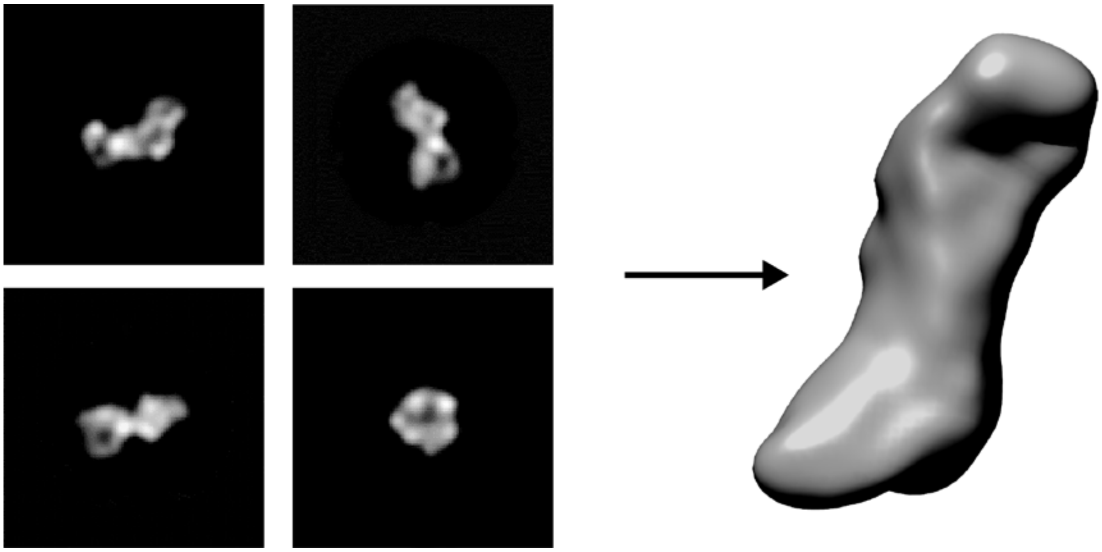

Figure 1. Negative Stain classes and model for the full *S. epidermidis* effector complex. Purified effector complex negative stain 2D classes and 3D reconstruction. The complex falls apart in ice and it has not been possible to solve the structure to high resolution. The structure of a subcomplex, with the missing subunits, has been solved to 5.2 Å resolution (Dorsey, B. W., Huang, L. & Mondragon, A. Structural organization of a Type III-A CRISPR effector subcomplex determined by X-ray crystallography and cryo-EM. *Nucleic Acids Res* **47**, 3765-3783, doi:10.1093/nar/gkz079 (2019)).

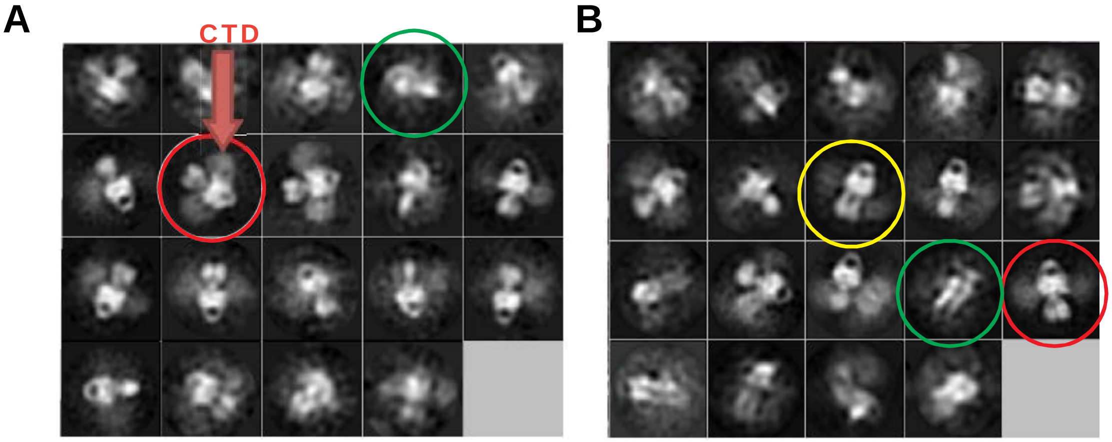

Figure 2. **Complex of gyrase with DNA.** 2D classification of particles from 2 small datasets collected by cryo-electron microscopy. (A) Representative 2D classification from 3,900 particles. (B) 2D classification from 6,660 particle. The particles in the red circles are representative of front views of the enzyme. The particles in green circles are representative of a side view. The particles in the yellow circle highlights an alternate conformation compared to the particles circled in red. The work is a continuation and expansion of previous work in the laboratory (Soczek, K.M., Grant, T., Rosenthal, P.B., Mondragón, A. CryoEM structures of open dimers of gyrase in complex with DNA illuminate mechanism of DNA passage. *eLife* e41215*,* 2018).