Supporting Information for

Chirality-dependent growth of self-assembled diphenylalanine microtubes

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Purity verification of the source peptide powders

To verify high purity of the used powders we have performed ^{1}H NMR and UHPLC-MS analyses to reveal the impurities mentioned above. ^{1}H NMR measurements of powders dissolved in D_2O in the presence of DCl and separately in DMSO-d6 did not reveal the presence of any impurities in both powders. Additional recrystallization of powders from H_2O-HFIP mixture did not affect the purity of the samples according to ^{1}H NMR spectroscopy. However the sensitivity of the method does not exceed 3-5% and thus cannot undoubtedly confirm the identical purity of the dipeptides.

Therefore we performed UHPLC-MS analysis using UHPLC Nexera X2 system combined with Shimadzu IT-TOF (ion trap coupled with time of flight) mass hybrid analyzer with electrospray ion source providing the sensitivity about 0.1%. The analysis was carried out on Aeris Peptide XB-C18 column (50 × 2.1 mm, 3.6 μm beads) with a gradient elution of 5 to 55% B in A (solvent A: 0.1% HCOOH in H_2O; solvent B: 0.1% HCOOH in MeCN). The FF powders were dissolved in 500 μl of water-acetonitrile mixture (80:20) each. The injection volume was 5 μL and the flow rate was 0.2 mL/min.

The total ion current (TIC) chromatograms obtained in positive ion mode show the only one signal located at about 6.6 min for both L-FF and D-FF powders (Fig. S1a). Corresponding high-resolution mass spectra contain the only one peak 313.153 *m/z* (313.154 *m/z* calculated for $[M+H]^{1+}$). No any other signals (except that one located at about 12.6 min and obviously attributed to the background signal) can be observed in the chromatograms.

It is necessary to note, that such possible impurities as Z-Phe-Phe-OH and Cyclo(-Phe-Phe) are difficult to detected in the positive ion mode due to the lack of protonation sites, therefore we repeated measurements in negative ion mode. The corresponding TIC chromatograms are presented in Fig. S1b. As in previous case, the only signal at about 6.6 min corresponding to diphenylalanine dipeptide is observed. Moreover, all the *m/z* values corresponding to possible impurities were additionally analyzed by generation of extracted ion chromatograms (XIC). None of these impurities was found.

Thus, the obtained results undoubtedly confirm ultra-high purity of the studied powders, much better than that mentioned in Analytical Data Sheets.

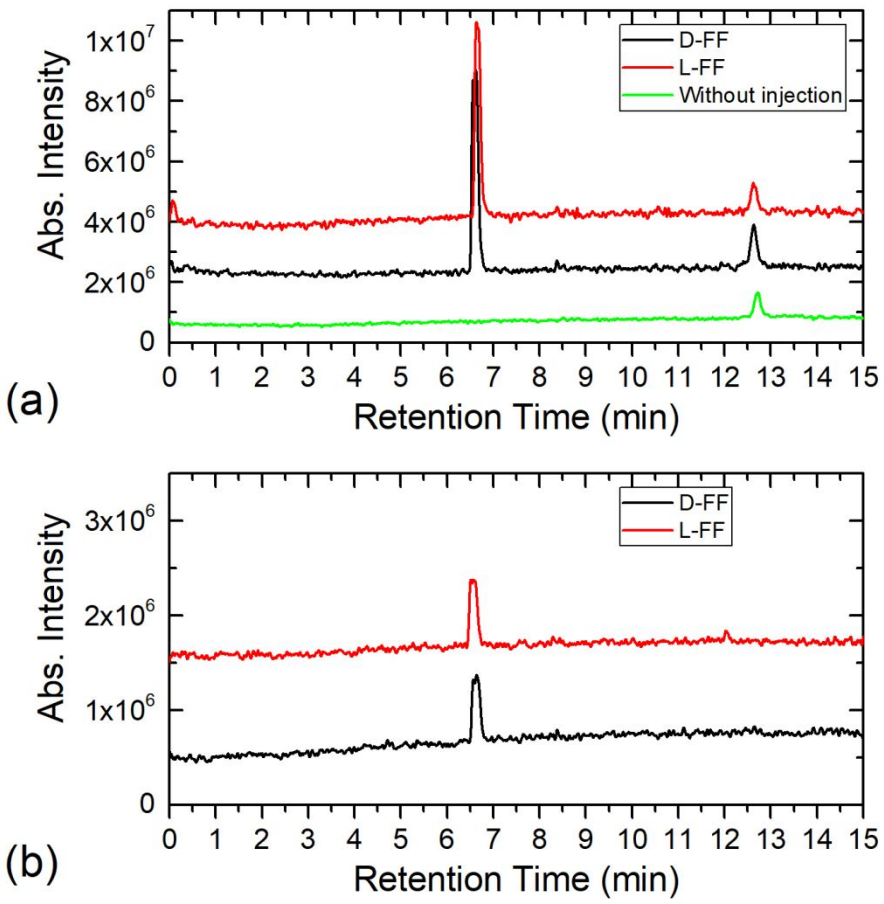

Figure S1. Total ion current chromatograms obtained in (a) positive and (b) negative ion mode.

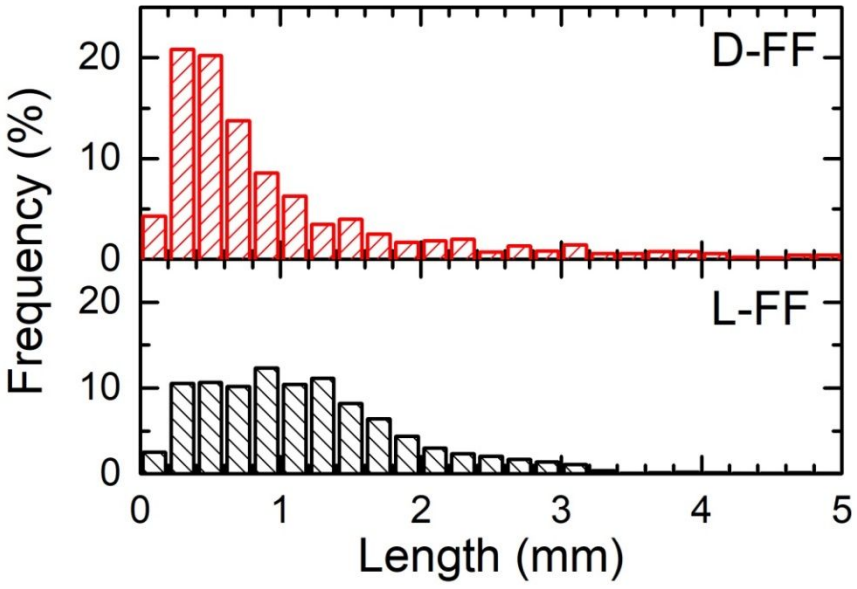

Figure S2. Length distribution of D-FF and L-FF microtubes grown on glass substrates.

Table S1. Comparison of morphologies of L-FF and D-FF MTs grown on glass substrates.

Enantiomer configuration	Number of MTs	Mode length, μm	Median length, μm	Diameter, μm
L-FF	1878	810 ± 310	1061	2.0 ± 0.5
D-FF	2257	430 ± 130	660	2.15 ± 0.6

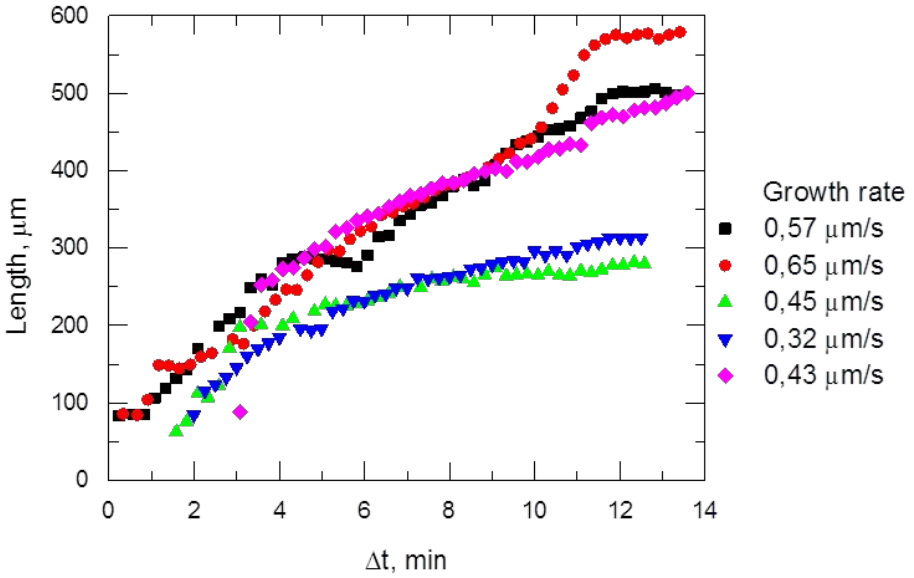

Figure S3. Time dependence of the L-FF microtubes length during the growth process in a drying droplet.

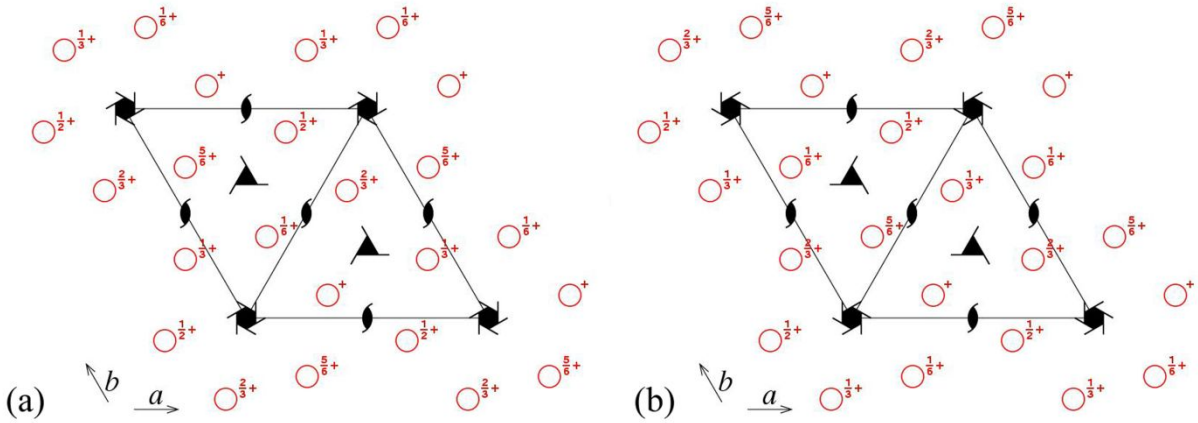

Figure S4. Diagrams for the symmetry elements and the general position for (a) $P6_1$ and (b) $P6_5$ space groups. Adapted from A Hypertext Book of Crystallographic Space Group Diagrams and Tables (http://img.chem.ucl.ac.uk/sgp/mainmenu.htm).

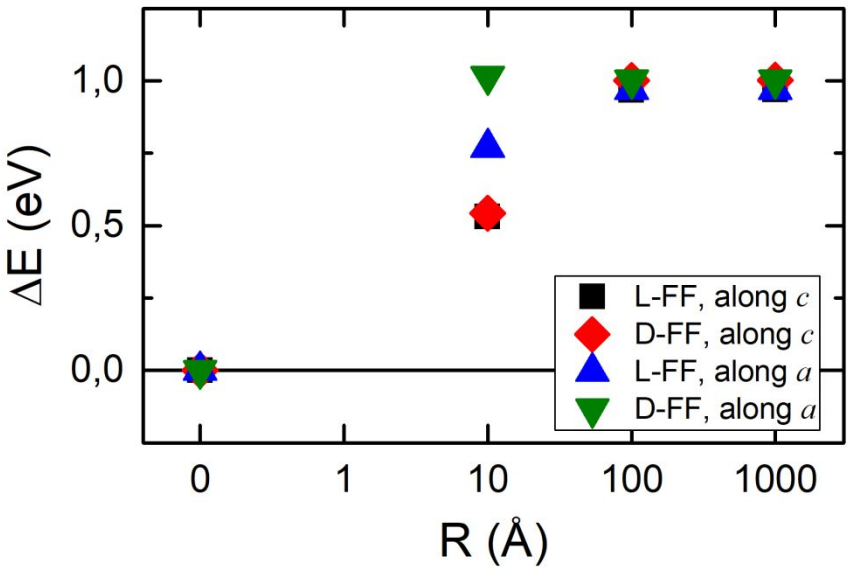

Figure S5. Variation of total energy of L-FF and D-FF rings with removing of one monomer at distance R along different crystallographic axes.

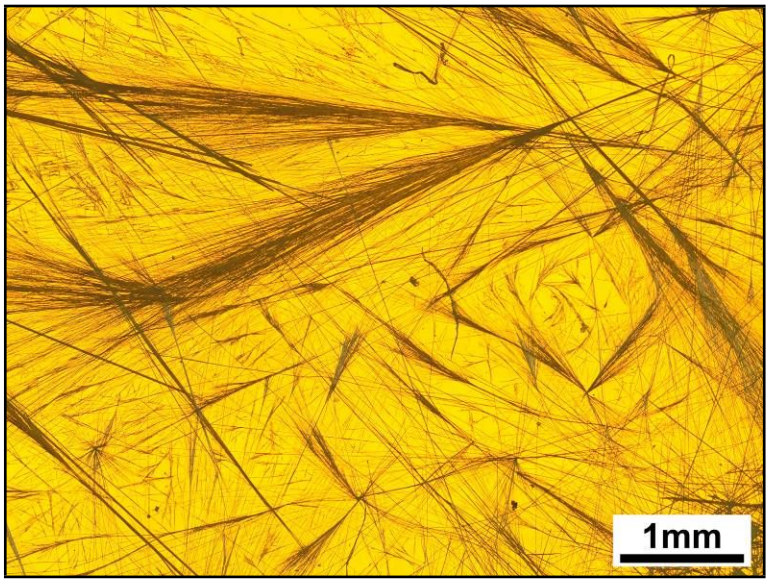

Figure S6. Splitting of L-FF microtubes into separate nanotubes.