



Figure S2 Alignment of BamA POTRA 5 and FhaC POTRA 2 domains. FhaC sequence comprises residues 165 to 238 of *Bordetella pertussis* FhaC. BamA sequence comprises residues 347 to 421 of *Escherichia coli* BamA. Sequences were aligned using COBALT. Secondary structure was determined for FhaC and BamA from crystal structures 2QDZ and 3OG5, respectively.