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MEETING ABSTRACTS

MOLECULAR MODELING IN SEARCH OF NEW, MULTI-TARGET LIGANDS AGAINST ALZHEIMER'S DISEASE. EXPLORING THE BIOCHEMICAL MULTIVERSE.

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In response to the complex and still not fully understood pathomechanism of Alzheimer's disease, many researchers have turned towards the promising paradigm of designing ligands with a multi-target nature[1]. One of the possible benefits of this approach in Alzheimer's disease is an opportunity to merge activity against cholinesterases, which are used in the current symptomatic therapies, with disease-modifying targets associated with β-amyloid and tau protein pathways[2]. Optimization of ligand with respect to several biological targets while maintaining good physicochemical parameters is not an easy task. Computer modeling can be a huge help in this task. Computer modeling in the design of biologically active substances can be used to effectively search through the huge, available chemical space, or provide support for drawing conclusions of results obtained during the study[3]. In the work presented here, we would like to describe how the molecular modeling methods were used to design and obtain new series of 1-benzylamino-2-hydroxyalkyl derivatives that are effective against both acetyl- and butyrylcholinesterase as valid, symptomatic targets with an anti-aggregating properties against Tau protein, β-amyloid and inhibition properties against β-secretase (BACE-1) as disease-modified targets[4].

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