In silico docking evaluation of α-Amylase inhibitory activity of N-(pyridine-2-ylcarbamothiol)benzamide

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Abstract: Inhibition of α-amylase, enzyme that plays a role in digestion of starch and glycogen, is considered a strategy for the treatment of disorders in carbohydrate uptake, such as diabetes and obesity[1]. Inhibitors of carbohydrate digesting enzymes, such as alpha-amylase and alpha-glucosidase, are now actively searched for, since they could ultimately make useful medicines against diabetes and obesity[2,3]. The objective of this study was to evaluate the α-amylase inhibitory activity of N-(pyridine-2-ylcarbamothiol)benzamideusing in silico docking studies. Acarbose, a known α-amylase inhibitor was used as the standard. In silico docking studies were carried out using recent version of AutoDock 4.2, which has the basic principle of Lamarckian genetic algorithm. Additional molecules to 1SMD.pdb, including solvent, were deleted prior to docking. The docking box was positioned at x = 6.805, y = 49.167, z = 12.297 with a size of 70x70x70. In order to get an approximation of the possible effectiveness of these ligands as a potential inhibitor of the enzyme, docking score was obtained for the 1SMD.pdb and new benzamide derivative. This score was −8.79 kcal/mol. In comparison, acarbose had a score of −11.04 kcal/mol, which is suggesting that our new benzamide derivative could inhibit amylase activity. A docking experiment suggests that binding site for new derivative is active site.Amino acids involved in the interactions are$D_{197,}E_{233}$ and$Y_{62.}$Interactions between enzyms and inhibitors was pi-pi and hydrogen bonds.

Keywords: diabetes; Alpha amylase ; N-(pyridine-2-ylcarbamothiol)benzamide

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