



Figure S1. (A) Peptidoglycan cross-linking reactions catalyzed by the DD-transpeptidases (PBPs, top) and the LD-transpeptidases (LdtD, LdtE and LdtF, bottom) resulting in 4-3 and 3-3 cross-links, respectively. G, *N*-acetylglucosamine (G); M, *N*-acetylmuramic acid; R indicates H, D-Ala or D-Ala-D-Ala. (B) Sequence alignment of LdtD, LdtE and LdtF. LdtD sequence starts at amino acid 201 of the protein sequence. Residues flanking the Cys residue (C) of catalytic site are indicated in bold. Consensus symbols: (*) indicates fully conserved residues; (:) indicates residues with high degree of conservation; (.) indicates residues with low degree of conservation. Alignment was performed with ClustaOmega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).