

Supporting Information

Destabilization Potential of Phenolics on A β Fibril: Mechanistic Insights from Molecular Dynamics Simulations

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Fig. S1. Final configuration of A β with (a) water, (b) DHC, (c) EGT, and (d) GDE.

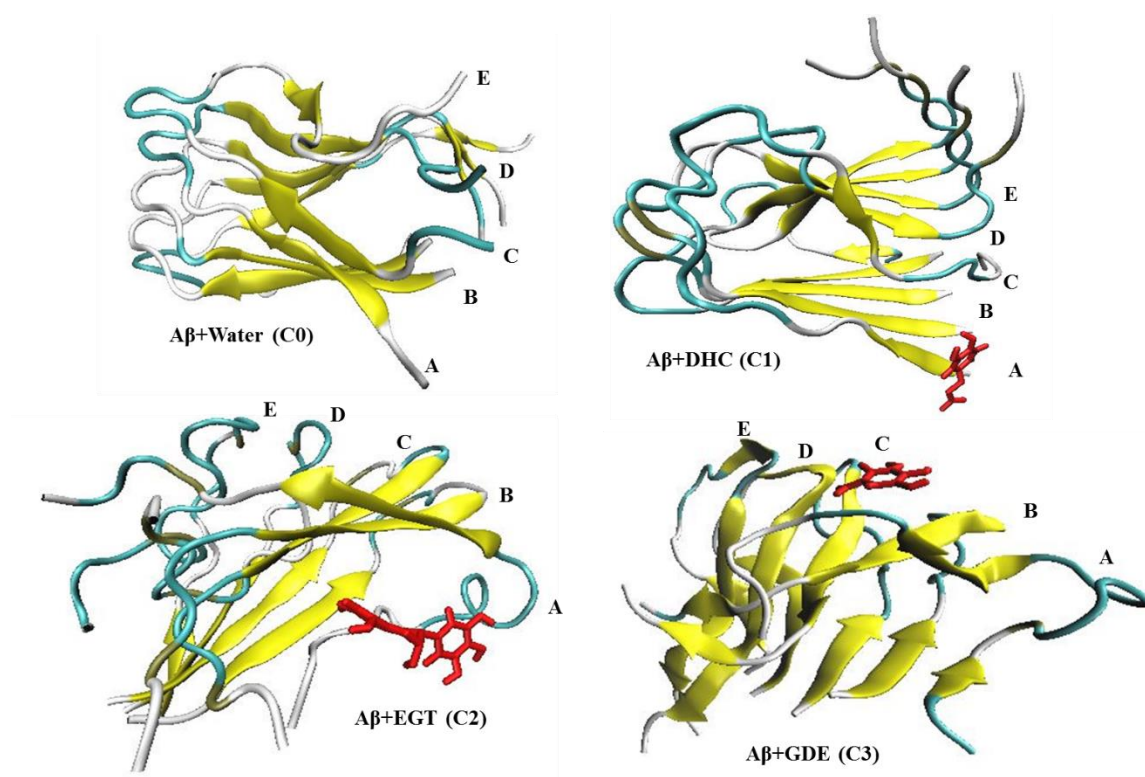


Fig. S2. (a) Average K28 C α distance of chain D-E in water and all 4 ligands, and (b) Average D23-K28 distance of 2BEG in water and all 4 ligands.

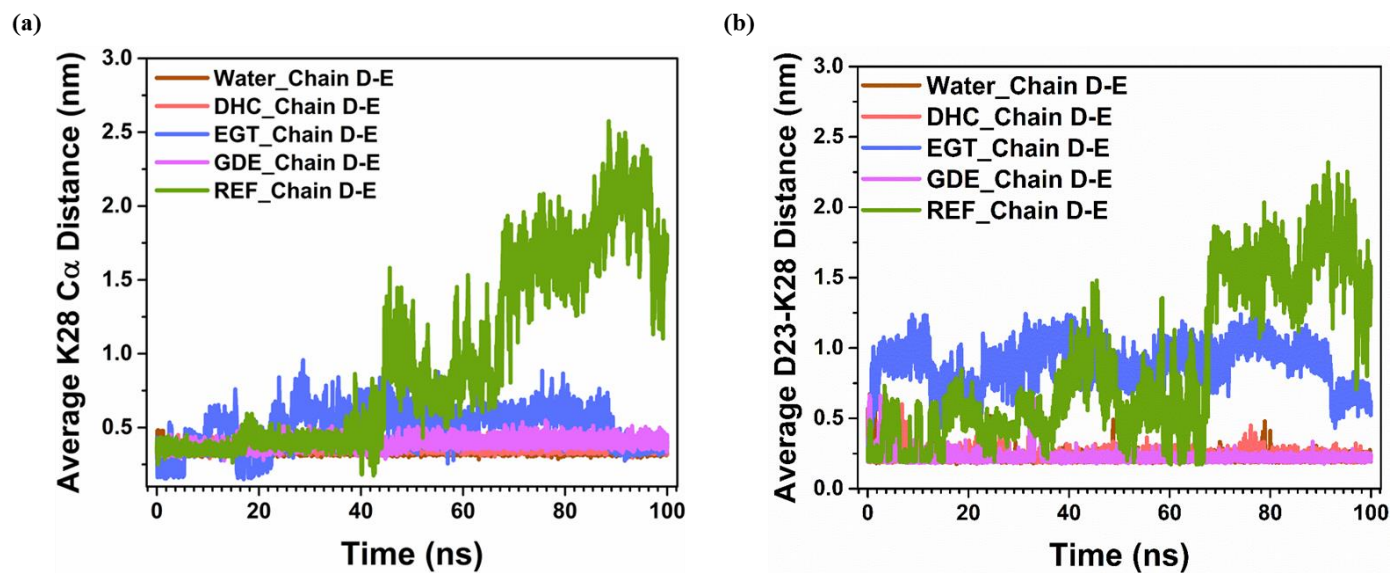


Fig. S3. Correlation between the theoretical and experimental NMR chemical shifts for $C\alpha$ and $C\beta$ atoms of $A\beta_{42}$ protofibril structure is shown in panel (a), and (b), respectively. The unit of NMR chemical shift is in ppm.

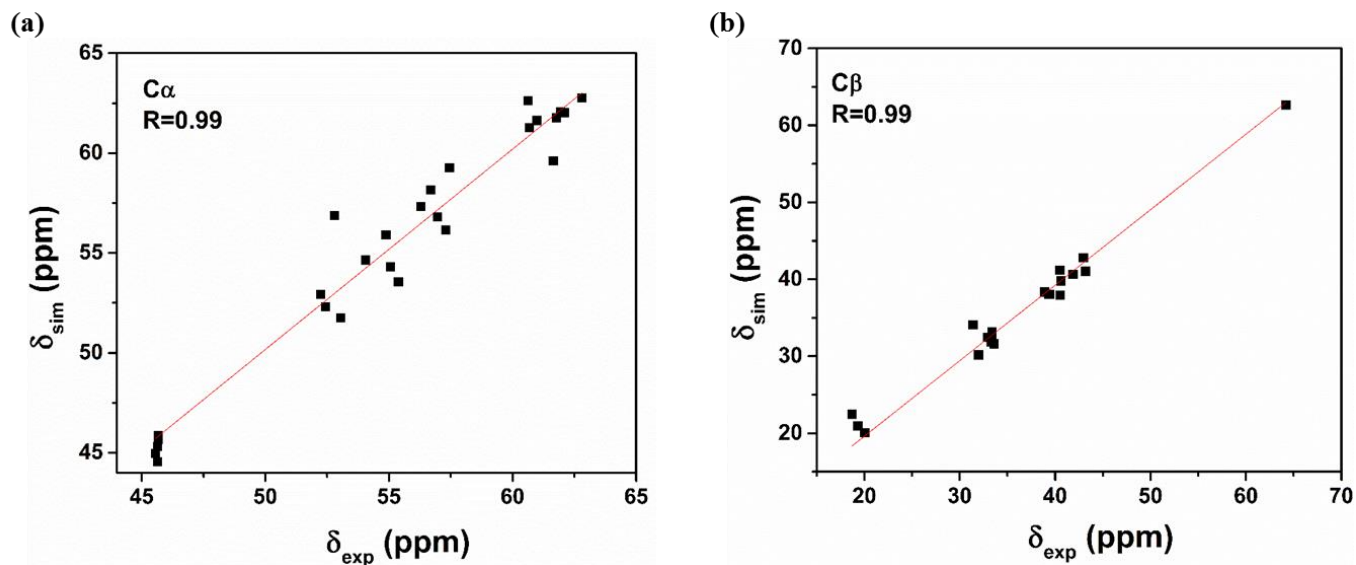


Fig. S4. Destabilization of A β fibril on addition of Ellagic acid by Average D23-K28 distance for all neighboring chains collectively A β -water and A β -REF system.

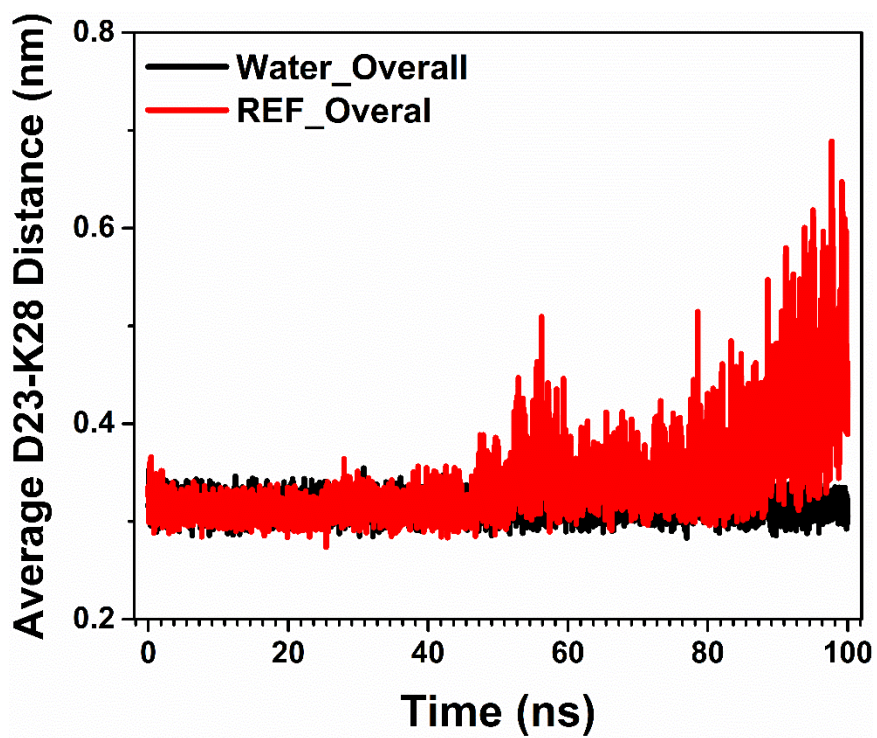


Fig. S5. Average D23-K28 distance for A β -water and A β -REF system (a) Within Chain A, and (b) Within Chain E.

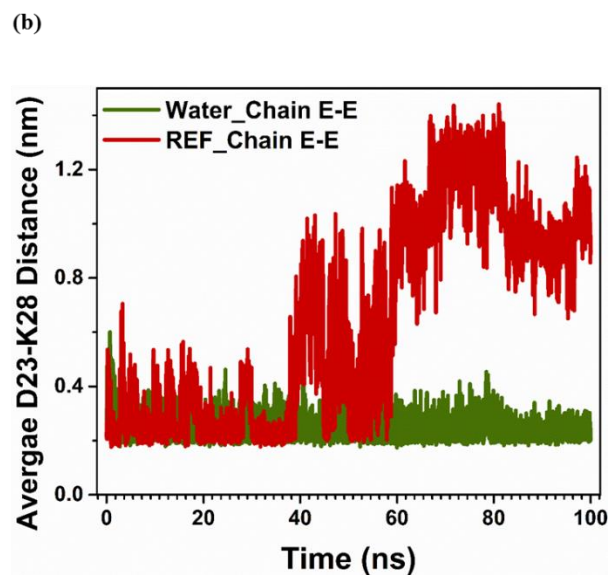
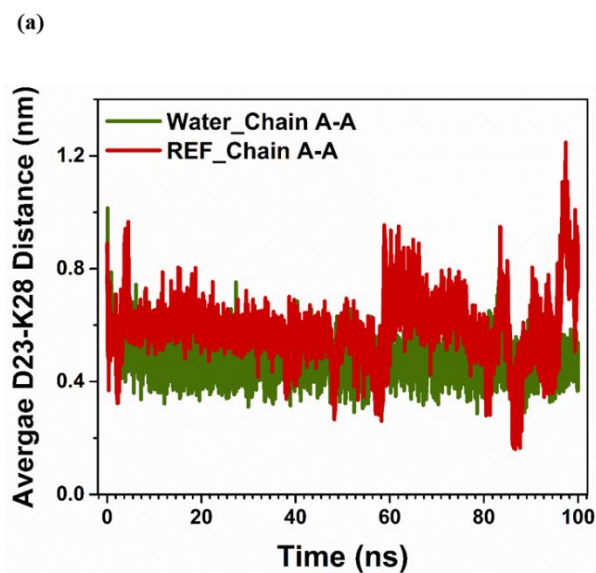


Fig. S6. Individual residue contribution to the total binding energy expressed in kcal/mol (a)- for the entire A β Fibril and (b)- Key residues which contribute the most to binding of DHC with chain A are indicated with a label in Orange.

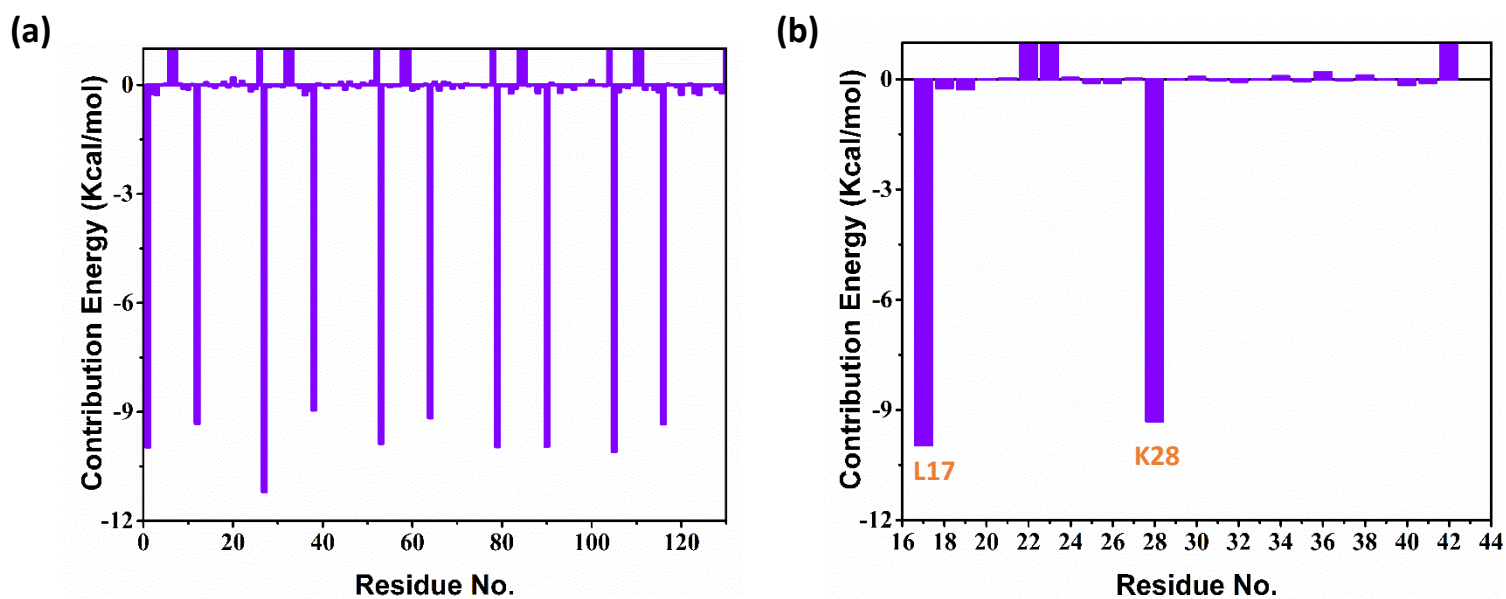


Fig. S7. Individual residue contribution to the total binding energy expressed in kcal/mol (a)- for the entire A β Fibril and (b)- Key residues which contribute the most to binding of EGT with chain A are indicated with a label in Orange.

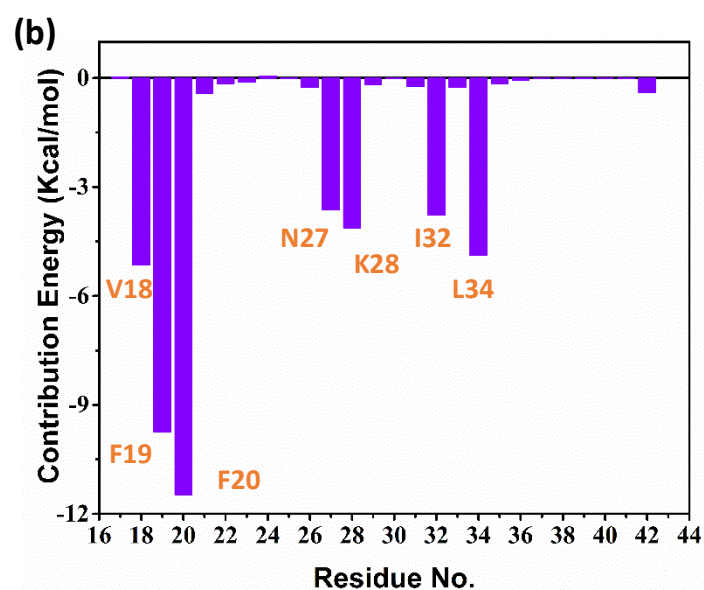
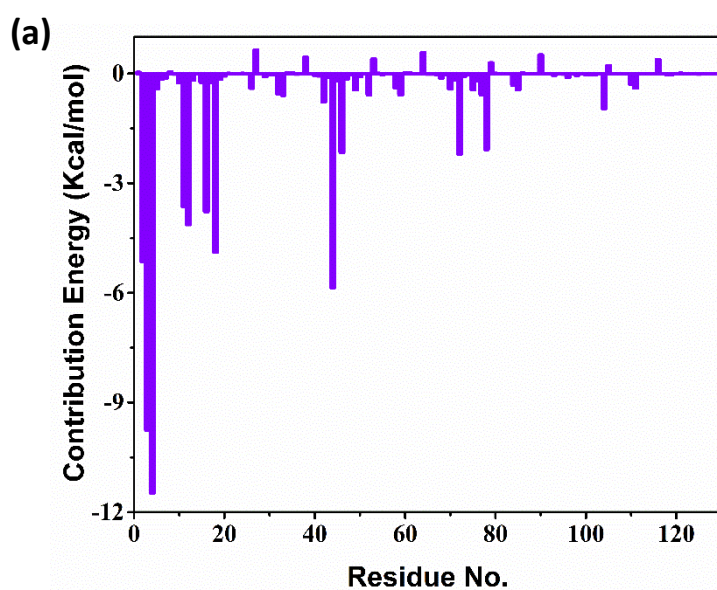


Fig. S8. Individual residue contribution to the total binding energy expressed in kcal/mol (a)- for the entire A β Fibril and (b)- Key residues which contribute the most to binding of GDE with chain A are indicated with a label in Orange.

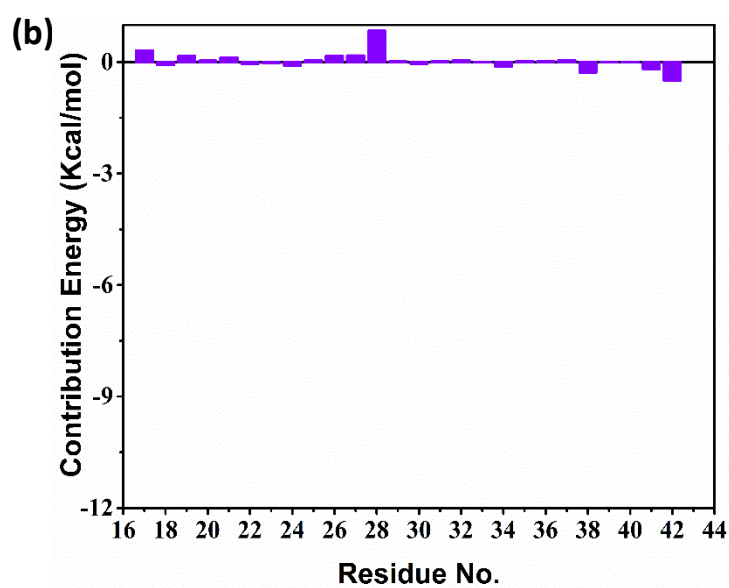
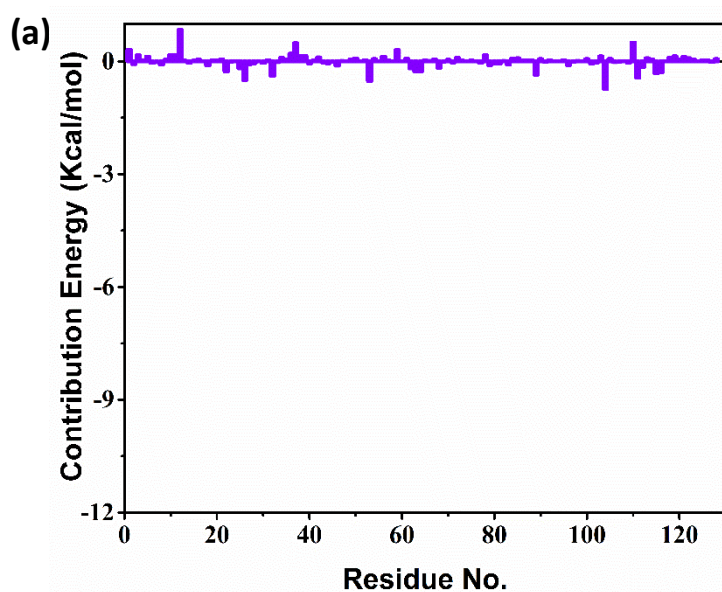


Table S1. Inter-chain binding free energy (Kcal/mol) for chain D and E for system A β -Water and A β -REF complex evaluated by MMPBSA method.

Energy Terms	Inter-chain (chain D and E) binding energy for Aβ-Water (Kcal/mol)	Inter-chain (chain D and E) binding energy for Aβ-REF (Kcal/mol)
ΔE_{vdW}	-333.26 \pm 2.03	-195.63 \pm 1.83
ΔE_{elec}	-272.51 \pm 1.48	-81.05 \pm 2.55
ΔE_{MM}^a	-605.77 \pm 3.51	-276.68 \pm 4.38
ΔG_{ps}	443.99 \pm 1.38	198.10 \pm 0.00
ΔG_{nps}	-40.84 \pm 0.84	-23.92 \pm 0.77
ΔG_{solv}^b	403.15 \pm 2.22	174.18 \pm 0.77
$\Delta G_{binding}^c$	-202.62 \pm 5.73	-102.50 \pm 5.15

$$^a \Delta E_{MM} = \Delta E_{vdW} + \Delta E_{elec}$$

$$^b \Delta G_{solv} = \Delta G_{ps} + \Delta G_{nps}$$

$$^c \Delta G_{binding} = \Delta E_{MM} + \Delta G_{solv}$$