

ELECTRONIC SUPPLEMENTARY INFORMATION

Self-assembly of human amylin-derived peptides studied by atomic force microscopy and single molecule force spectroscopy

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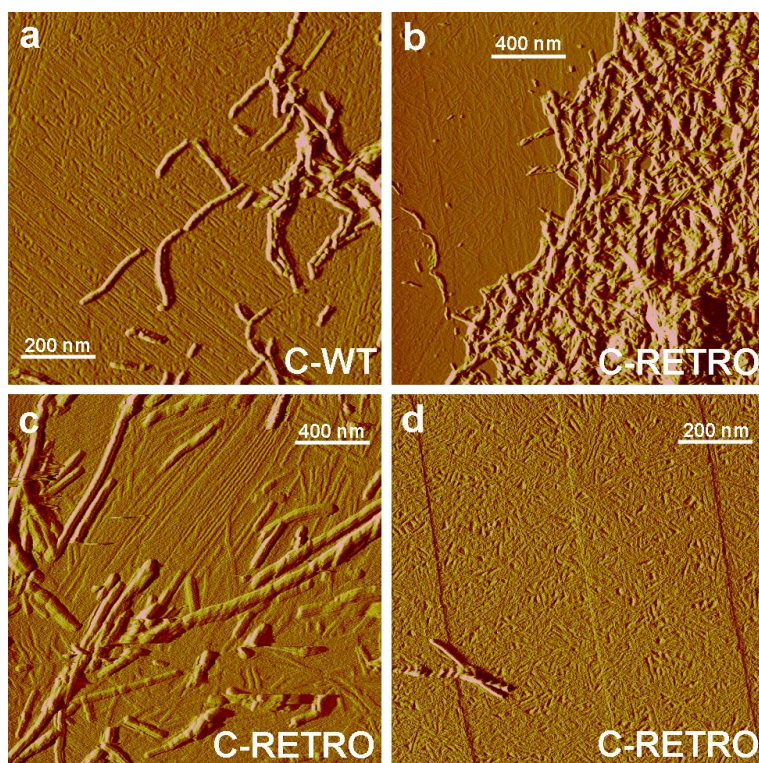


Figure S1. Amplitude AFM images of fibrils and protofibrils of C-WT and C-RETRO formed after incubation for 1-2 weeks in different aqueous solutions: a) C-WT in 10 mM acetate buffer, pH 5.4, 137 mM NaCl, KCl 2.7 mM; b) C-RETRO in PB, pH 7.4; c) C-RETRO in 10 mM acetate buffer, pH 5.4; d) C-RETRO in HCl diluted in PBS, pH 2.0.

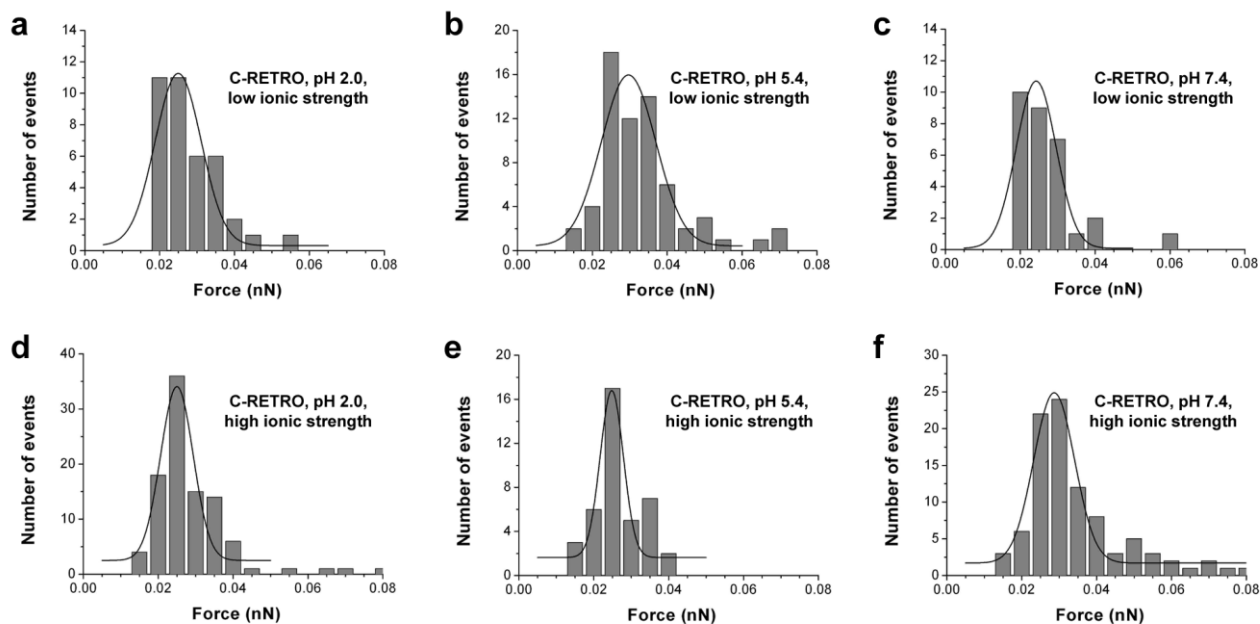


Figure S2. Binding force histograms for C-RETRO peptides in different solutions: a) dilution of HCl in PB, pH 2.0; b) 10 mM acetate buffer, pH 5.4; c) PB, pH 7.4; d) dilution of HCl in PBS, pH 2.0; e) 10 mM acetate buffer, pH 5.4, 137 mM NaCl, KCl 2.7 mM; f) PBS, pH 7.4. The histograms were fitted to Gaussian curves.

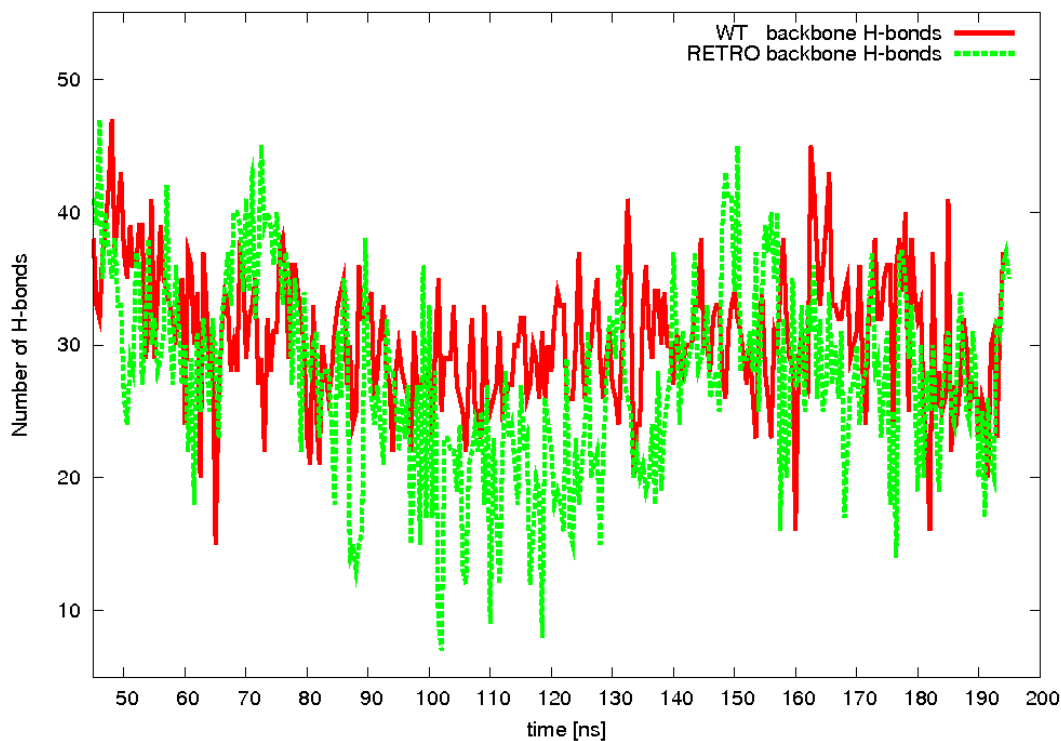


Figure S3. Number of backbone hydrogen bonds in WT (red, solid line) and RETRO (green, dotted line) peptide six-stranded β -sheets during the course of the molecular dynamics simulations.