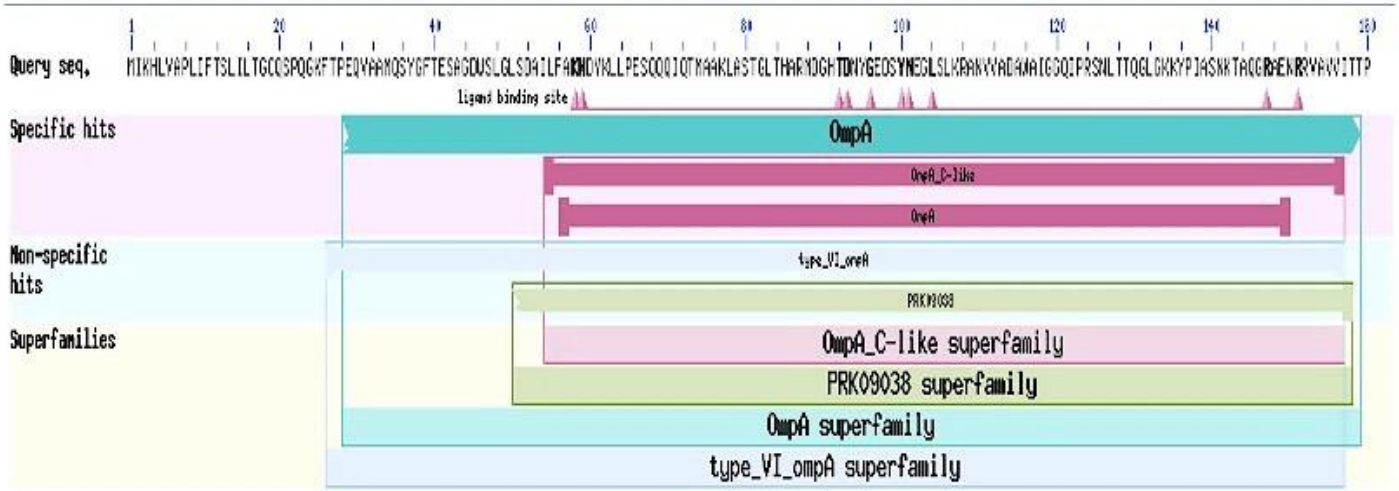
Supplementary Figure S1. Results for conserved domain analysis, Clustal-Omega alignment of YfiB from *Pseudomonas* and *Shigella*, and predicted protein structure by I-TASSER. (a) Conserved domains found in the YfiB protein, analysed using NCBI-protein BLAST and conserved domain database (CDD). **(b)** Clustal-Omega sequence alignment of YfiB protein from *Pseudomonas and Shigella*. Highlighted sequences indicate: Blue- conserved linker sequence; Purple- 35-55 amino acid cluster important for activating YfiB; Yellow - PAL Domain associated amino acids. Symbols denoting- : strongly similar amino acid residue; . weakly similar amino acid residue; * conserved amino acid residue. **(c)** The 3D protein structure predicted for YfiB, computed by the I-TASSER tool, using *Pseudomonas* YfiB solved crystal structure as a template; the 3D structure consists of Core OmpA-like domain, four-stranded anti- parallel β-sheet with topology β1-β4-β2-β3 and helices α1-3.

A



B

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YfiB_Pseudomonas        MLPQRLHPSRLLALALFSLVLGLAGCQTKPPQTGLSAEQIAVLQEQGFELRDEGWEFGMS 60
YfiB_Shigella           MIKH-------LVAPLIFTSLILTGCQ--SPQGKFTPEQVAAMQSYGFTESAGDWSLGLS 51
                        *: :       *.  *:   * *:***   **  :: **:*.:*. **     .*.:*:*

YfiB_Pseudomonas        SKVLFGNNLDRLNPDSRNTLTKIARALLAVDIDKVRLEGHTDNYGDEGYNQKLSERRAES 120
YfiB_Shigella           DAILFAKNDYKLLPESQQQIQTMAAKLASTGLTHARMDGHTDNYGEDSYNEGLSLKRANV 111
                        . :**.:*  :* *:*:: : .:*  * :..: :.*::*******::.**: ** :**:

YfiB Pseudomonas        VAAVFREA-GMPAANIEVRGLGMSKPVADNKTRAGRSENRRVAIIVPAE  168
YfiB_Shigella           VADAWAIGGQIPRSNLTTQGLGKKYPIASNKTAQGRAENRRVAVVITTP  160
                        ** .:  .  :* :*: .:*** . *:*.***  **:******::: :
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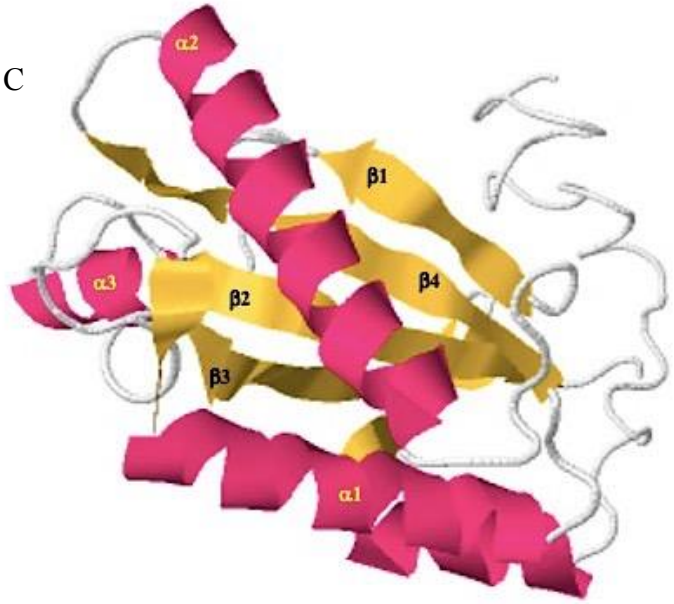
C