

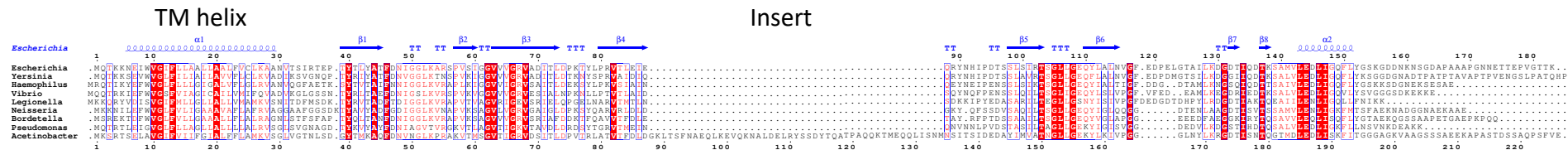
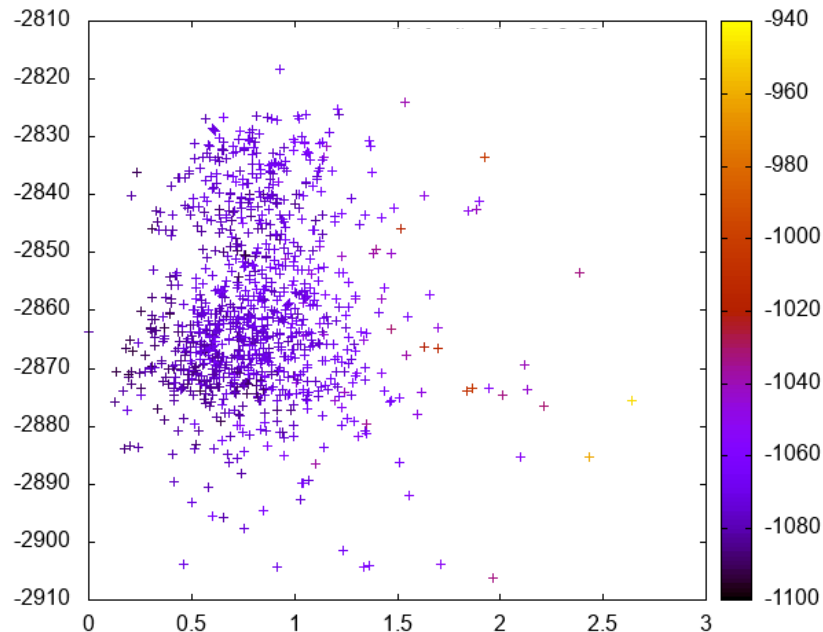
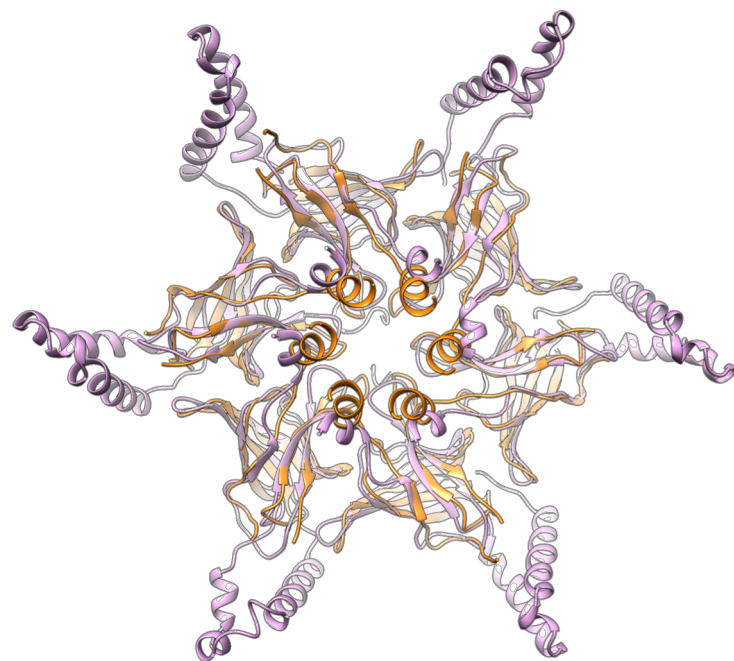
A**B****C**

Figure 2 - figure supplement 3. Modeling of the abMlaD hexamer. (A) Multiple alignment of MlaD sequences from various gram-negative human pathogens. The secondary structure for ecMlaD is shown at the top. The position of the abMlaD insert is indicated. (B) Result of the all-atom refinement step for the MlaD hexameric model. The energy of each model is plotted versus the RMSD relative to the initial model, and color-coded for the fit to the EM map density. (C) Cartoon representation of our abMlaD hexameric model (magenta), superimposed to the crystallographic ecMlaD hexamer structure (grey).