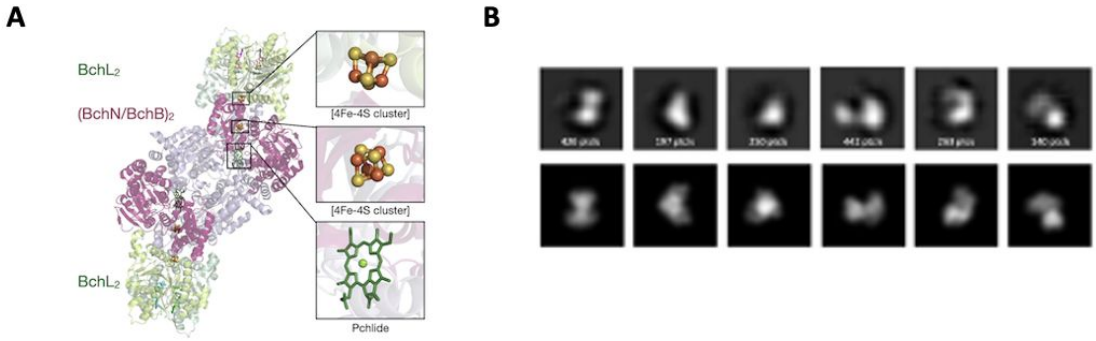

Figure 2. (A) Crystal structure of the ADP-AlF4-stabilized full DPOR complex (360 kDa). The architecture is analogous to the nitrogenase system. (B) Preliminary negative-stain EM data on the core subunit of DPOR (209 kDa). Top: 2D class averages from initial negative-stain EM done on a T12 microscope. Bottom: Projections of the crystal structure simulated at 20-Å resolution.

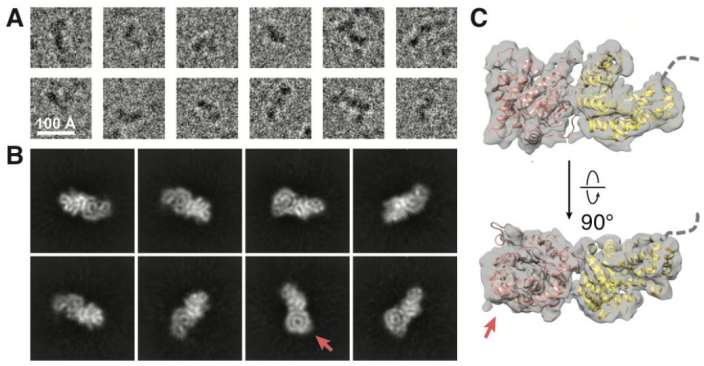

Figure 3: (A) Representative individual particles showing the full-length methionine synthase protein. (B) Reference-free 2D classes align to the more rigid N-terminal half of the protein (~71 kDa). High-resolution classes do not show the highly flexible C-terminal half. (C) Initial 5-Å reconstruction of the N-terminal half of the protein, with homology models of the relevant domains fit to the map as rigid bodies.