Figure 1. CryoEM structure of ArnT from *Salmonella enterica* at 3.2Å global resolution. (**A**) Representative micrograph from the dataset of 1457 micrographs that yielded the 3.2Å global resolution reconstruction. The dataset was collected at Columbia U. Krios 3 (at SEMC/NYSBC) equipped with energy filter and Gatan K2 direct detector. Scale bar corresponds to 100nm (**B**) Representative two-dimensional class averages after reference-free classification of the final particle stack (extracted in a 256 pixel box, ~210Å) after particle polishing in Relion. (**C**) Fourier shell correlation (FSC) curve generated after the final non-uniform refinement in cryoSPARC.v2. (**D**) CryoEM map of ArnT$_{Se}$ embedded in nanodisc is shown in purple (semi-transparent). The model built based on this map is colored in blue and is superimposed to the CryoEM map. Some partial densities for the nanodisc (weak densities in the periphery) are visible at this contour level. (**E**) ArnT$_{Se}$ model is shown in hazel. Models for the ligands (Lipid A in magenta and undecaprenyl phosphate in blue) are superimposed to the corresponding densities from the cryoEM map shown in teal. (A-E) Petrou, V, and Mancia, F, unpublished data.