

**S3 Fig. Alignment of amino acid sequences of NT*Hi* SapA (UNIPROT=Q4QL73) with its closest structural homologs** *Hp*HbpA (UNIPROT=B8F653), *Ec*DppA (UNIPROT=P23847) and *Pseudoaltermonas* sp. SM9913 DppA (UNIPROT=A7Y7W1). Non-conserved NTHi SapA residues discussed in the main text are highlighted in solid green. α-helices are displayed as squiggles respectively. β-strands are rendered as arrows, strict β-turns as TT letters. Figure generated with *ESPript 3.0*[67]*.*