**Fig. 6B. Synergistic effects in NagB protein-protein interactions (PPIs) may be the result of simultaneous binding of protein partners.** (A-C) Structural models of simultaneous binding are shown for NagB + HPr + NanE (A) as well as NagB + HPr + U-PII (B). The binding of HPr to NagB does not sterically obstruct the binding of either NanE (A) or U-PII (B) in the model, but the binding of NanE to NagB does sterically obstruct the binding of U-PII (and vice versa) (C). *Inset:* Binding sites for HPr, NanE, and U-PII on the surface of NagB. Interacting residues are colored according to the binding partner, and shared residues between NanE and U-PII are colored in grey. Note that the majority of the NanE and U-PII interfaces on NagB overlap with each other. Residues indicated by black lines are shared among all three NagB partners. Functional NagB is a hexamer in which the cavity (not shown) interacts with solvent; the inter-subunit trimer contacts, a loop spanning residues 216-223, are indicated by a heavy dashed line, while the inter-trimeric contacts (residues 244-250) are indicated by a light dashed line. The orientation of the NagB monomer with respect to the greater hexamer is indicated by dashed arrows. PDB IDs and chains used for NagB, HPr, and U-PII were 1FS5:A, 3CCD:A, 5L9N:A. 1FS5:A is a structure of the open, “R” conformation of NagB, and 5L9N:A is a structure of uridylated PII. For NanE, the full-length Swiss Model Repository model based on the template 3IGS:A (79.7% sequence identity) was used.