Modeling the interaction of acetylcholinesterase inhibitor

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Currently used in medicine, acetylcholinesterase (AChE) inhibitors do not have sufficient specificity. Pyridoxine derivatives synthesized in the Butlerov Chemical Institute showed anticholinesterase activity in vivo experiments in mice. Pyridoxine derivatives were docked in the active site of the mouse and human cholinesterases. Kalimin and neostigmine served as controls. Docking results showed that the binding energy derivatives pyridoxine enzymes more than the control inhibitors [1]. Analysis of results showed that the interaction between the derivatives of pyridoxine and amino acid residue Ser203 of the catalytic triad is strongly influenced by its surroundings. To check the result was simulated interaction of the inhibitor with the catalytic triad in different environments. The experiment revealed that the individual sites of the active center in the simulation contributed to the reduction of the energy barriers for the whole duration of the interaction, while others perform a barrier function [2].

In this study acetylcholinesterase inhibitor molecular dynamics was carried out. Files for the dynamics were obtained from the program Amber 99, calculation was carried out in the program Namd 2.8, the primary location of the inhibitor in the active cavity were obtained from the docking program AutoDock. The primary analysis of the dynamics shows that there is a significant convergence of the atom C to atom O, which are supposed to interact non-covalently or form reversible covalent bond.

The detailed analysis revealed the most important parts in the AChE active site responsible for the interaction with the inhibitor.

Literature

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