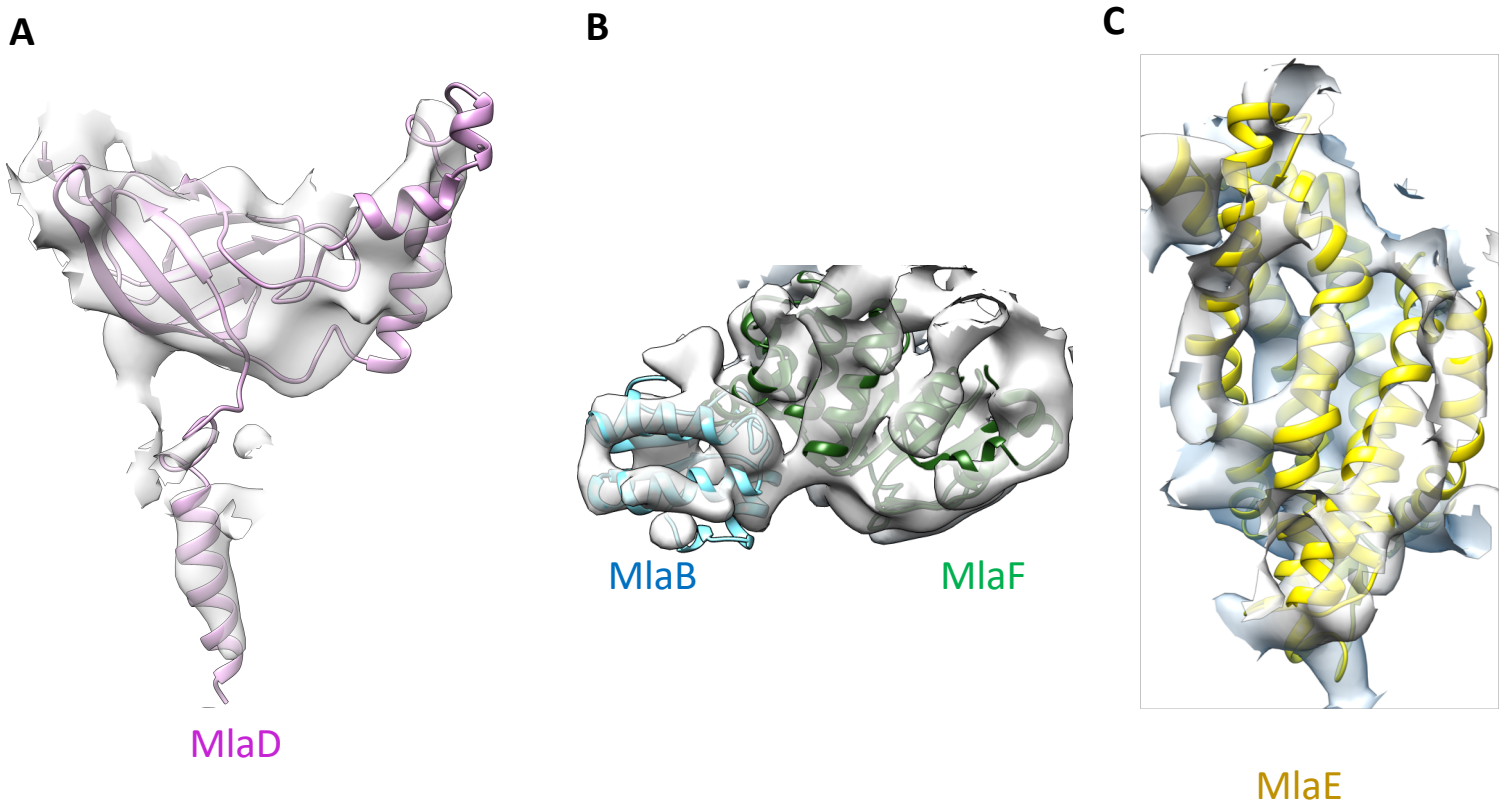


**Figure 2 - figure supplement 4. Close-up view of the MlaB, MlaD, MlaE and MlaF models in the abMlaBDEF cryo-EM map.** (**A**) Region of the density corresponding to a MlaD monomer, with the corresponding atomic model in magenta. The density of the N-terminal helix is well resolved, as well as that of the A. baumannii-specific insert. (**B**) Region of the density corresponding to a MlaF-MlaB hetero-dimer, with the corresponding atomic models in green and cyan respectively, shown from two different angles. Density for helices are well defined for most of the model. (**C**) Region of the density corresponding to a MlaE monomer, with the corresponding atomic model in yellow.