Supporting Information

Zhang et al. 10.1073/pnas.0901085106

Iterative Helical Real Space Reconstruction (IHRSR)

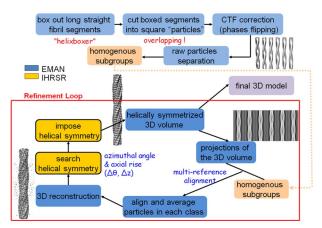


Fig. S1. The pipeline of image reconstruction. The operations in blue and yellow boxes were done by EMAN software and the IHRSR package, respectively.

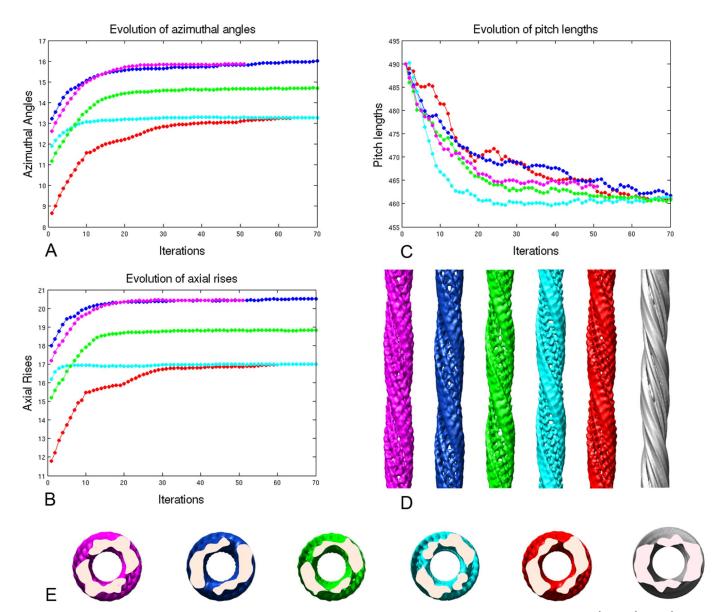


Fig. S2. Structural refinement of $A\beta_{1-42}$ fibrils by the IHRSR method. Five different sets of initial helical symmetries (axial rise Δz : 11.80 Å, 15.20 Å, 16.20 Å, 17.20 Å, 18.00 Å, and their corresponding azimuthal angle $\Delta\theta$ which would give the same 490-Å pitch length) were used. Note that this pitch was deliberately chosen to disagree with the measured pitch (460 Å) for this pitch class. (A–C) The azimuthal angles for these 5 cases evolve over 70 iterations (A), as does the axial rises (A) and pitch lengths (A). All parameters converged to a consistent value α 400 Å. (A0 and A0 The global protofilament packing was unaffected by imposing different helical symmetries (A0), and the cross-sections were unaffected by imposing different helical symmetries (A0), and the cross-sections were unaffected by imposing different helical symmetries (A0), and the cross-sections were unaffected by imposing different helical symmetries (A0), and the cross-sections were unaffected by imposing different helical symmetries (A0).

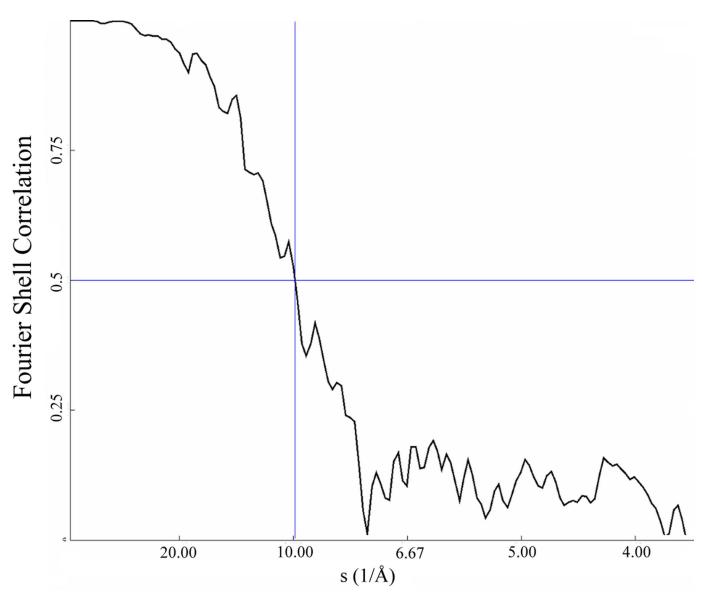


Fig. S3. Resolution of the reconstruction. The Fourier shell correction (FSC) between two independently-reconstructed volumes (obtained by dividing the whole dataset into halves and carrying out two independent reconstruction processes) indicates that the resolution of the reconstruction is \approx 10 Å when using a 0.5 cutoff.

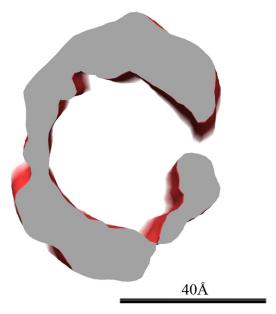


Fig. S4. The cross-section of the asymmetric C1 reconstruction after 20 iterations, which suggests a C2 symmetry along the fibril axis.