Molecular docking study of 3-(3-chloro-4-R-phenyl)-1,1-dimethylurea, with R=Cl and CH_3

SOUHILA Laib[1,2*] and WAHIBA Boussebbat[2]

[1]*Departement de Socle Commun, Faculté des Sciences de la Nature et de la vie, Université de Batna-2*

[2]*Laboratoire de Chimie des Matériaux et des Vivants: Activité & Réactivité (LCMVAR), Université de Batna-1*

Code CCO 7

E-mail* : laibsouhilal@yahoo.com/s.laib@univ-batna2.dz

Introduction & Objectives: Phenylureas pesticides are substances or mixtures used to control plant and animal life for the purposes of increasing and improving agricultural production, protecting public health from pest-borne disease and discomfort, reducing property damage caused by pests, and improving the aesthetic quality of outdoor or indoor surroundings [1]. Molecular Docking is a computational procedure that attempts to predict the non-covalent binding of a macromolecule obtained from data banks or MD simulations, etc. with a small molecule as a lead for further drug development [2]. The lead candidates can be found using a docking algorithm that tries to identify the optimal binding mode of a small molecule to the active site of a macromolecular target [3]. Docking can also be used to try to predict bound conformation, binding energy and affinity [2]. Thus, the purpose of drug discovery is to derive drugs that more strongly bind to a given protein target than the natural substrate [4–6]. As a reason, understanding the processes of interaction between HSA protein and 3-(3-chloro-4-R-phenyl)-1,1-dimethylurea, with R=Cl **(1)** and CH_3 **(2)** is critical for determining the potential risks of these compounds to humans.

Methodology (Material and methods): The Molecular Docking calculation for 3-(3-chloro-4-R-phenyl)-1,1-dimethylurea, with R=Cl **(1)** and CH_3 **(2)** are performed by Gaussian 09 [7], Autodock Vina [8], the polar hydrogen atoms and Kollman charges were added to the protein by using the AutoDockTools4 [9], the visualization of the results was depicted by Discovery Studio Visualizer software 2016 [10].

Results and Discussion: The two studied structures were docked to HSA using Autodock Vina. The lowest energy (best) poses were selected as the binding mode (**1**) (-7.4 kcal/mol). The results suggested that the studied molecules could interact with HSA at the binding site using hydrogen bonding hydrophobic and van der Waals interactions. The molecule **(1)** interacts by hydrogen bonding with the residues Arg-485 (2.30A°), Arg-348 (1.96A°) and Met-446 (3.64A°) and the molecule **(2)** with the residues Asp-187 (3.48A°) and Gln-459 (3.46A°).

Conclusion: The molecular docking results suggest that the first compound is the least stable and the most harmful compound. Thus, the binding energy with HSA follows the trend: **(1)** (-7.4 kcal/mol) < (**4**) (-6.9 kcal/mol).

Keywords: Molecular Docking, Pesticides, AutoDockTools, Binding energy, Potential risks, hydrogen bond.

References

1. Arnold, DJ (1990), Environmental Fate of Pesticides. Wiley & Sons. New York.
2. Trott, O., Olson, AJ. (2010) J Comput Chem, 31: 455-461. 3. René, T., Mikael, MH. (2006) J Med Chem, 49: 3315-3321.
4. Yao, Y., Han, W., Zhou, Y., Li, Z., Li, Q., Zhong, D. (2007) J Theor Comput Chem, 06: 541-548.
5. Carlos, HTP., Silva, D., Ivone, C., Carlton, A. (2006) J Theor Comput Chem, 05: 579–586.
6. Riahi, S., Moghaddam, AB., Ganjali, MR., Norouzi, P. (2007) J Theor Comput Chem, 06: 331-340.
7. Frisch, MJ. et al. (2009), Gaussian 09 Revision.Wallingford CT.
8. Biovia, DS (2017), San Diego. CA. USA.
9. Morris, GM., Huey, R., Lindstrom, W. et al. (2009), J Comput Chem 30: 2785-2791.
10.Trott, O., Olson, AJ. (2010) J Comput Chem, 31: 455-461.