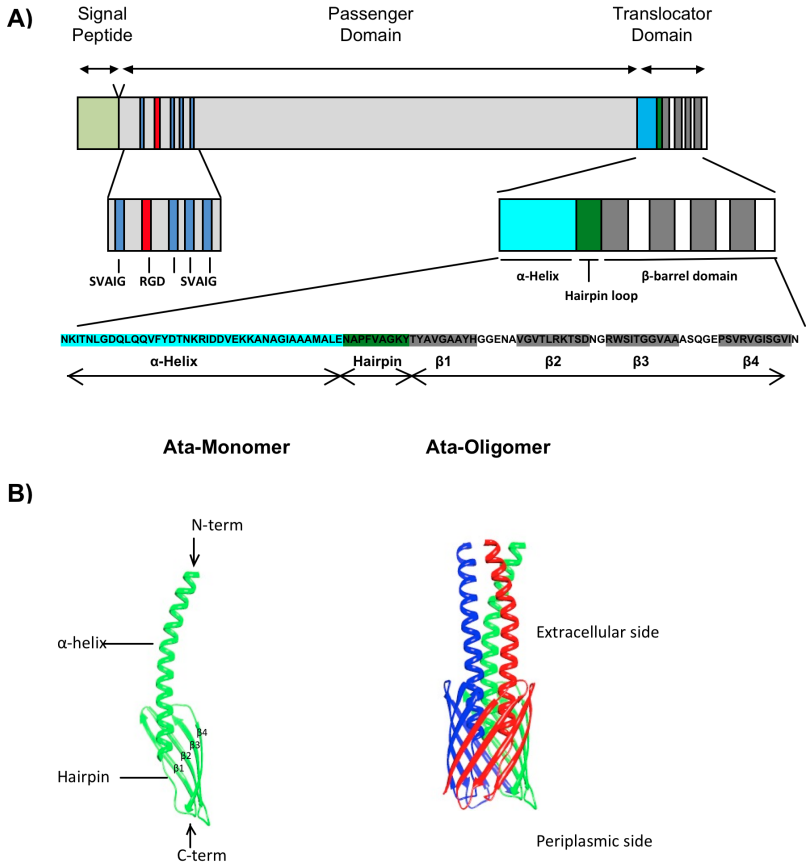

Fig. S1. *In silico* analysis of the Ata protein. A) Schematic representation of the domain architecture of the *A. baumannii* ATCC 17978 Ata protein. Indicated are the signal peptide, the N-terminal domain encoding an RGD and four SVAIG collagen binding motifs and the C-terminal translocator domain consisting of a proximal α-helix and a hairpin loop, which connects the α-helix to the beta-barrel domain. The beta-barrel domain consists of four transmembrane antiparallel beta-sheets (β1 to β4). B) Stereo ribbon diagram of monomeric and trimeric Ata generated by computer modeling of the crystal structure of the C-terminal translocator domain of Ata. Secondary structures and loop regions are labeled in the monomeric Ata structure.

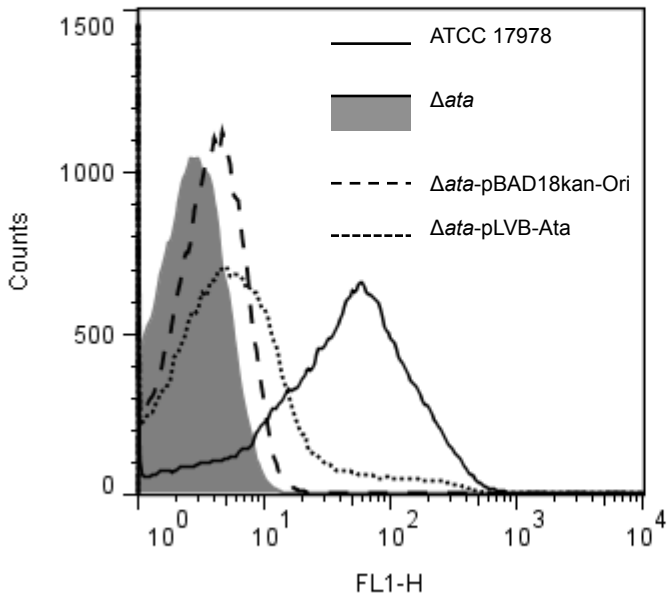

Fig. S2. Flow cytometry analysis of wild type *A. baumannii* ATCC 17978, Δ*ata,* Δ*ata*-pLVB-Ata and Δ*ata*-pBAD18Kan-Ori strains grown to OD_{650}nm 0.025 and labeled with anti-Ata rabbit sera and a secondary goat antibody to rabbit IgG conjugated to Alexa 488 fluorescent dye. Fluorescence is expressed in relative units, and the data are representative of multiple independent flow analyses.