## Figures.

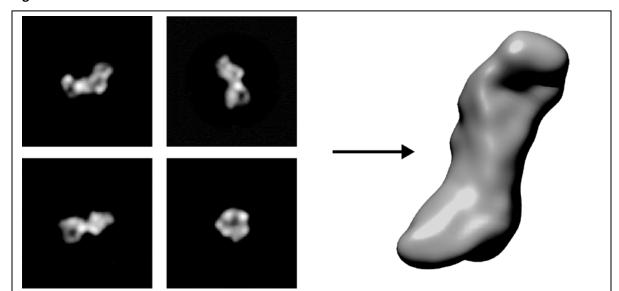


Figure 1. Negative Stain 2D classes and model for the full *S. epidermidis* effector complex. Purified effector complex negative stain 2D classes and 3D reconstruction. The complex falls apart in ice and it has not been possible to solve the structure to high resolution. The structure of a subcomplex, 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)).

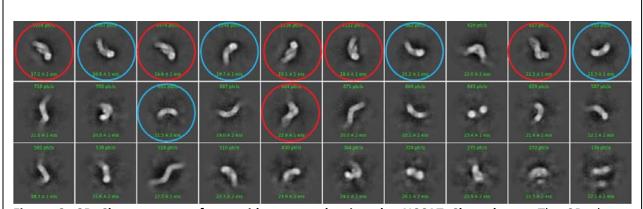


Figure 2. 2D Class averages from grids prepared using the NCCAT Chameleon. The 2D classes correspond to the ones expected from the full complex (red circles), but that we have not seen before in ice. The cyan circles represent classes associated with the subcomplex. Note in particular the presence of a second strand or ribbon in the red-circled classes. We interpret this second strand as the ribbon formed by the csm2 protein, which is missing in the subcomplex. Compare also the red-circled class in the second row with the classes in Figure 1. We have not seen the full complex classes before in ice, only in negative stain grids. Given the number of particles in the main classes, we anticipate an approximate 50/50 distribution of the full complex and the subcomplex. Classes shown were calculated using CryoSPARC by the staff at NCCAT. We have reproduced them in our laboratory using both CryoSPARC and Relion.

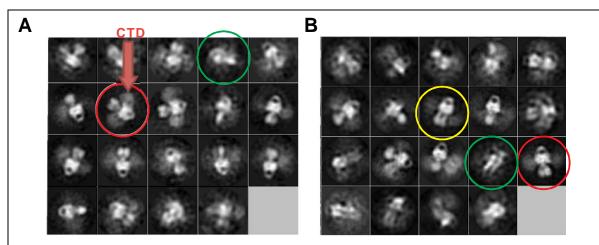


Figure 3. Complex of Synable Inc. 2008 September 2. Particles from two small datasets collected by cryo-electron microscopy. (A) Representative 2D classification from 3,900 particles. (B) 2D classification from 6,660 particle. The particles in the red circles are representative of front views of the 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).