**Structural modeling.** HPr, NanE, and U-PII were each docked to NagB individually using the HADDOCK webserver with CPORT predicted interface residues as active and passive restraints. All structures from clusters with negative z-scores (below average energy scores, among clusters of the top 200 structures) were considered in the modeling. Docked complexes for HPr+NagB, NanE+NagB, and U-PII+NagB were aligned by NagB in Pymol. The #4, #1, and #3 clusters for HPr+NagB, NanE+NagB, and U-PII+NagB were selected for further analysis, as these allowed unobstructed orientations for HPr and NanE, as well as HPr and U-PII, in their bound state with NagB. The HPr+NagB and NanE+NagB clusters were both the largest (greatest number of docking models) clusters from their respective docking runs, while the U-PII+NagB cluster was the second-largest. The 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.