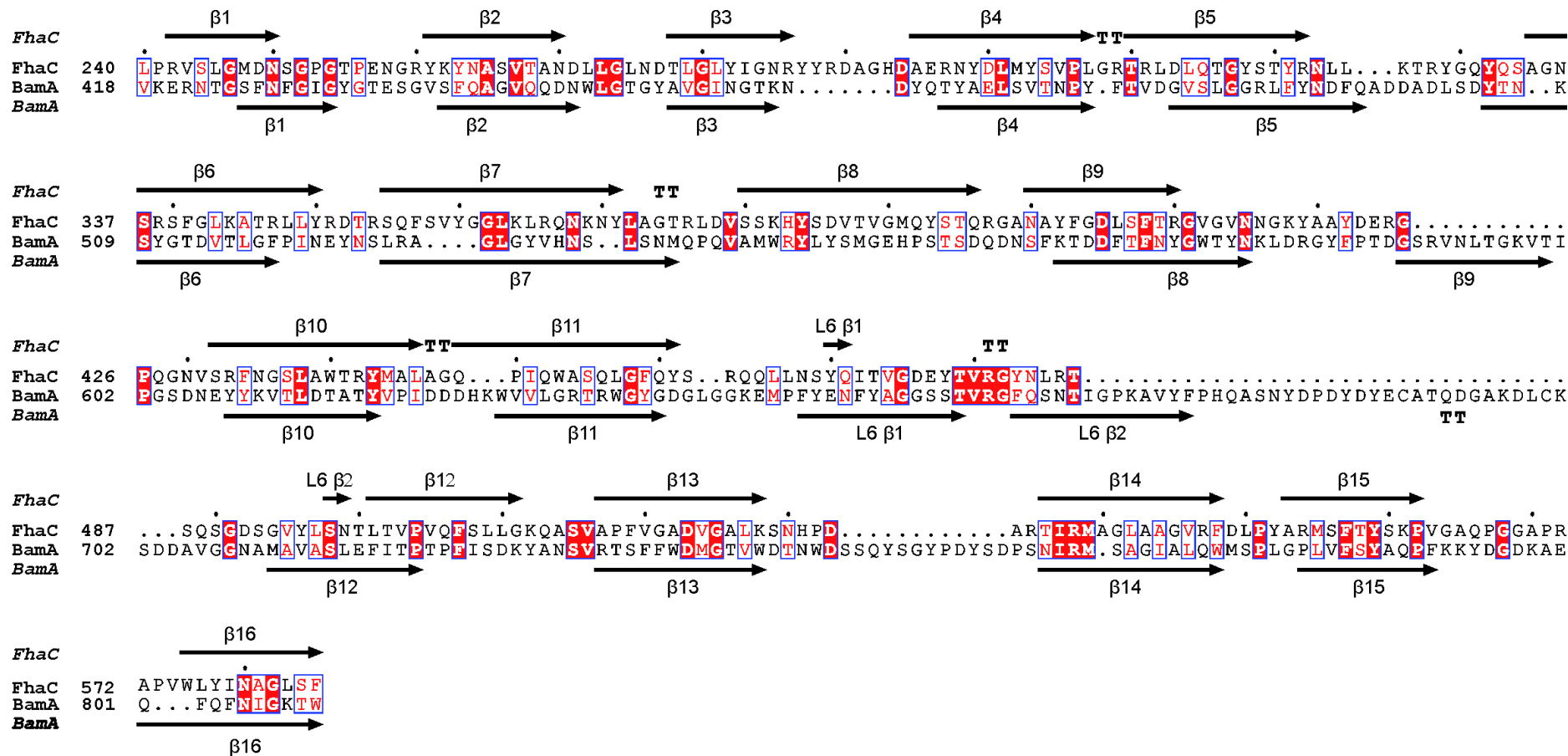


**Fig. S7.**



**Figure S7. Alignment of the  $\beta$ -barrel domains from BamA and FhaC.** The figure shows the alignment of the  $\beta$ -barrel domain of FhaC from *Bordetella pertussis* (GenBank CAA46092) with that of BamA from *E. coli* K-12 (GenBank AAC73288). Secondary structure for FhaC is derived from the crystal structure of FhaC (2QDZ) [13] and is shown above the alignment, whilst that for BamA is from our model predictions and is displayed below (see Fig. 2). Predicted  $\beta$ -strands in loop L6 are labelled as L6  $\beta$ 1 and L6  $\beta$ 2.