Alternative folding to a monomer or homopolymer is a common feature of the type 1 pilus subunit FimA from enteroinvasive bacteria

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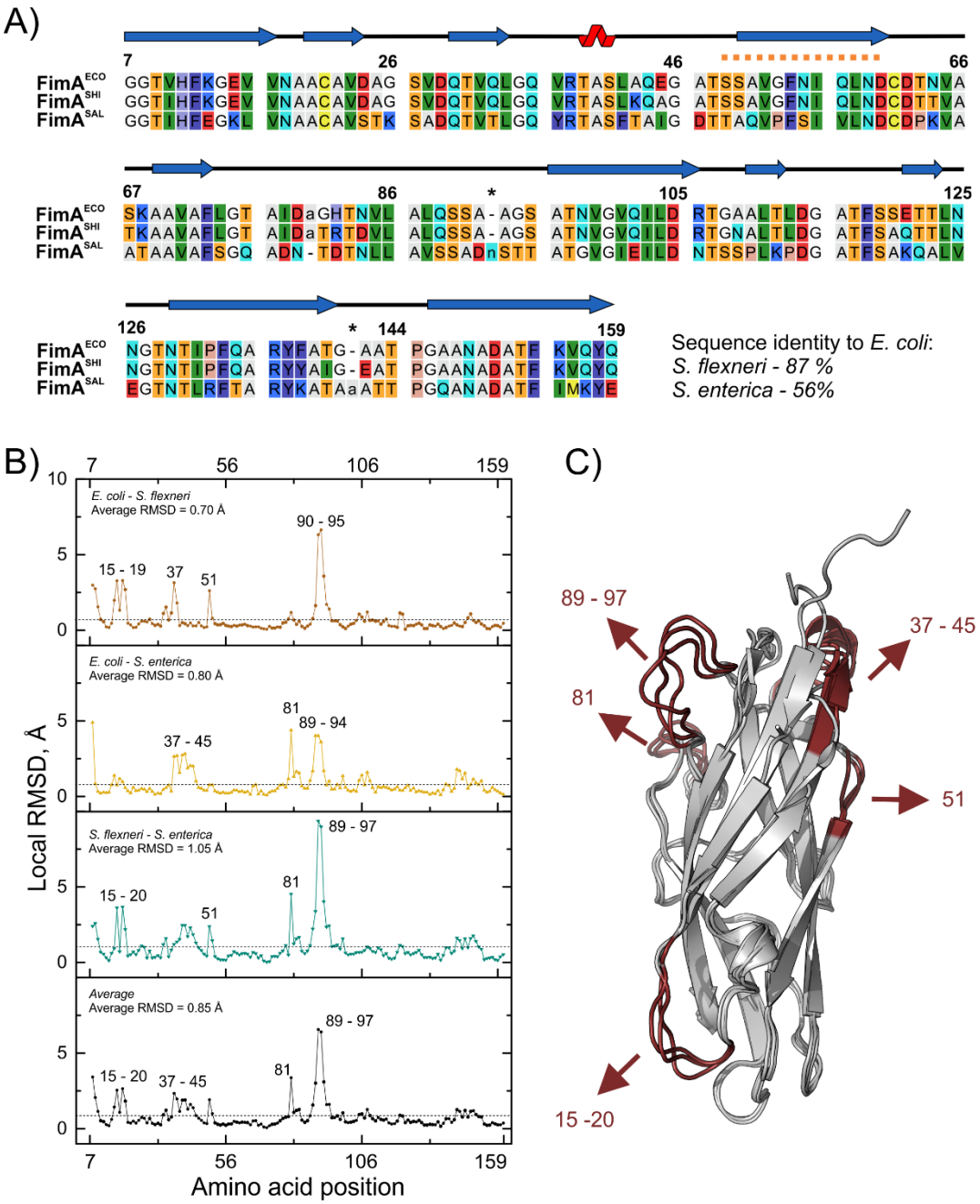

Figure S1: Pairwise structural alignment of the solved X-ray structures of the self-complemented monomers FimA^{ECO}, FimA^{SHI} and FimA^{SAL}.

A) Structure-based sequence alignment of FimA^{ECO}, FimA^{SHI} and FimA^{SAL} for the regions that were uniformly well resolved in the X-ray structures of all three. Secondary structures are indicated above the primary sequences. Amino acid numbering corresponds to mature *E. coli* FimA. Positions, where the sequences differ due to insertion of an additional residue (lower case letters), are marked with asterisks. The FimA fragment 50–60 that proved to be sufficient for targeting a GFP fusion protein to mitochondria is indicated as an orange dotted line [21].

B) The plot of the pairwise, local RMSD values against residue number.

C) Superposition of all solved structures. Polypeptide segments with the highest structural variability are highlighted in red.

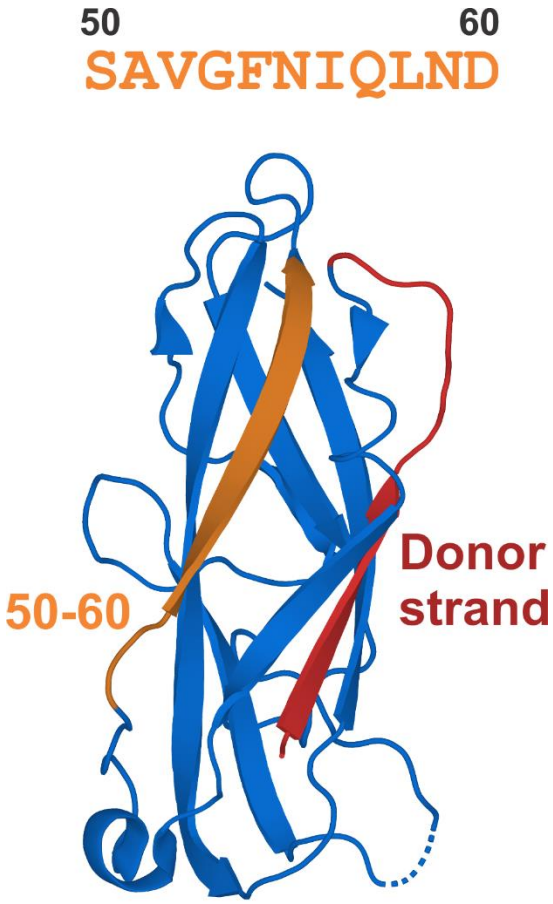

Figure S2: Localisation of the FimA anti-apoptotic peptide segment 50–60 in the context of the solved X-ray structure of $FimA^{ECO}$ (orange). The segment 50–60, which corresponds to the FimA β-strand (amino acid sequence indicated) proved to be sufficient to specifically target GFP to mitochondria when fused to the GFP N-terminus [21]. The self-complementing donor strand is coloured in red.

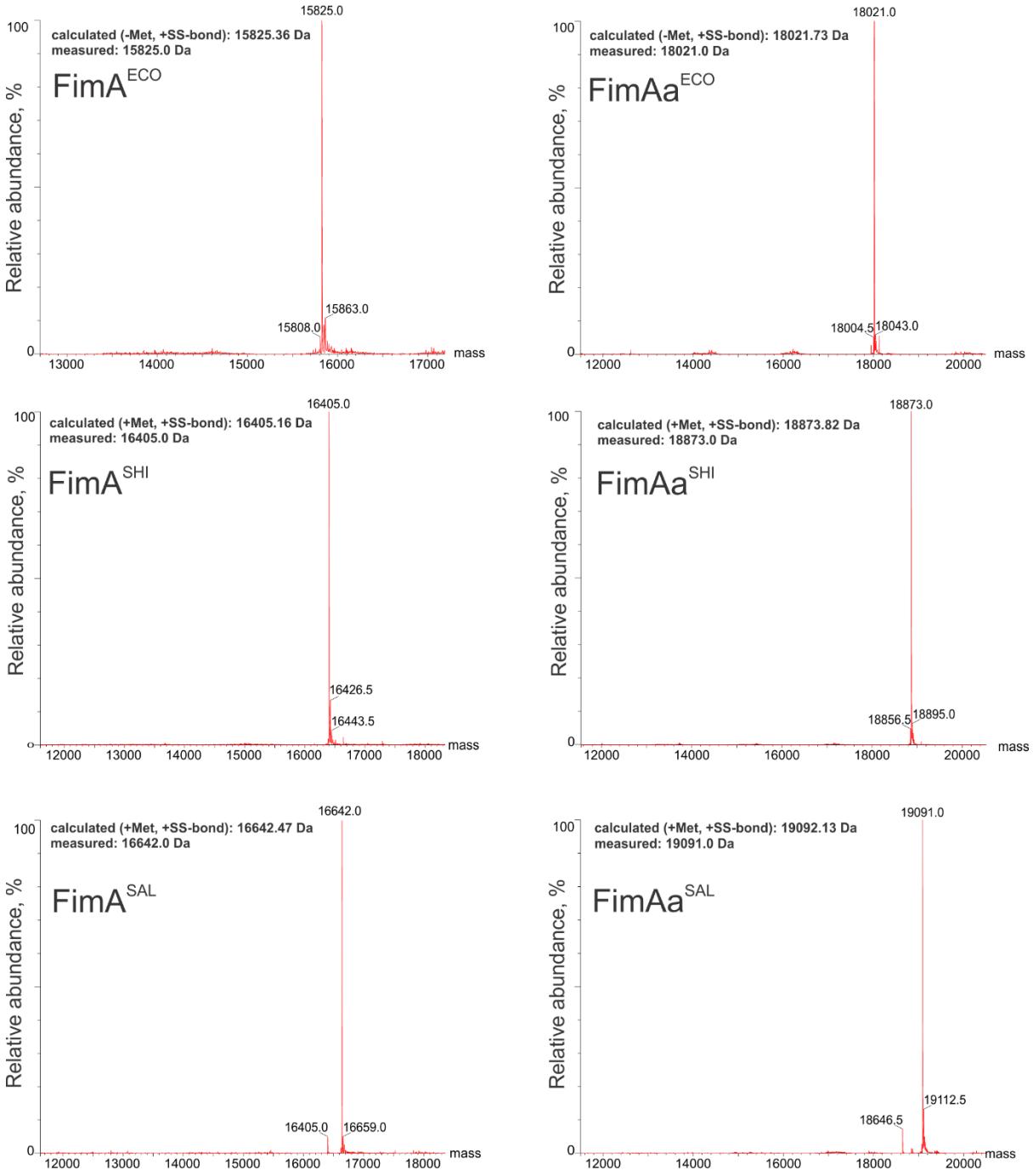

Figure S3: ESI-MS spectra of FimA and FimAa orthologues. All measured masses are consistent with calculated masses. All proteins contain a single disulfide bond. For FimA^{SHI} and FimA^{SAL} variants, the N-terminal methionine was not cleaved.