**Supplementary material**

***Placement of neighbouring strand in β-strip helix***

The figure shows two strands in 2D depiction. In 3D Cα atoms of one strand (the lower strand) have been placed using the parametric equation of a helix with the appropriate radius and pitch. To create the neighbouring upper strand in a β-strip helix arrangement, the lower strand can be displaced by the vector indicated by the red broken arrow. However, the quantities needed to position the strand in practice, are the projections of this displacement on the direction aligned to the helical axis and the direction perpendicular to the helical axis (as shown by the blue broken arrows) as these correspond to translation along the axis and rotation about the axis, respectively.

Thus the helix of the upper strand can be found be translating the helix of the lower strand along the axis direction by:

and by translating perpendicular to the axis by:

which means rotating about the helical axis by:

where *r* is the helical radius. Repeating this process allows one to build up a β-strip helix with the desired number of strands. The β-strip helix shown in Figure 1B can be constructed in this way.

***Placement of neighbouring*** ***β-strip helix as a protofilament subunit***



To create subunit B by duplication of subunit A, subunit A can be displaced by the vectors indicated by the red broken arrows. As above these are projected on to the direction aligned with the helical axis and perpendicular to the helical axis as indicated by the blue broken arrows.

Displacement along the direction parallel to the axis is given by:

Translation perpendicular to the axis is given by:

which means:

These equations were used to create the 3D protofilament model shown in Figure 10.

*****Condition for gap between protofilament subunits and its length***

The figure shows in 2D representation two β-strip helices A and B of length *L* residues which would be joined end-to-end in 3D (see Figure 10). The register shift is *t*. From the numbering of residues on A it can be seen that:

*t* +1 > *L* – *t*

and

*t* +1 ≤ *L*

which combine to give:

*L* ≤ 2*t* ≤ 2(*L*-1)

One can see that the length of the gap, *g*, as a shift in the number of residues between strip A and B is given by:

*g* = 2*t* – *L* +1