Supporting Information

The Inhibitory Mechanism of a Fullerene Derivative against Amyloid-β peptide aggregation: an Atomistic Simulation Study

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This material contains the temperature list of REMD simulation for isolated Aβ dimer and Aβ dimer with DMF molecules systems, two supplementary tables and 11 supplementary figures.

Temperature lists of REMD simulation:

The temperature list for isolated Aβ dimer system is: 306.30, 308.16, 310.03, 311.91, 313.80, 315.70, 317.60, 319.51, 321.44, 323.37, 325.32, 327.26, 329.22, 331.19, 333.16, 335.14, 337.13, 339.14, 341.15, 343.17, 345.20, 347.24, 349.29, 351.35, 353.41, 355.49, 357.58, 359.67, 361.78, 363.90, 366.08, 368.22, 370.37, 372.52, 374.69, 376.86, 379.05, 381.24, 383.45, 385.66, 387.89, 390.12, 392.37, 394.62, 396.89, 399.17, 401.45, 403.75, 406.06, 408.38, 410.71, 413.05, 415.41, 417.77.

The temperature list for Aβ dimer with DMF molecules system is: 306.30, 308.17, 309.98, 311.86, 313.76, 315.66, 317.56, 319.48, 321.41, 323.34, 325.29, 327.24, 329.20, 331.17, 333.15, 335.14, 337.14, 339.15, 341.17, 343.19, 345.23, 347.27, 349.33, 351.36, 353.43, 355.51, 357.60, 359.70, 361.81, 363.93, 366.06, 368.20, 370.35, 372.51, 374.68, 376.86, 379.04, 381.24, 383.45, 385.67, 387.90, 390.14, 392.51, 394.77, 397.05, 399.33, 401.62, 403.92, 406.24, 408.56, 410.89, 413.24, 415.60, 417.97.

Two supplementary tables:

Table S1. The secondary structure details of each β-hairpin observed in the top ten most-populated clusters for isolated Aβ dimer system, the β-1 and β-2 refers to the first and second β-strand of the β-hairpin, and the loop refers to the region connecting the two β-strands of the β-hairpin.

	β1	loop	β2
Cluster-1	--	--	--
Cluster-2	17LVFFAED23	24VGSNKG29	30A IIGLMV36
Cluster-3	11EVHHQKLVFFAE22	23DVGSN27	28KGAIIGLMVGGV39
Cluster-4	16KLVFFAE21	22EDVGSNKGAII32	33GLMVGG38
Cluster-5	16KLVFF20 18VFFAE 22	21AEDV24 23DVGSN27	25GSNKG29 28KGAII32
Cluster-6	18LVFFAEDV24 17LVFFA21	25GS26 22ED23	27NKGA IIG33 24VGSNK28
Cluster-7	17LVFFA21	22ED23	24VGSNK28
Cluster-8	16KLVFFAE22	23DVGSN27	28KGAIIGL34
Cluster-9	--	--	--
Cluster-10	--	--	--

Table S2. The secondary structure details of each β-hairpin observed in the top ten most-populated clusters for Aβ dimer with DMF molecules, the β-1 and β-2 refers to the first and second β-strand of the β-hairpin, and the loop refers to the region connecting the two β-strands of the β-hairpin.

	β1	loop	β2
Cluster-1	--	--	--
Cluster-2	--	--	--
Cluster-3	--	--	--
Cluster-4	--	--	--
Cluster-5	18VFFAE22	23DVGSN27	28KGAIIG 32
Cluster-6	10YEVHH14	15QK16	17LVFFA21
Cluster-7	--	--	--
Cluster-8	7DSGYEV12	13HHQ15	16KLVFFA21
Cluster-9	17LVFFA21	22EDVGSNKGAI31	32GLMVG36
Cluster-10	--	--	--

11 supplementary figures:

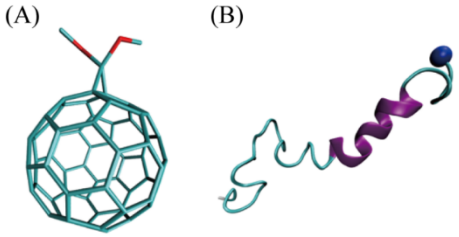

Figure S1. The chemical structure of DMF molecule, carbon atoms are in cyan, oxygen atoms in red, nitrogen atoms in blue, and hydrogen atoms in white(A). The initial conformation of the Aβ1-42, the Cα-atom in the N-terminal is represented by a blue bead (B).

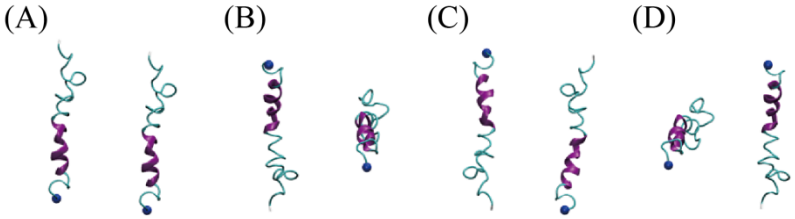

Figure S2. The initial conformation of $A\beta_{1\text{-}42}$ dimer used for our REMD simulations: (A) dimer with parallel orientation, (B) (D) dimer with cross orientation, (C) dimer with anti-parallel orientation

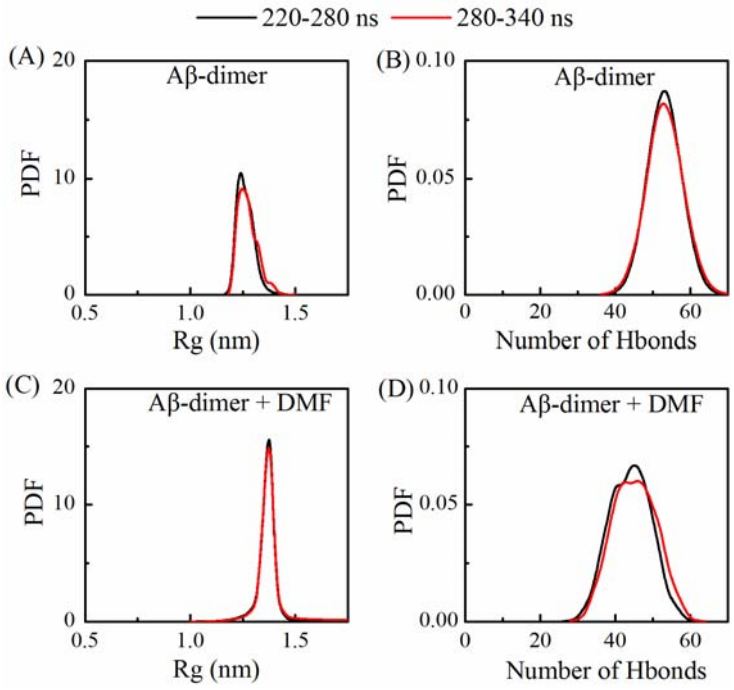

Figure S3. Simulation convergence assessment. Probability density function (PDF) of radius of gyration (Rg) and the number of hydrogen bonds (H-Bonds) for both Aβ dimer system (A,B) and Aβ dimer with four DMF system (C,D) within the time intervals of 220-280 ns (black) and 280-340 ns (red) at 310 K.

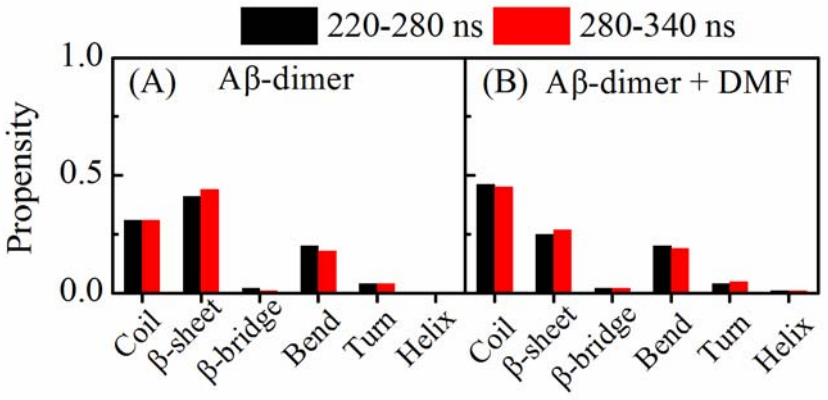

Figure S4. The averaged secondary structure propensities for the Aβ dimer system (A) and Aβ dimer with four DMF system (B) using 220-280 ns (black) and 280-340 ns (red) intervals, respectively at 310 K.

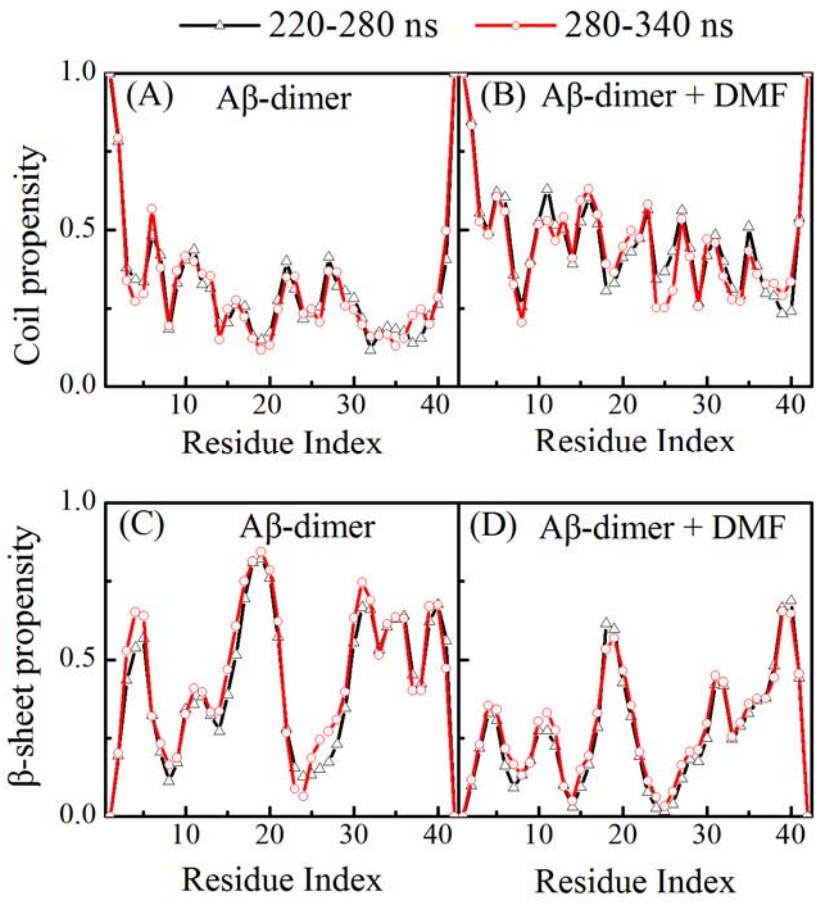

Figure S5. The calculated secondary coil and β-sheet structure propensity of each residue in REMD runs with the time intervals of 220-280 ns (black) and 280-340 ns (red) for Aβ dimer system (A，C) and Aβ dimer with four DMF fullerenes system (B，D) at 310 K.

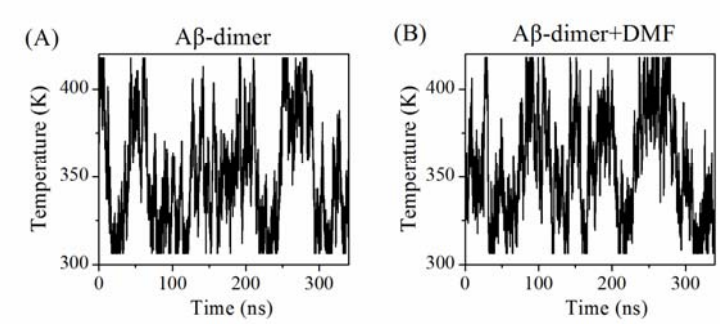

Figure S6: The time evolution of temperature swapping of one representative replica in temperature space for Aβ-dimer system (A) and Aβ-dimer+DMF system (B).

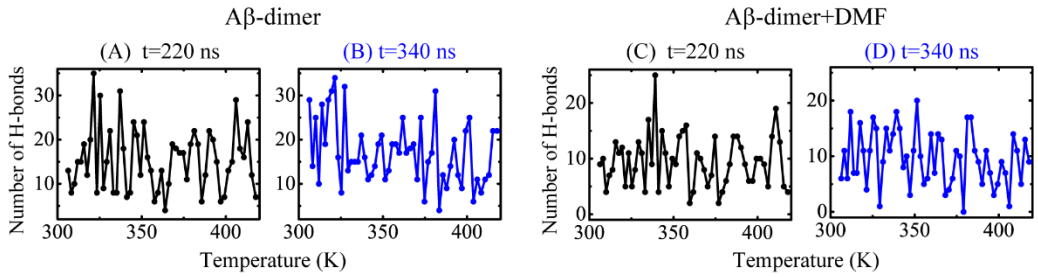

Figure S7: Number of inter-chain H-bonds of the 54 replicas from 306 to 417 K at t=220 and 340 ns for Aβ-dimer (A, B) and Aβ-dimer+DMF (C, D) systems.

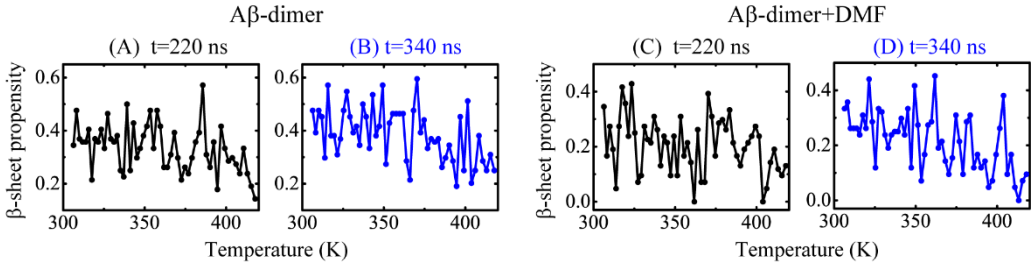

Figure S8: β-sheet propensity of the 54 replicas from 306 to 417 K at t=220 and 340 ns for Aβ-dimer (A, B) and Aβ-dimer+DMF (C, D) systems.

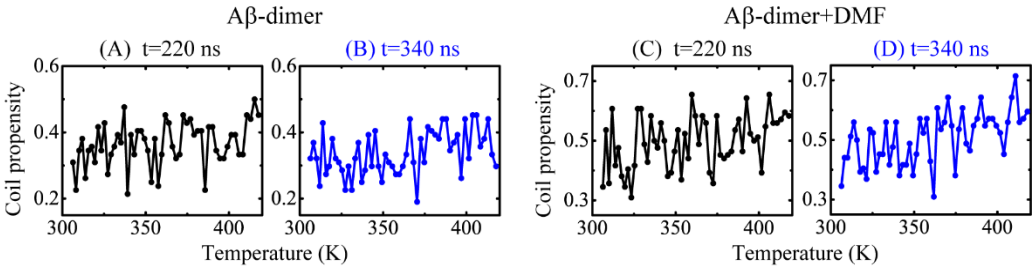

Figure S9: Coil propensity of the 54 replicas from 306 to 417 K at t=220 and 340 ns for Aβ-dimer (A, B) and Aβ-dimer+DMF (C, D) systems.

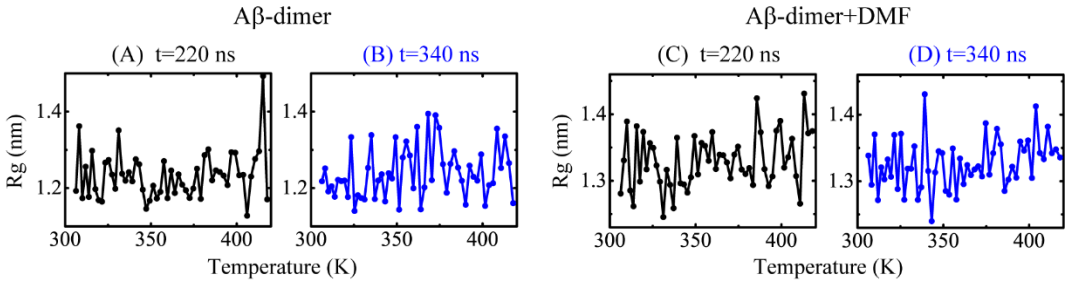

Figure S10: Rg of the 54 replicas from 306 to 417 K at t=220 and 340 ns for Aβ-dimer (A, B) and Aβ-dimer+DMF (C, D) systems.

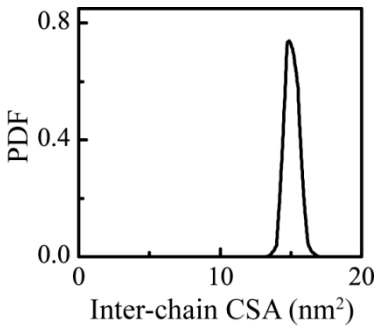

Figure S11. The probability density function (PDF) of average contact surface area (CSA) between DMF molecules and each chain in Aβ dimer.