Acta Cryst. (2019). F**75**, doi:10.1107/S2053230X1900178X Supporting information

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Supporting information for article:

Crystal structure of the putative peptide-binding protein AppA from *Clostridium difficile*

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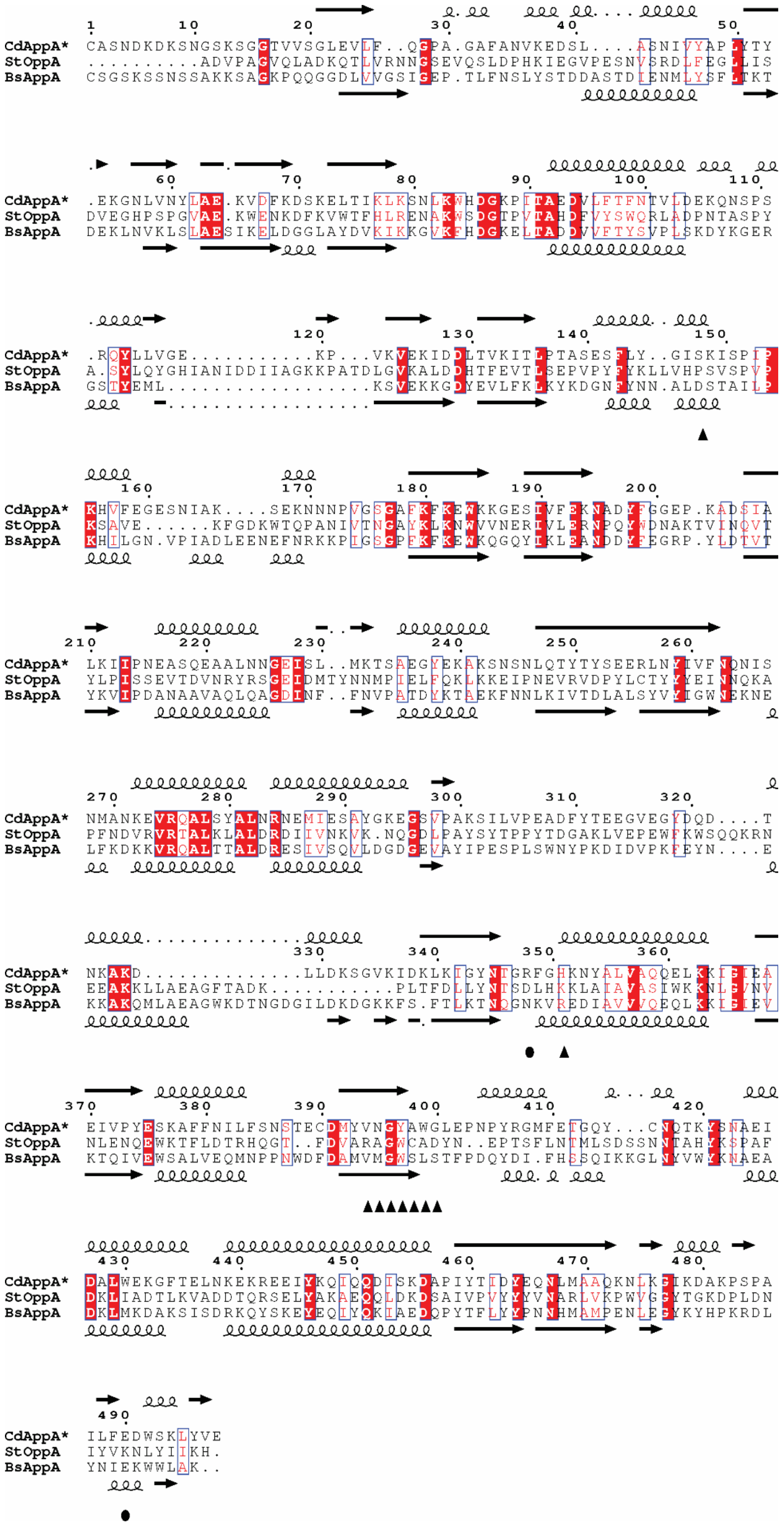
CdAppA*
StOppA
BsAppA

Figure S1 Alignment of the sequence of *Cd*AppA with those of *St*OppA and *Bs*AppA. Secondary structure elements in *Cd*AppA and *Bs*AppA are displayed above and below the alignment respectively. Invariant and conserved residues are in red filled boxes and blue outlined boxes respectively. Residues/motifs involved in peptide binding in *St*OppA and *Bs*AppA, which are discussed in the text, are highlighted by black triangles below the sequence. These features are not conserved in *Cd*AppA. Residues that might be involved in peptide binding in *Cd*AppA are highlighted by black circles below the sequence. The asterisk of *Cd*AppA* indicates that residues 1-30 are a hybrid N-terminal sequence containing part of the recombinant fusion tag (residues 20-30).