

S8 Table. Residues conserved within a bacterial β -glucan synthase sub-family but different across sub-families.

Res	SS	Clade 1 (AcsA)	Clade 2 (BcsA)	Clade 3 (CrdS)	Clade 5 (BgsA)
183	α 2	Arg	Thr/Ser	Arg	Arg
249	β 5	His	His	Phe	Phe
276	β 6- α 6	His	His	Mainly Gln/ some His	Gln
285	α 6	Glu	Glu	Gln	Gln
295	α 7/IF1	Pro	Pro	Val	Pro
296		Asn	Mainly Ser	Asp	Asp
298		Gly	Asn	Gln	Gln
299		Thr	Mainly Glu/ some Asp	Arg	Arg
302		Tyr	Tyr	Phe	Phe
309		Asn	Leu	Lys	Arg
317		Phe	Phe	Cys	Cys
318	α 7/IF1- β 7	Cys	Cys	Val/Ile	Cys
320		Ser	Ser	Thr	Ser
321		Cys	Ala	Ser	Mainly Cys/ some Asn
322		Ala	Ala	Mainly Phe/ some Cys	Ser
336		α 8- α 9	Ala	Ser/Some Ala	Pro
351	α 9	His/some Gln	His	Various	Leu
357	B8	Ser/Thr	Ser	Thr	Thr
359		Tyr	Tyr	Trp	Tyr
370	β 9- α 10/IF2	Thr	Pro	Ala	Mainly Ala/ some Pro
376	α 10/IF2	His	Mainly Phe	Tyr	Mainly Tyr/ some Phe
387		Met	Met	Thr	Mainly Gly/ some Ala
395	α 10/IF2-TM3	-	-	Gly	Gly
402		Leu	Leu	Mainly Tyr/ some Phe	Leu
410	TM3	Tyr	Tyr	Mainly Tyr/ some Phe	Phe
412		Asn/some Ser	Ser/ some Asn	His	-
417		Phe	Trp	Trp	Leu
465	TM4	Arg/Lys	Various	Trp	Trp
479	TM5/IF3	Tyr	Tyr	Mainly Thr/ some Ser	Mainly Val
480		Glu	Glu	Gln/His	Mainly Gly
500	Gating Loop	Various	Various	Gly	Gly
501		Pro	Pro	Arg	Mainly Lys
562	TM7	Asn	Asn	Ala/Ser	Asn

Gaps in sequences indicated by “-”.

Residues are numbered relative to the RsBcsA crystal structure.