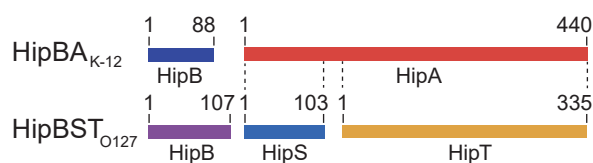
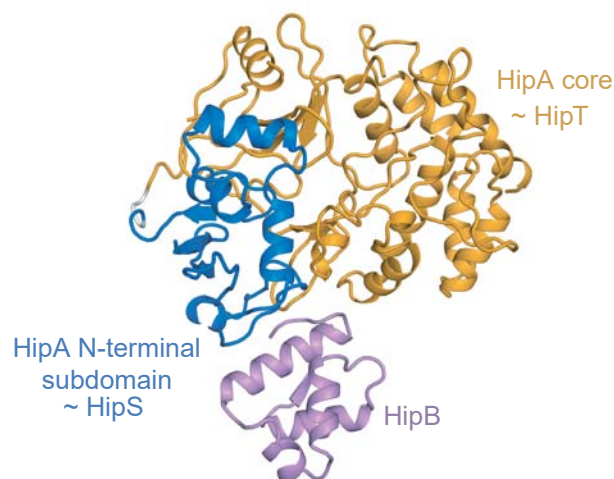
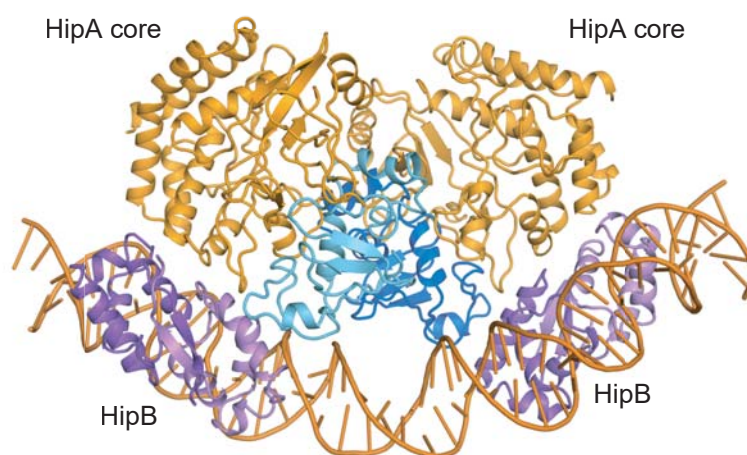


A



B



C

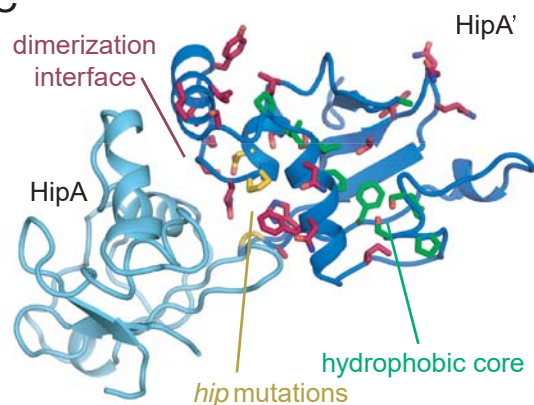


Figure S9

Figure S9. Modelling of the HipBST_{O127} complex structure.

(A). Top; the crystal structure of *E. coli* HipBA (PDB ID: 4YG7) colored according to a sequence alignment with HipBST_{O127}, with the part corresponding to HipB_{O127} in purple, HipS_{O127} in blue, and HipT_{O127} in yellow. Bottom; schematic overview of the sequence alignment with colors as above. HipA of *E. coli* K-12 is shown in red.

(B) The structure of HipBA bound to DNA shows that the part corresponding to HipS_{O127} (the HipA N-terminal subdomain) mediates complex dimerization in the DNA-bound form.

(C) The N-terminal subdomain of HipA contains a hydrophobic core conserved in HipS_{O127} (green) but a divergent dimerization interface (red). Two high-persister mutations in the N-subdomain-1 of HipA conserved among HipS orthologs are shown in yellow.