Structures and dynamics of hibernating ribosomes from *S. aureus* mediated by intermolecular interactions of HPF

Iskander Khusainov, Quentin Vicens, Rustam Ayupov, Konstantin Usachev, Alexander Myasnikov, Angelita Simonetti, Shamil Validov, Bruno Kieffer, Gulnara Yusupova, Marat Yusupov and Yaser Hashem

APPENDIX

Appendix Figure legends Appendix Figure S1 Appendix Figure S2 **Appendix Figure S1.** Binding of SaHPF induces conformational changes of flexible elements. RMSD calculated between the coordinates of the unrotated vacant ribosome (PDB ID 5LI0; (Khusainov et al., 2016b)) and the unrotated SaHPF-bound ribosome in our reconstructed dimer. RMSD were overlaid on the three dimensional structure of the vacant ribosome.

Appendix Figure S2. Binding of SaHPF likely interferes with dynamics at the decoding site in helix 44, which is targeted by aminoglycosides like gentamicin (red). Ribosome bound SaHPF was overlaid on the structure of the E. coli ribosome bound to gentamicin (PDB ID 4V53, (Borovinskaya et al., 2007)).



