Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Supplementary Information

Replica Exchange Molecular Dynamics Study of the Truncated Amyloid Beta (11-40) Trimer in Solution

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The Electronic Supporting Information file includes the list of temperatures parameterizing REMD simulations. Additional figures consist of initial conformations of the trimer and two dimer systems, the REMD convergence of both dimer systems, the β-content in time-dependence of the dimers over REMD simulation, the β-content of the dimer in time-dependence over 16 independent MD trajectories, the mean exchange rates between neighboring replicas, the diffusion of temperature space of the REMD simulations, and the distribution of the salt bridge D23-N27 and D23-K28 of the peptide.

The structure of solvated 3Aβ_{11-40} oligomer was investigated using temperature replica exchange molecular dynamics simulations with explicit solvent and 48 different temperatures. The temperatures of replicas was ranged from 295 to 382 K, such as 295, 296.68, 298.37, 300.07, 301.78, 303.49, 305.22, 306.95, 308.68, 310.42, 312.17, 313.92, 315.68, 317.45, 319.23, 321.01, 322.8, 324.6, 326.4, 328.25, 330.07, 331.89, 333.72, 335.57, 337.42, 339.28, 341.14, 343.02, 344.9, 346.79, 348.68, 350.59, 352.5, 354.42, 356.35, 358.29, 360.23, 362.18, 364.14, 366.11, 368.09, 370.07, 372.07, 374.07, 376.08, 378.1, 380.13, and 382.16 K. The solvated Aβ_{16-22} dimer was evaluated utilizing the T-REMD simulations with explicit solvent and 32 different temperatures. The temperatures of replicas were ranged from 294 to 397 K including 294, 296.98, 299.97, 302.99, 306.02, 309.08, 312.17, 315.27, 318.4, 321.56, 324.74, 327.94, 331.16, 334.41, 337.69, 340.99, 344.31, 347.66, 351.04, 354.44, 357.87, 361.33, 364.81, 368.32, 371.86, 375.39, 378.98, 382.59, 386.24, 389.91, 393.61, and 397.34 K.

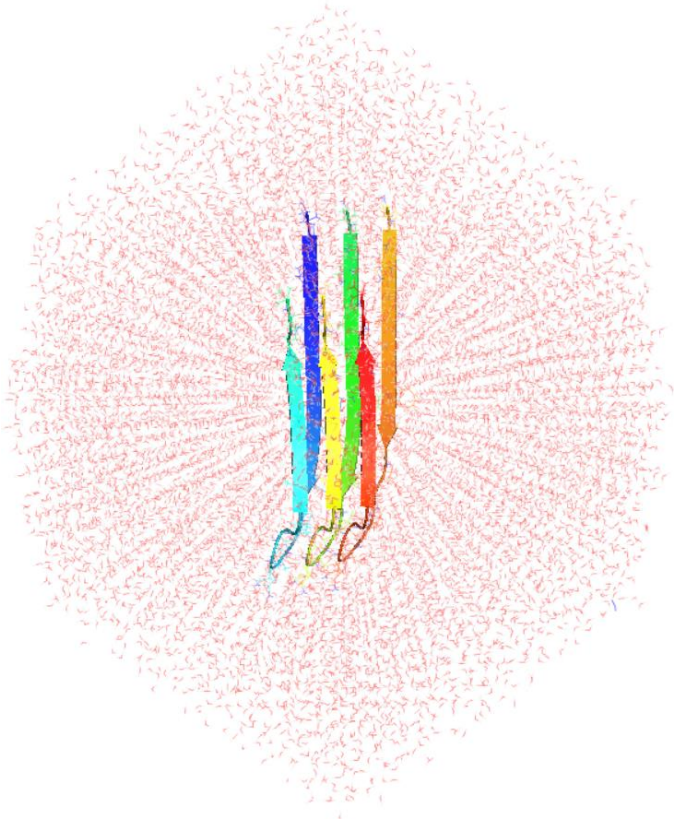

Fig. S1 The conformation of the solvated 3A$\beta_{11\text{-}40}$ oligomer that was used as initial structure of T-REMD simulations.

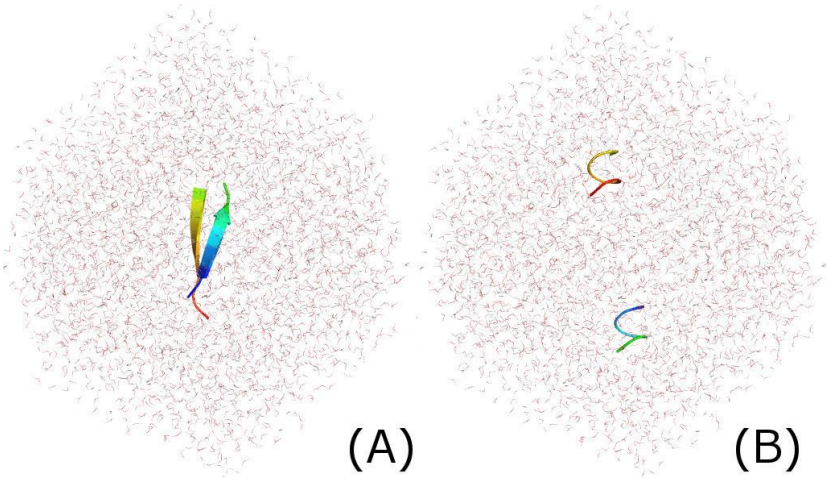

Fig. S2 The initial conformations of the solvated $A\beta_{16-22}$ dimers that were used as initial structure of T-REMD simulations. (A) is antiparallel $A\beta_{16-22}$ dimer system and (B) is random $A\beta_{16-22}$ dimer system.

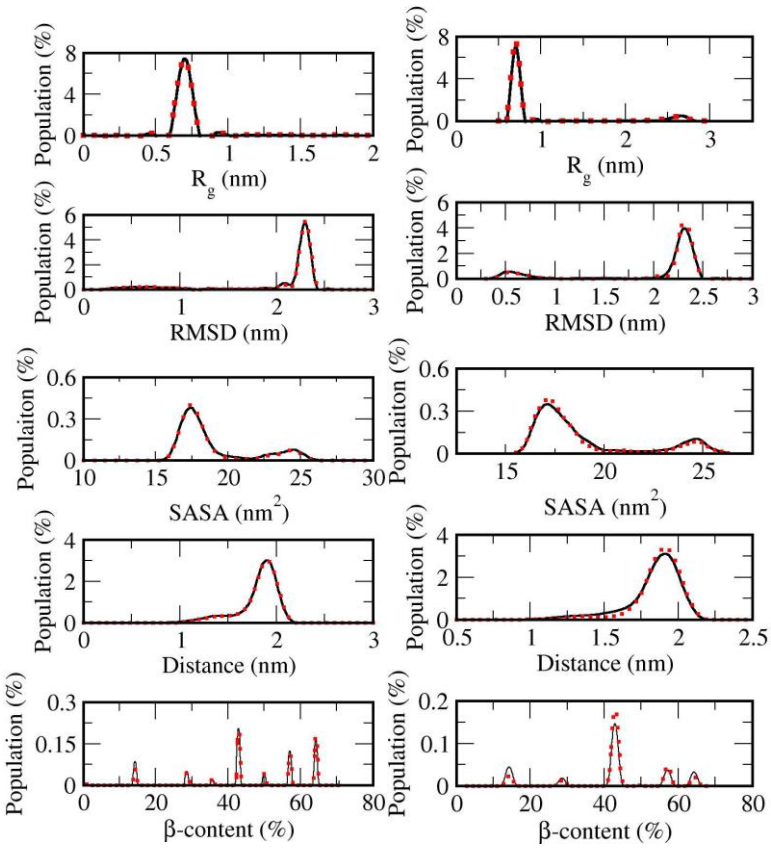

Fig. S3 The REMD simulation convergence of three solvated $A\beta_{16-22}$ dimer systems including antiparallel (left) and random (right) $A\beta_{16-22}$ dimers. All of metrics are measured in two time intervals that black color corresponds to the 15-60 and 174-182 ns, while the discontinued red lines represent the simulation time 65-100 and 184-191 ns of antiparallel and random systems, respectively. The fitted lines suggest the convergence of the REMD simulations.

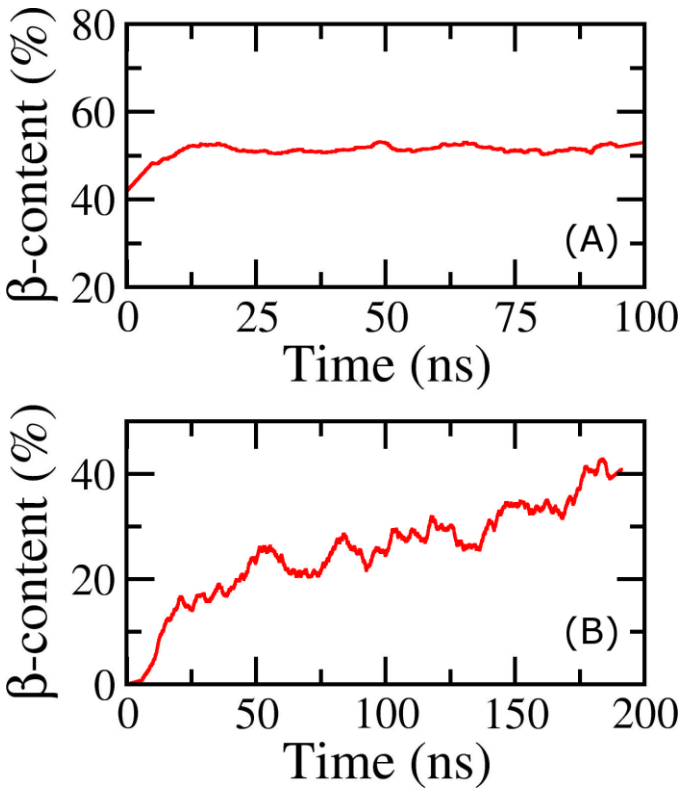

Fig. S4 (A) is the β-content of antiparallel $A\beta_{16-22}$ dimer and (B) is β-content of random $A\beta_{16-22}$ dimer. The results are estimated the REMD data at 300 K using DSSP tool.

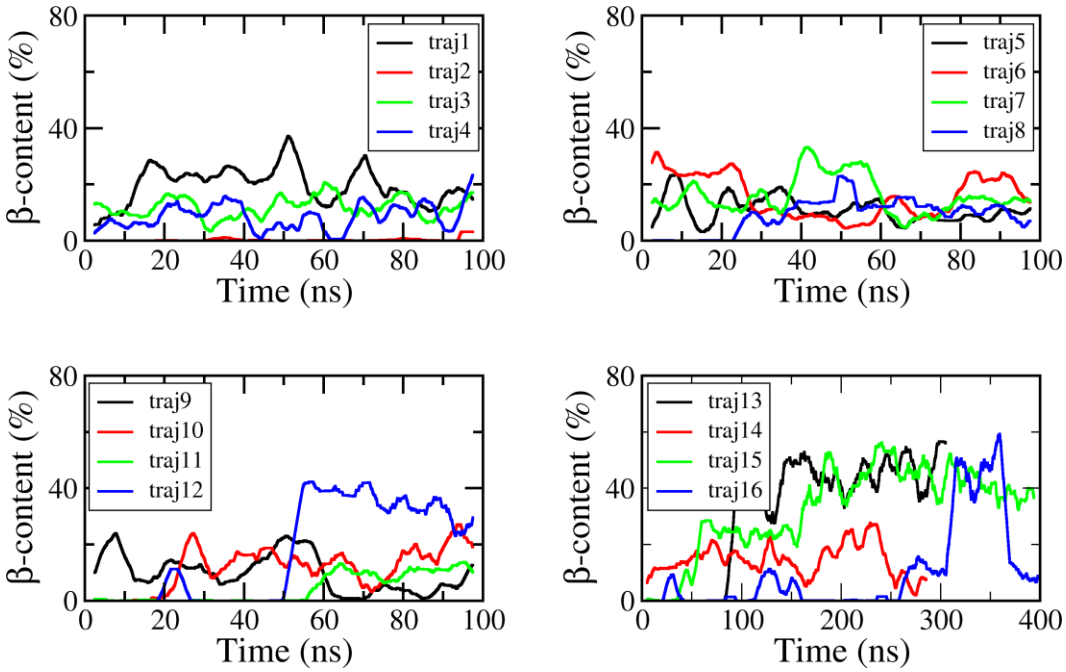

Fig. S5 The β-content of the solvated $A\beta_{16\text{-}22}$ dimer, which has the same initial conformation with random $A\beta_{16\text{-}22}$ dimer starting of T-REMD simulations, is estimated over the 16 independent trajectories MD data at 300 K using DSSP tool. The trajectories noted from traj1 to traj12 are simulated in 100 ns. The trajectories noted from traj13 and traj14 are simulated in 300 ns. The last trajectories are simulated in 400 ns. The high fluctuation of β-content suggests that the MD simulations are not convergent.

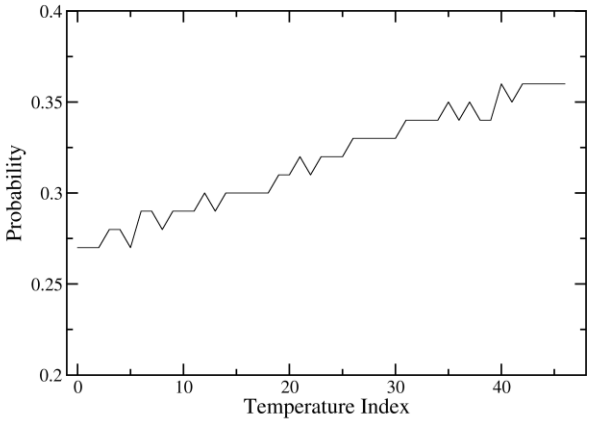

Fig. S6 The average of exchange rates between neighboring replicas, being about 30%.

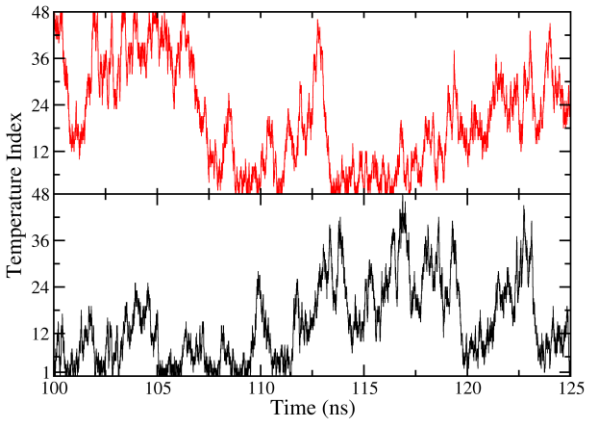

Fig. S7 The diffusion of temperature space of the REMD simulations is monitored by the replica temperature index that is exchanged between the 1st (black) and 48th (red) replicas.

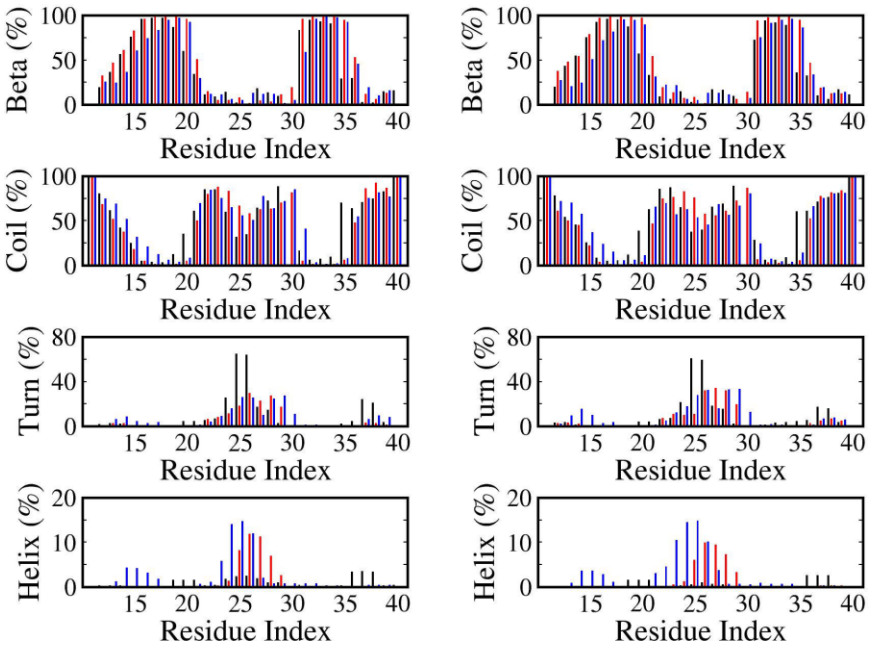

Fig. S8 The secondary structure terms per residue in different time intervals 300-355 ns (left) and 365-417 ns (right). The mean of secondary structure terms difference in isolated time windows is extremely small with approximately < 1% of the total secondary structure of the trimer.

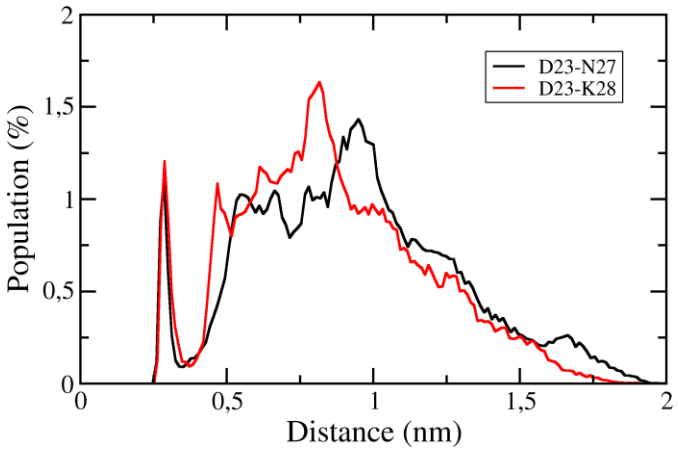

Fig. S9 The distribution of the salt bridges D23-N27 and D23-K28 of the solvated $3A\beta_{11\text{-}40}$ oligomer.

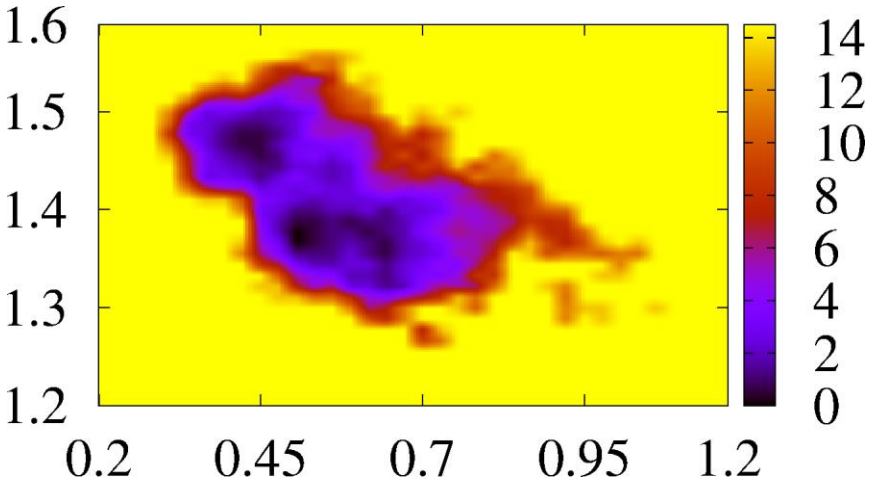

Fig. S10 The FES of the Aβ trimer as a function of the two principal component radius of gyration and the C_α RMSD of the peptide. The FES was determined over the last 206 ns of T-REMD simulations at 300 K.

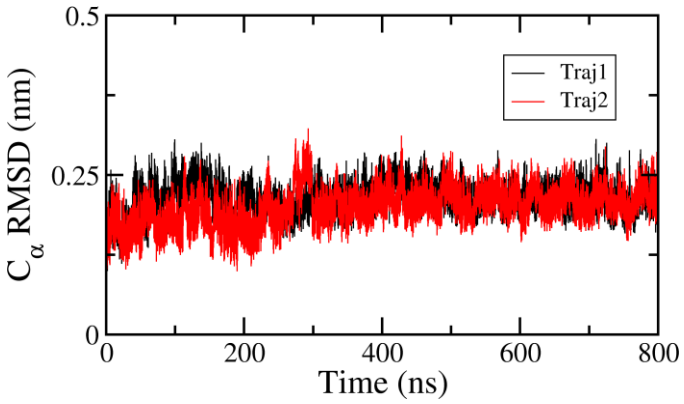

Fig. S11 The C_α RMSD of the trimer during two independent MD simulation trajectories length 800 ns starting from MA conformation. The stable of metric implies that MA is very stable conformation.