Acta Crystallographica Section F

Volume 70 (2014)

Supporting information for article:

Recombinant expression, purification, crystallization and preliminary X-ray diffraction analysis of the C-terminal DUF490963-1138 domain of TamB from *Escherichia coli*

Inokentijs Josts, Rhys Grinter, Sharon M Kelly, Khedidja Mosbahi, Aleksander Roszak, Richard Cogdell, Brian O Smith, Olwyn Byron and Daniel Walker

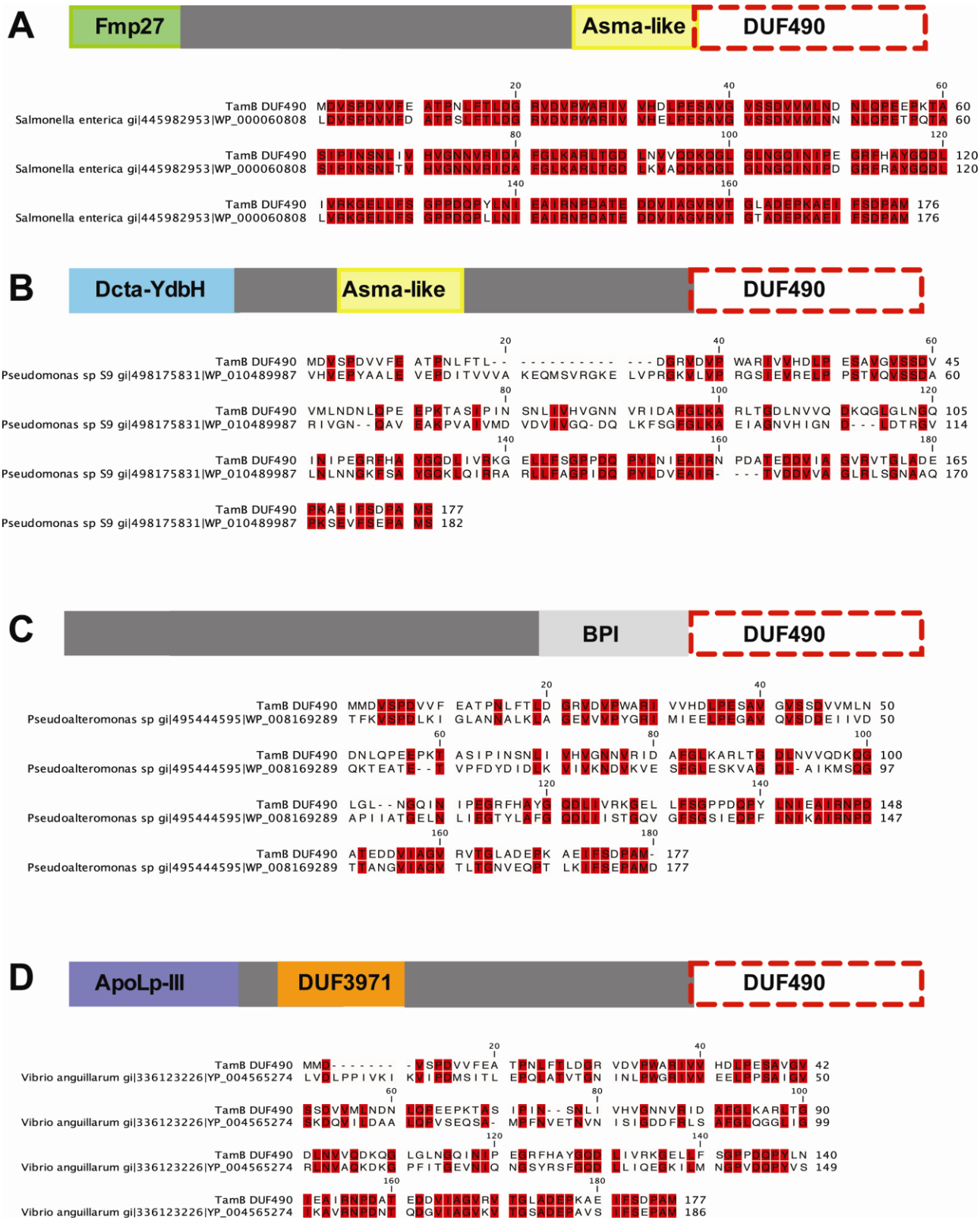

Figure S1 Sequence alignment between TamB DUF490$_{963\text{-}1138}$ and several other proteins possessing this domain. (A) Hypothetical protein from *Salmonella*, which bears 86% sequence identity to TamB, with additional annotated domains: Asma-like domain, associated with OMP biogenesis and an N-terminal

domain related to mitochondrial oxidative stress resistance protein Fmp27 (B) Hypothetical protein from *Pseudomonas sp.* which bears 29% sequence identity to TamB, yet 44% identity in the DUF490 domains. This protein also possesses an Asma-like domain upstream of DUF490 as well as an N-terminal DctA-YdbH-like domain associated with dicarboxylate transport (C) Hypothetical protein from *Pseudoalteromonas sp* with 28% sequence identity to TamB and 42% identity in the DUF490 domains. Additional sequence annotation suggests the presence of a bactericidal permeability-increasing protein (BPI) domain implicated in antimicrobial activity upstream of DUF490. (D) Hypothetical protein from *Vibrio anguillarum* with 33% sequence identity with the whole TamB protein and 48% identity in their DUF490 domains. The protein has an additional uncharacterized DUF3971 domain and an N-terminal apolipophorin-III-like domain associated with lipid transport.

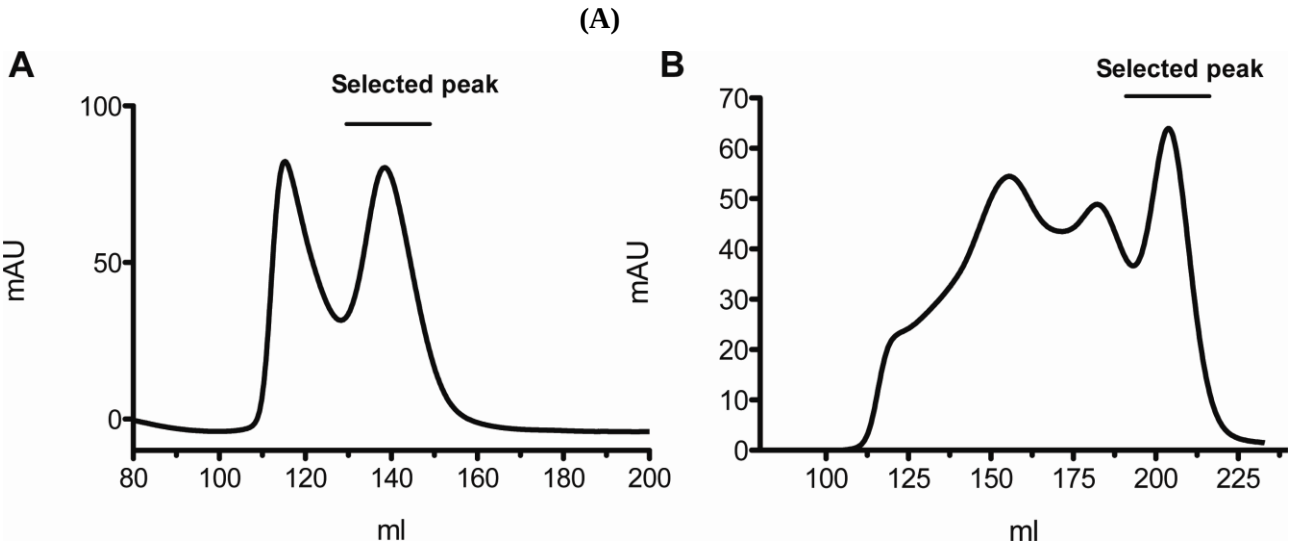

Figure S2 Size-exclusion chromatograms of $DUF490_{963-1138}$ from two independent purifications. Chromatograms from SEC using (A) Superdex S200 and (B) Superdex S75 are shown. Both chromatograms show the multimeric nature of the protein. For the purposes of crystallization and CD analyses only the monomeric species was utilized.