S7 Table. Fully (>99%) and strongly conserved (>75%) residues across all bacterial β-glucan synthases used in the initial, unrefined phylogenetic analysis, grouped by secondary structure.

	Fully Conserved (>99%)			Strongly Conserved (>75%)		
TM1	Tyr80	Arg84		Trp83	Thr88	
TM2	Glu108					
Pre-β1	Pro140					
β1	Asp143			Val142	Phe145	
β1-α1	Tyr149	Glu151		Thr148	Asn150	
α1				Thr159	Ala163	
α1-β2				Tyr168	Pro169	
β2				Val175		
β2-α2	Asp179	Asp180				
α3				Cys209		
β3				Tyr216	Thr218	
β3-α4	Arg219	Asn222	Ala225			
α4	Lys226	Gly228	Asn229	Ala227	Asn231	
β4-β5	Asp246	Asp248		Ala247		
β5	Pro251					
α5				Leu256	Phe263	Asp266
β6	Gln273			Val272		
β6-α6	Pro275			Thr274	Asn280	Asp282
α6	Pro283	Asn287		Leu288		
α6-α7/IF1				Glu297		
α7/IF1	**Phe301**	Asp310				
α7/IF1-β7	Gly319			Trp312	Phe316	
β7				Arg325		
α8	Arg326					
α8-α9				Gly333	Gly334	
α9	Glu342	Asp343				
α9-β8				Gly354		
β9	Gly367					
β9-α10/IF2	Leu368					
α10/IF2	Gln379	Arg380	Arg382			
	Trp383	Gly386	Gln389			
α10/IF2-TM3				Gly401		
TM3	Pro430			Gln406	Arg407	**Tyr433**
TM4-TM5/IF3				Pro473		
Gating loop	Pro498	Phe503	Val505			
	Thr506	Lys508				
TM7				**Trp558**		
Post-TM7				Glu575		

RsBcsA residue numbering used. See **S2** and **S4 Fig.** for positioning of the secondary structures. Amino acids in bold are those identified in simulations to form stacking interactions with the (1,4)-β-glucan and (1,3)-β-glucan chains within the RsBcsA and AtumCrdS TM channel, respectively (see **Table 2**).