

Amyloid peptide $A\beta_{40}$ inhibits aggregation of $A\beta_{42}$: evidence from molecular dynamics simulations

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Effects of amyloid beta peptide $A\beta_{40}$ on secondary structures of $A\beta_{42}$ are studied by all-atom simulations using the GROMOS96 43a1 force field with explicit water. It is shown that in the presence of $A\beta_{40}$ the beta content of monomer $A\beta_{42}$ is reduced. Since the fibril-prone conformation N^* of full-length $A\beta$ peptides has the shape of beta strand-loop-beta strand this result suggests that $A\beta_{40}$ decreases the probability of observing N^* of $A\beta_{42}$ in monomer state. Based on this and the hypothesis that the higher is the population of N^* the higher fibril formation rates, one can expect that, in agreement with the recent experiment, $A\beta_{40}$ inhibit fibril formation of $A\beta_{42}$. It is shown that the presence of $A\beta_{40}$ makes the salt bridge D23-K28 and fragment 18-33 of $A\beta_{42}$ more flexible providing additional support for this experimental fact. Our estimation of the binding free energy by the molecular mechanics-Poisson-Boltzmann surface area method reveals the inhibition mechanism that $A\beta_{40}$ binds to $A\beta_{42}$ modifying its morphology.

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