Amino acid sequence alignment of *H. pylori* DnaB (HpDnaB), related *Campylobacter jejuni* DnaB (CjDnaB) and *E. coli* DnaB (EcDnaB). The alignment was done using CLUSTALW multiple alignment software. The WALKER A nucleotide binding domain (ARPSMGKT) and 34 amino acid insertion region at the ‘C’ terminus of HpDnaB, not present in EcDnaB are marked in bold. The relative positions of different deletion mutants of HpDnaB are marked by ‘Ñ’. The start point of *E. coli* deletion mutant (EcDelN156) that shows *in vitro* ATPase activity but no helicase activity (comparable to HpDelN2) is marked by arrowhead (↑).