



S3 Fig. Notable residues displayed on the BcsA crystal structure. (A) TM channel residues that were identified as potentially having a role in the specificity of bacterial β -glucan synthases, displayed in stick form coloured by atom type (carbon – cyan; oxygen – red; nitrogen – blue) or with labels coloured by residue type (acidic – red; basic – blue; aromatic or Pro – purple; polar – green). BcsA is coloured as per **Fig 1** and residues labelled with BcsA numbering. (B) TM channel residues in CrdS model, coloured as in panel A. Distinct H-bond forming residues listed in **Table 2**. (C) Positioning of residues with strong (>75%) conservation in bacterial β -glucan synthase proteins. Residues with strong conservation across the Cesa, CrdS and BgsA sub-families of β -glucan synthases, as identified in **S7 Table**, are shown with their C α atoms as yellow spheres. (D) Mutations in plant Cesa/CsIFs (**S15 Table**) from regions with prominent differential conservation (as defined in **S8 Table**) have their C α atom coloured purple while mutations from other regions (generally sites of either full or strong conservation) are coloured green.