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DESIGN AND SYNTHESIS OF NOVEL MANNICH BASES CONTAINING 1,2,4-TRIAZOLE MOIETY AS POTENTIAL ANTIHYPERTENSIVE AGENTS: MOLECULAR DOCKING STUDY

Ismoilov Sh., Yeromina H. O., Perekhoda L.O.

National University of Pharmacy

annerem2012@gmail.com

As biological research has become increasingly data intensive and expensive, biomedical projects require informatics tools such as molecular docking and database mining. Molecular docking can be defined as the prediction of the structure of receptor-ligand complexes, where the receptor is usually a protein or a protein oligomer and the ligand is either a small molecule or another protein. Nowadays molecular docking is a tool in drug discovery to find and optimize lead compounds, often by database screening [1].

Few Mannich bases derived from 1,2,4-triazoles containing morpholine substituent were biologically active [2-4]. In view of this and as a part of our continuing research on potential antihypertensive agents new series of Mannich bases containing both 1,2,4-triazoles and morpholine moiety were synthesized by one-pot multicomponent Mannich reaction. Structure and purity of target compounds have been established by means of ¹H NMR, ¹³C NMR-spectroscopy and TLC. Docking studies in order to find biologically active substances with antihypertensive activity were conducted. As a biological target for docking the active site of the macromolecules from Protein Data Bank (PDB) the angiotensin receptor II (PDB ID: 1R4L,3NXO, 4BZR) were used. In result of the molecular docking, a number of the consensus scoring function values, which estimate quality and binding energy of the studies substances with the molecules of biological targets, were obtained. It was established, that the inhibitory activity of test compounds relative to angiotensinconverting enzyme can be realized through the formation of complexes between them. The stability of this complexes is provided mainly by energy-favorable geometric arrangement of ligands at the active site of the acceptor and the formation of hydrogen bonds between them by intermolecular electrostatic and donor-acceptor interactions. The best affinity binding was observed in the case of molecules with crystallographic model of angiotensin-converting enzyme PDB ID: 1R4L.

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