

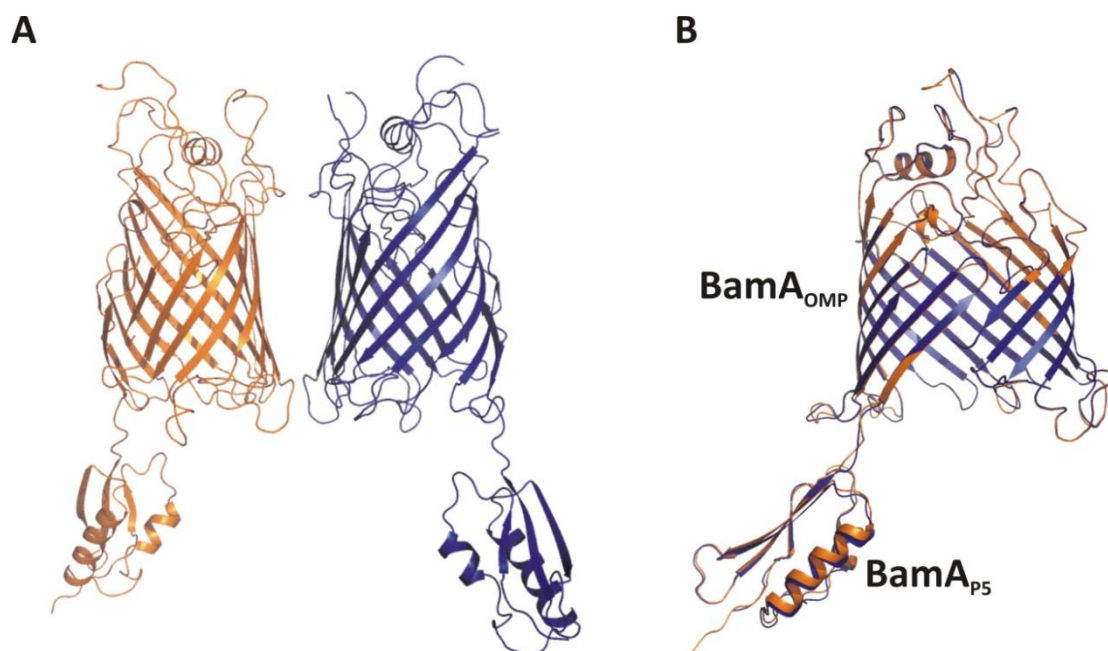
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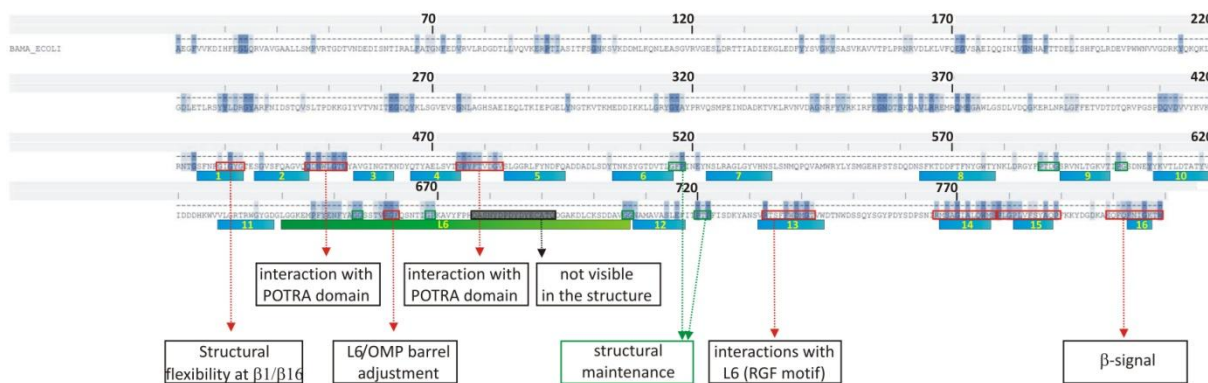
Supporting information for article:

**Structure of BamA, an essential factor of outer membrane protein biogenesis**

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**Figure S1** Asymmetric unit composition and superposition of monomers. (A) The asymmetric unit of BamA<sub>P5</sub> is composed of two molecules shown in orange and blue which interact by hydrophobic contacts. (B) The superposition of the two structures shows a strong similarity of the monomers with an r.m.s.d. of 0.7 Å.



**Figure S2** Alignment of BamA sequences and conservation analysis of BamA from *E. coli*. The alignment demonstrated resembles in line with our previous publication on the BamB – BamE structures in JBC [(Albrecht & Zeth, 2011)]. The alignment was performed by CS-BLAST (<http://toolkit.lmb.uni-muenchen.de/>) and conserved positions were identified, ranked and presented using the program FRpred from the toolkit server of the LMU, Munich, Germany (<http://toolkit.lmb.uni-muenchen.de/>). Conserved positions are colour coded by four different blue tone levels (light - dark blue). Residues colour coded in light blue are less conserved than residues coloured in dark blue. The topology of the  $\beta$ -barrel strands of BamA<sub>OMP</sub> is indicated with blue bars which are numbered in yellow. The longest and most highly conserved loop structure L6 is marked as green bar and the highly conserved and functionally important RGF motif is encircled in red. Additionally conserved motifs were encircled in red and assigned to functions according (e.g.  $\beta$ -signal, POTRA-OMP interaction) to data of the structure and literature. Small conserved motifs of BamA are marked in green and can be assigned to the structural maintenance of the overall fold, e.g. GG or GP motifs in periplasmic turns.