



### S3 Figure: Molecular modelling of PG0189 using Phyre-2.

Three models are shown based on the three best matching (but different) template structures. A) OmpW full length from *E. coli*, PDB accession 2F1T; B) OmpA trans-membrane domain from *E. coli*, PDB accession 1QJP; C) OprG full length from *P. aeruginosa*, PDB accession 2X27. The N- and C-termini are shown and the cross-linked lysine residue is indicated by an arrow.