

Figure S5

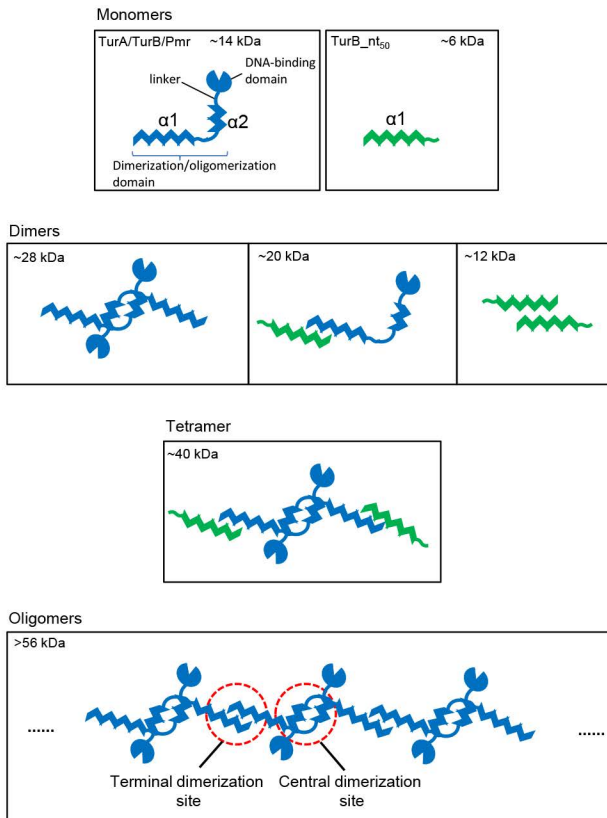


Figure S5 Model of expected mode of interaction between full-length TurA, TurB or Pmr and TurB_nt₅₀ variant inactivated at the central dimerization site. Dimerization/oligomerization domain, flexible linker and DNA-binding domain in the full-length TurA, TurB and Pmr model are indicated. Secondary structural features of the dimerization/oligomerization domain (helices $\alpha 1$ and $\alpha 2$) are presented based on the solved structure of TurB_nt₆₁-R8A [21]. Expected dimers, tetramers and oligomers are shown (see also Fig. 2). Central and terminal dimerization sites in the oligomer model are shown.