Figure S1

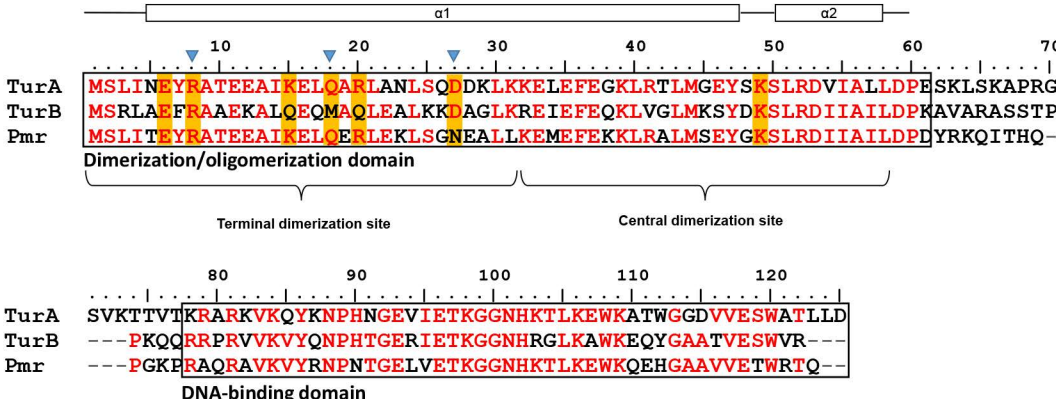

Figure S1 Amino acid sequence alignment of TurA, TurB and Pmr. Alignment was performed using ClustalW software version 2.1 (http://clustalw.ddbj.nig.ac.jp/). Amino acid residues identical in at least two members are shown in red. Dimerization/oligomerization and DNA-binding domains connected by the linker are indicated. Secondary structural features based on the solved structure of TurB_nt$_{61}$-R8A [21] are shown. Boxes indicate helices (α1, α2) and lines indicate unstructured loops. Central dimerization site (residues 1-31) and terminal dimerization site (residues 32-58) are indicated. The seven amino acid residues found in a previous study [20] to be important for homo-oligomerization of Pmr and the corresponding residues in the other proteins are highlighted in orange. The three amino acid residues found to be important for homo-oligomerization of TurB [21] are indicated with blue arrows.