



Figure S2. The predicted bilobal structure of PA0674 based on homology modeling.

(A) Predicted domain architecture of VreA. The N-terminal domain (NTD) of VreA (shown in green) is preceded by a signal sequence (SS). The NTD and the C-terminal domain (CTD) (shown in blue) are separated by a short linker region. (B) The VreA/NTD (modeled residues 39-120) is classified as belonging to the Secretin/TonB N-terminus domain superfamily. Members of this superfamily have domains that are homologous to the N-terminal signaling domains of TonB-dependent outer membrane receptors (e.g. FpvA; PDB ID: 2O5P). The VreA/CTD (modeled residues 133-233) is expected to belong to the TolA/TonB C-terminal domain superfamily. The linker region separating the domains is shown in grey.