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Supporting Information

for

Chiral Structure Fluctuations Predicted by a Coarse-Grained Model of Peptide Aggregation

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Figure S1: Example histogram of atom distances in all clusters for a simulation with N = 9, $\varepsilon = 2 \text{ kJ/mol}$, $k_{\theta} = 1000 \text{ kJ/mol}$. The first maximum at 5.5 Å marked by a vertical line determines the cluster cut-off distance.



Figure S2: Example histogram of atom distances in all clusters for a simulation with N = 9, $\varepsilon = 2 \text{ kJ/mol}$, $k_{\theta} = 10 \text{ kJ/mol}$. The first maximum at 5.5 Å marked by a vertical line determines the cluster cut-off distance.



Figure S3: Cluster twist trajectory q(t) for an aggregate of size M = 41. The normalized trajectory histogram (estimated probability density) is presented on the right panel. Three maxima marked by violet lines are visible on the histogram at $q \approx 0.16$, $q \approx 0.0$, and $q \approx -0.16$.



Figure S4: Cluster twist trajectory q(t) simulated by the stochastic diffusion model for an aggregate of size M = 20. The normalized trajectory histogram (estimated probability density) is presented on the right panel. Two maxima marked by violet lines are visible on the histogram at $q \approx 0.45$ and -0.45.



Figure S5: Cluster twist trajectory q(t) simulated by the stochastic diffusion model for an aggregate of size M = 41. Normalized histogram (estimated probability density) is presented on the right panel. Two maxima marked by violet lines are visible on the histogram at $q \approx 0.15$ and -0.15.



Figure S6: Cluster twist trajectory q(t) simulated by the stochastic diffusion model for an aggregate of size M = 68. Normalized histogram (estimated probability density) is presented on the right panel. The maximum marked by violet line is located at $q \approx 0$.



Table S1: The chain twist $\cos(\tau) = (\mathbf{b} \times \mathbf{t}) \cdot \mathbf{A}$ for three cases: achiral, right and left-handed chain twists.