

SUPPLEMENTARY INFORMATION FOR

**Crystal structure of the phosphate binding protein (PBP-1) of an
ABC-type phosphate transporter from *Clostridium perfringens***

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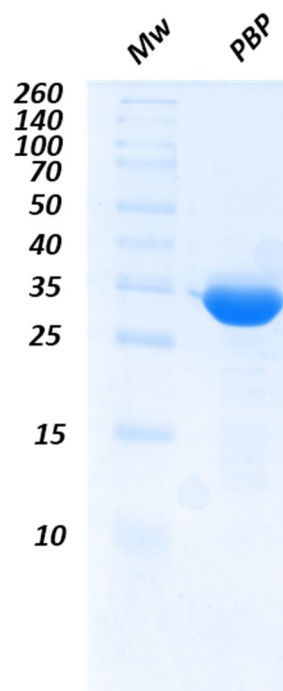


Figure S1: Coomassie-stained SDS-PAGE 15% of the PBP-1 from *C. Perfringens*. The left lane correspond to the molecular weight marker (Mw). Each bands correspond to a molecular weight indicated in kiloDalton (kDa, Spectra Multicolor broad range protein ladder). The right lane corresponds to the PBP-1 from *C. perfringens* after the expression and purification steps.

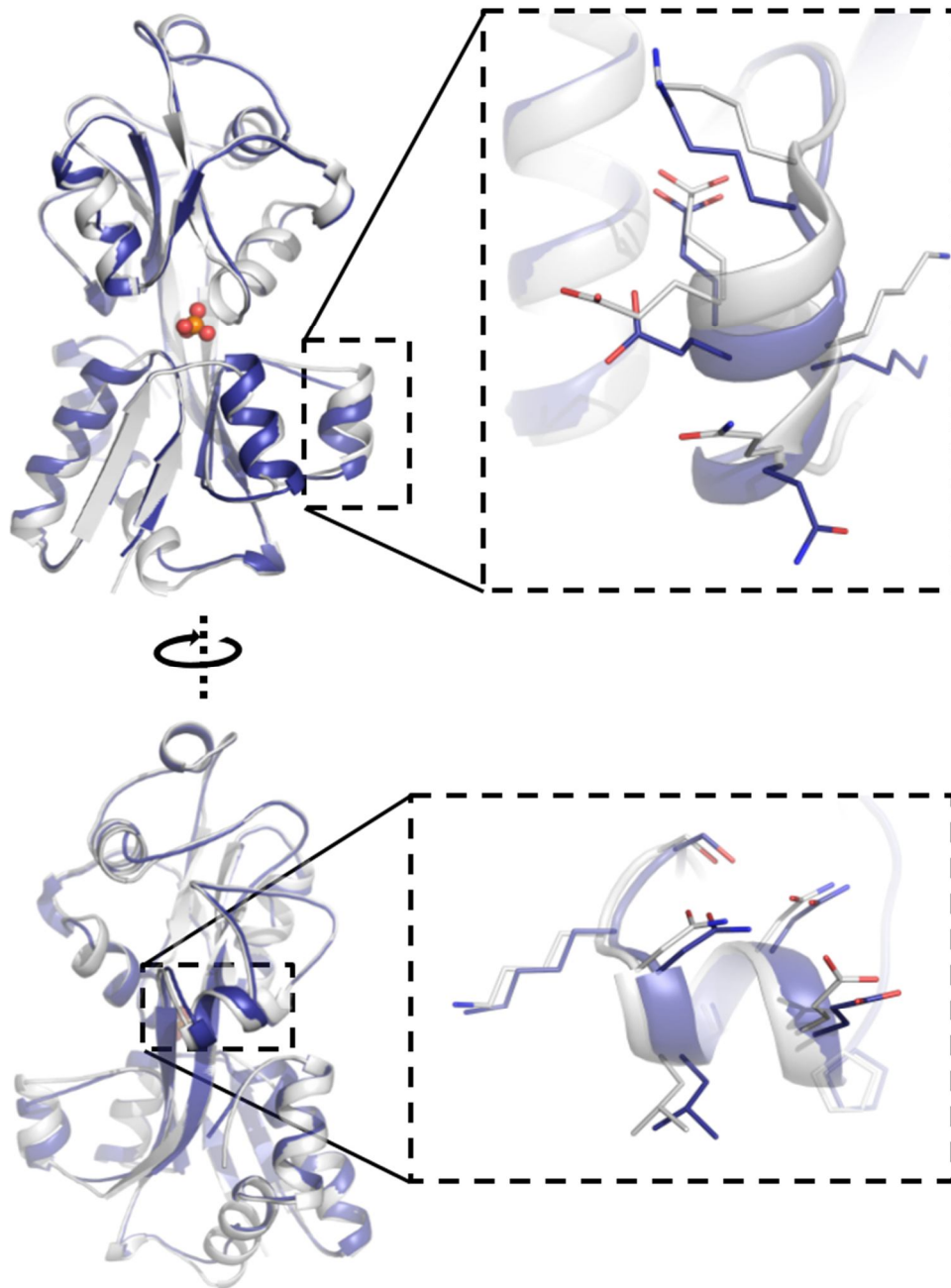


Figure S2: Structural alignment with *C. perfringens* PBP-1 from the CSGID. Structure available on the protein data bank (pdb 4GD5, colorized in light grey) was aligned to the structure solved herein (PDB ID 4Q8R, colorized in deepblue). Both structures are represented in cartoon. Residues of the boxed α -helix are represented in sticks.

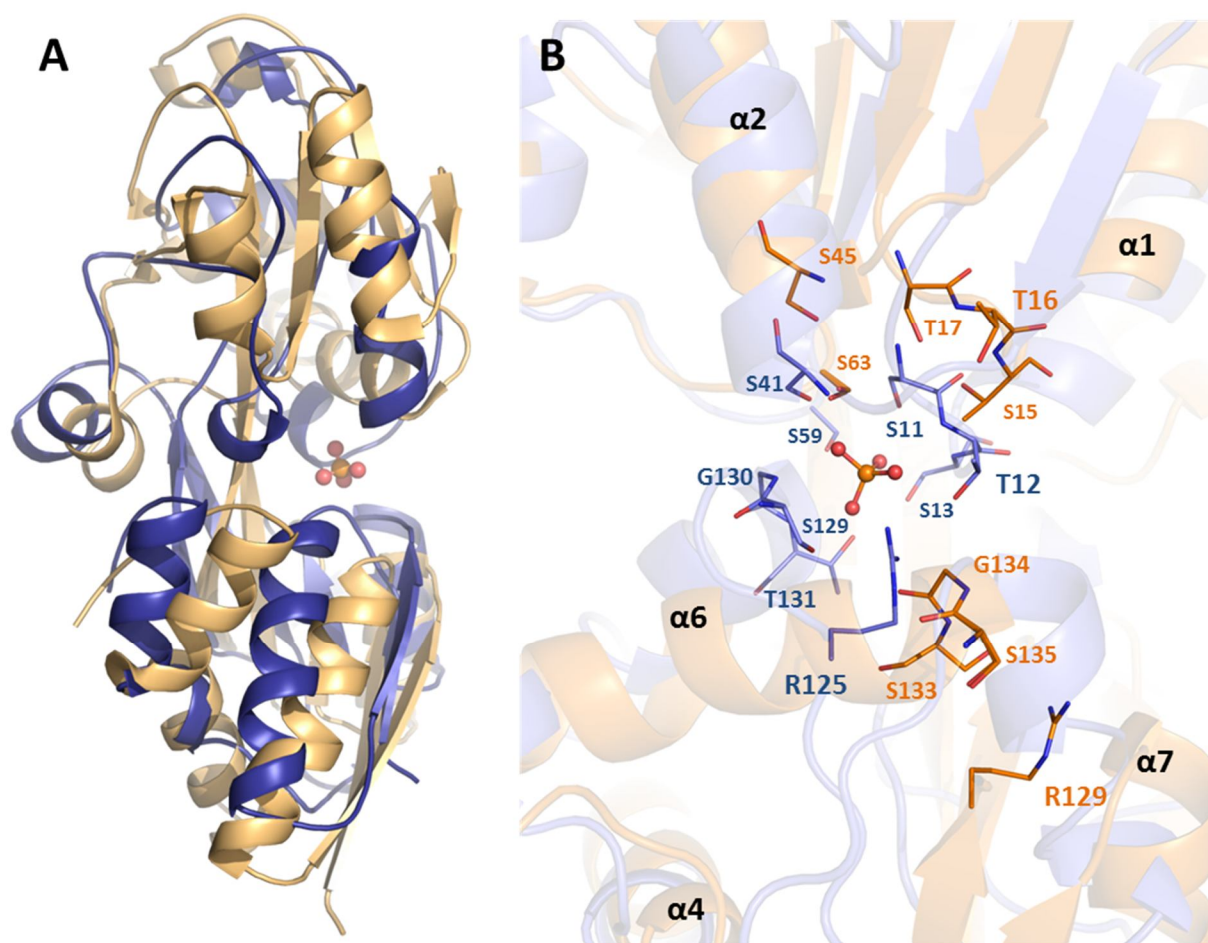


Figure S3: Structural comparison of *C. perfringens* and *B. Burgdorferi* B31 PBPs. A.

Structures of PBP-1 from *C. perfringens* and *B. Burgdorferi* are depicted in cartoon and colorized in blue and orange, respectively. Phosphate molecule is represented as spheres. **B.** Residues involved in phosphate binding in both structures are depicted in sticks and colorized using the same color code as (A.). Helix number (from tri-dimensionnal structure) are indicated in black.

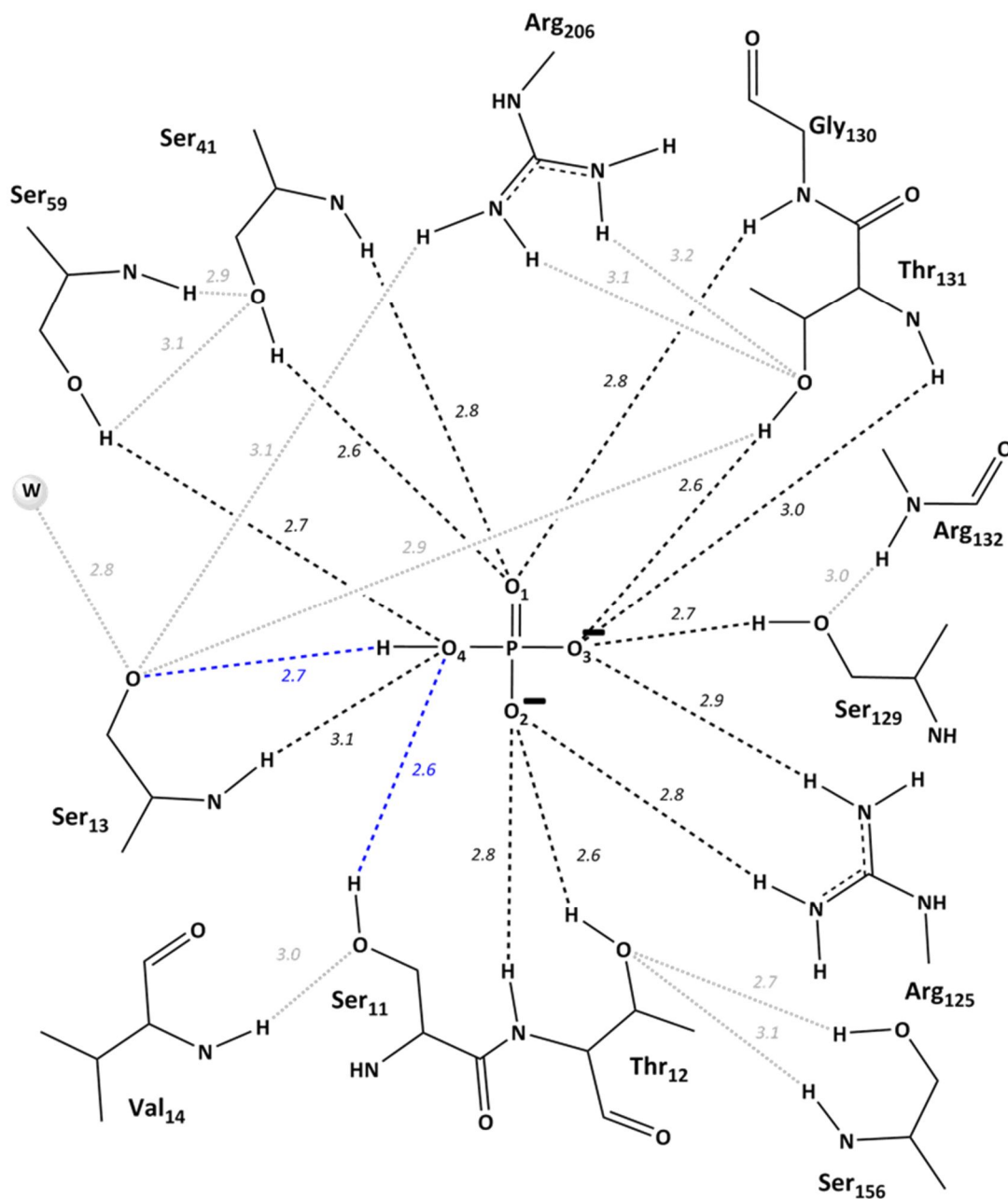


Figure S4: Schematic diagram of the hydrogen bond network in the phosphate binding site of PBP-1 from *C. perfringens*. Hydrogen bonds performed between the protein and the phosphate anion are shown in black dash lines. Hydrogen bonds unique to PBP-1 are colored in blue. Second shell hydrogen bonding to residues involved in phosphate binding is colored in grey. Distances are indicated in Ångstroms.