The wild-type flagellar filament of the Firmicute *Kurthia* at 2.8 Å resolution *in vivo*

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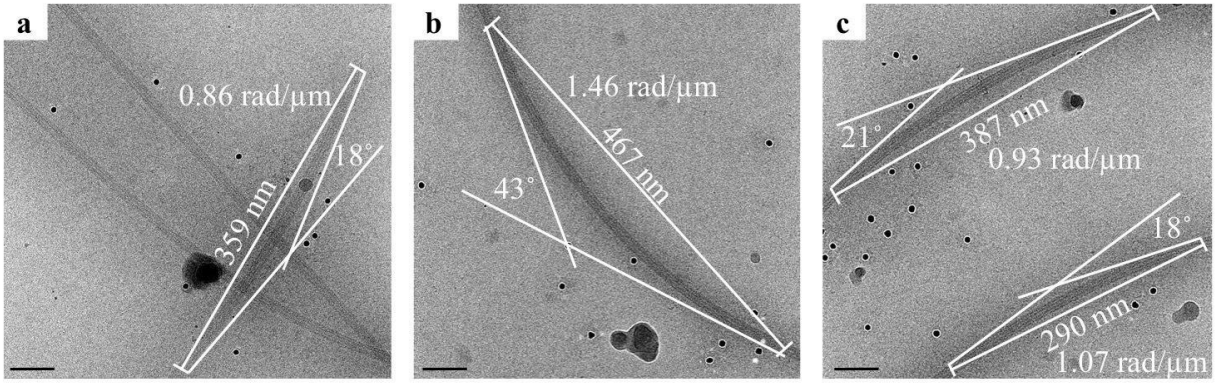
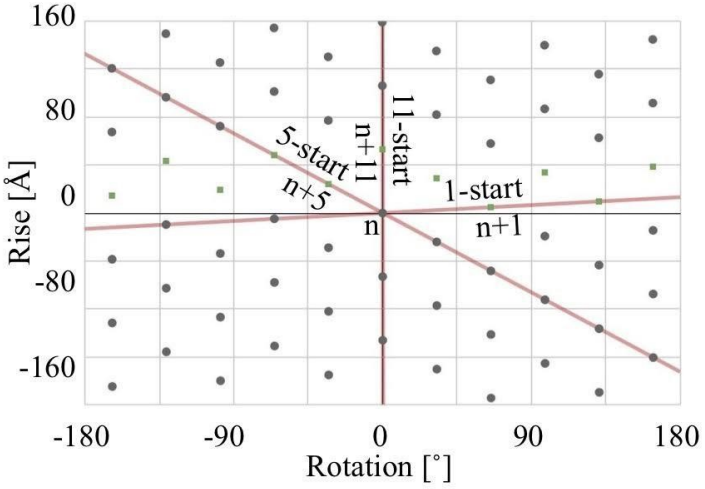
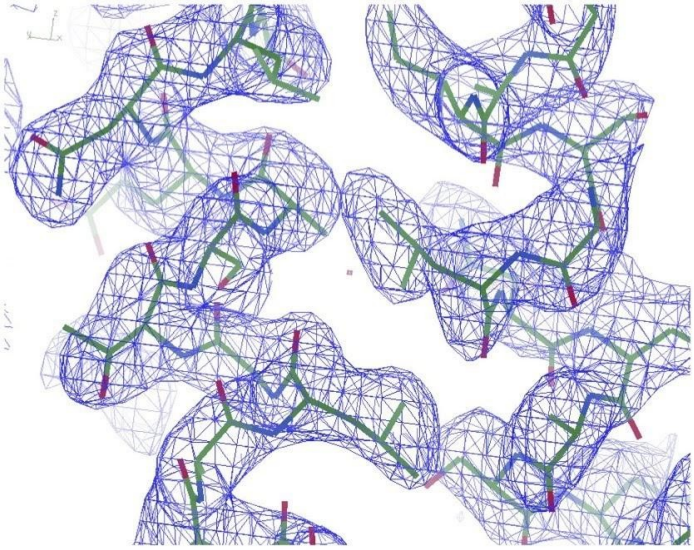


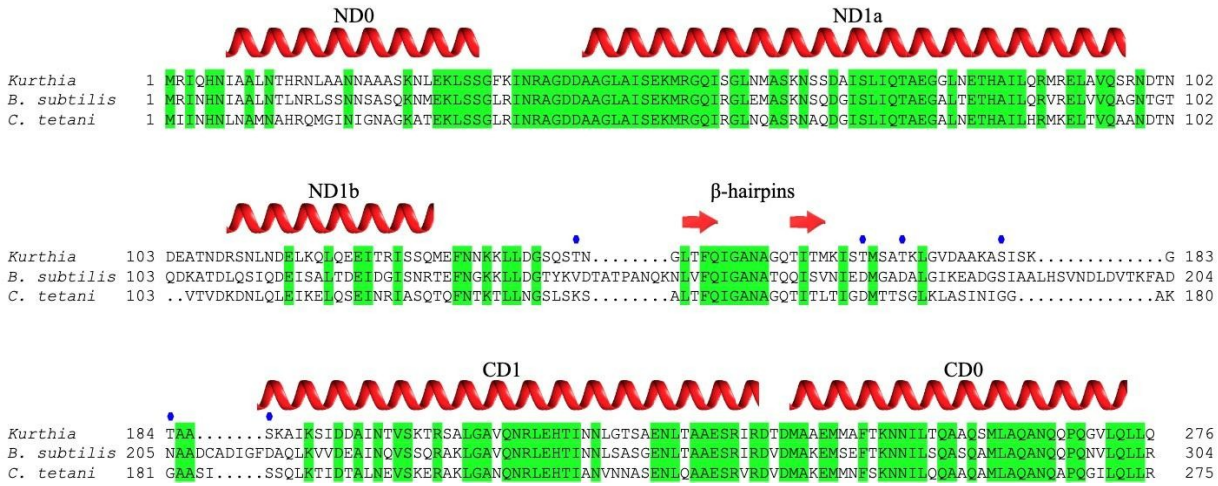
Supplementary Figure 1. The majority of the picked flagella are bent and had a curvature between 0.8 and 1.5 rad/µm. Scale bars: 50 nm.



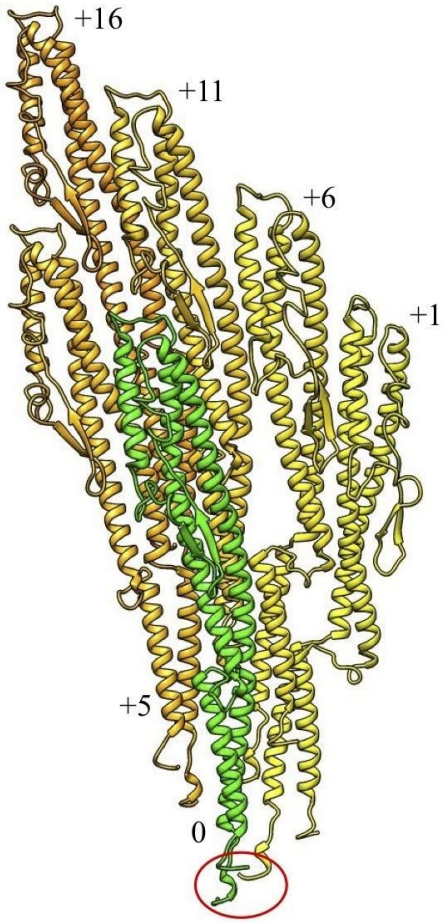
Supplementary Figure 2. Helical net of the flagellar filament. Each point represents one flagellin. One asymmetrical unit containing 11 flagellins is indicated in green. The 11-start helix is tilted by ~ 0.06˚ to the left.



Supplementary Figure 3. Cryo-EM density map with part of the refined model.



Supplementary Figure 4. Amino acid sequence alignment of the gram-positive bacteria *Kurthia* sp. 11kri321, *Bacillus subtilis* and *Clostridium tetani*. The six O-glycosylations sites of Kurthia are marked by blue hexagons.



Interfacial subunit-subunit areas

11-start	1947Å^2
5-start	1809Å^2
6-start	569Å^2
16-start	293Å^2
1-start	9Å^2

Supplementary Figure 5. One flagellin subunit (green) with it 5 interacting neighbours (yellow) in the + direction shows a new interaction with the 1-start subunit (red circle). This new interaction is tentative because the C-terminus is flexible and therefore the electron density map is not well resolved.

Supplementary Video 1. Time lapse movie showing the active movement of *Kurthia* sp. 11kri321 cells in a growth chamber in liquid medium.