Supplemental Figure 4. Structural modeling of the Hk1 SBP domains. Left. Predicted three-dimensional structures of the Hk1 substrate-binding domains D1 and D2 (cyan) aligned with (A) ArtJ from *Geobacillus sterothermophilus* and (B) GlnBP from *E. coli* (orange), respectively. Right. Predicted ligand coordination residues for D1 and D2 (cyan) aligned with those of ArtJ and GlnBP (orange); residue numbers in parentheses correspond to the *B. burgdorferi* Hk1. The corresponding ligands for ArtJ (lysine) and GlnBP (glutamine) are shown in magenta. The 3D models for Hk1 D1 and D2 domains were generated on the Swiss-Model server (http://swissmodel.expasy.org) using ArtJ (Protein Data Bank: PDB 2Q2A) and GlnBP (Protein Data Bank: PDB 1WDN) structures, respectively, as templates. Figures were generated using the program PyMol (http://www.pymol.org).