BfpI secondary Structure

Secondary structure and disorder prediction	
1	
Sequence L S L I E A S L V I I L S G L V I V L V Q S A I S K I I K Y A V Secondary	HENALHDVSYVMSYI QDTLQTSCYGKEN
structure	*****
SS confidence	
Disorder ? ? ? ? ? ?	
Disorder confidence	
Sequence I VCDGVI SSVKSNVNSGNKI KVDVKKDGKYVS	
Secondary structure	
SS	
confidence Disorder	
Disorder confidence	
Sequence AYSGRMDSSTGVVSSVLGWWKVNSDDTIFLGG	
Secondary structure	
55	
confidence Disorder	
Disorder	
confidence	
Confidence Key	
High(9) Low (0)	
? Disordered (12%)	
Alpha helix (49%) Beta strand (28%)	
TM helix (9%)	

BfpJ secondary structure

Secondary structure and disorder prediction			
Sequence Secondary structure SS	SI VSL SVY NY YNRS	A E Q H Y MN N V S V V M	CRYADALSYYLQDSTATNGN
confidence Disorder Disorder confidence	······		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
Disorder	L P P MQETS GV GE YE	IKMYVDKNKNGLI/	ALYGGEYYSLTSENI KKFLG
	AGGYYSLPVSDFTG	FRTVNLRGLMLIPS	SI QT S GQN CDR GGYDF
Disorder confidence	onfidence Key		
? Di An Al Be	Low (0) sordered (28%) pha helix (20%) eta strand (42%) 4 helix (9%)		

BfpK secondary structure

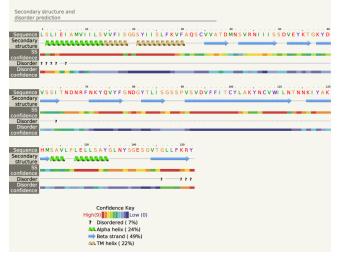


Figure S1. **Secondary structure prediction of BfpI, BfpJ and BfpK.** Prediction of secondary structure of mature BfpI, BfpJ and BfpK minor pilins. Modeling was done using Phyre2, showing the presence of alpha helix in the hydrophobic N-terminal.

BfpI BfpK BfpA BfpJ	-MFILRNKRKESGLSLIEASLVIILSGLVIVLVQSAISKIIKYAVHENALHDVSYV MIFEGRQQKGLSLIEIAMVIILSVVEISGGSYIISLFKVFAQSCVVATDMNSV MVSKIMNKKYEKGLSLIESAMVLALAATVTAGVMFYYQSASDSNKSQNAISEVMSA MIRKESGLSLIEVMIGVLFFSIVSLSVYNYNRSAEQHYMNNVSVVMCRYADAL ::****** :::: : : :	53 56
BfpI BfpK BfpA BfpJ	MSYIQDTLQTSQYGKENIV DGVISSVKSNVNSGNKIKVDVKKDGKYVSVYILYTLSGNE RNIIISSDVEYKTGKYDVSSITNDNRFNKYQVYFGNDG-YTLISGSSPVSVDV TSAINGLYIGQTSYSGLDSTILLNTSAIPDNYKDTTNKKITNPFGGELNVGPANNNTAFG SYYLQDSTATNGNGSVSLSTLVASGYLPPMOETSGVGEYEIKMYVDKNKNGLIALYGGEY	105 116
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BfpI BfpK BfpA BfpJ	YFGRNEDFGSMLFTHVSAYSGRMDSSTGVVSSVLGWWKVNSDDTIFLGGDNN FFITCYLAKYNCVWILNTNNKIYAKHMSAVLPLELLSAYGLNYSGESGV YYLTLTRLDKAACVSLATLNLGTSAKGYGVNISGENNITSFGNSADQAAKSTAITPAEAA YSLTSENIKKFLGIRGASAKDNKIISAGGYYSLPVSDFTGFRTVNLRGLMLIPSIQT :	
BfpI BfpK BfpA BfpJ	KNLFFYNNFRVDVL 181 TGLLFKRY 162 TA <mark>C</mark> KNTDSTNKVTYFMK 193 SGQN <mark>C</mark> DRGGYDF 183	

Figure S2. Alignment of BfpA, BfpI, BfpJ and BfpK sequences.

The signal peptide is show in Red letters, the Gly residue where BfpP cuts the leader peptide is shown in red. All three mature proteins start with Leu and all three have the Glu conserved at position 5. In green the conserved C residues in the C-terminal regions are shown. In yellow is where the truncated protein was cloned for purification in the present study.