ID 3039

Molecular Docking Analysis of 4-Iminoflavan Derivative as an Anti-Inflammatory Agent Targeting Mitogen-Activated Protein Kinase 1 (MAPK 1)

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ABSTRACT

The current study focuses on the molecular docking of 4-iminoflavan derivatives obtained through a condensation reaction with a primary amine as an anti-inflammatory drug that targets Mitogen-activated protein kinase 1 (MAPK1), which is an important signaling molecule that regulates cell survival, differentiation, and proliferation. The molecular docking program used in this investigation was Moe software. The result showed the binding energy of N-(hydroxyl-Phenyl) 4-iminoflavan to MAPK1 was found to be -5.5 kcal/mol, indicating a strong binding affinity.

Keywords: 4-iminoflavan, molecular docking, anti-inflammatory, (MAPK 1).

1. Introduction:

The 4-iminoflavan derivatives have been demonstrated to have important biological activities such as aldose reductase inhibition, cancer chemoprevention, antibacterial, and anti-inflammatory effects. The 4-iminoflavan derivatives are derived from flavanones, a subclass of natural flavonoids found in plants, through a condensation reaction with a primary amine [1-4]. The current study focuses on the molecular docking of N-(hydroxyl-Phenyl) (Figure 1) as anti-inflammatory drugs that target MAPK1. Mitogen-activated protein kinases are a subclass of protein kinases that phosphorylate substrate residues or their own dual serine and threonine residues (autophosphorylation) to either activate or de-activate their targets. Mitogen-activated protein kinase 1, often referred to as extracellular signal-regulated kinase 2 (ERK2), is a crucial signaling molecule involved in several physiological processes, including cell survival, differentiation, and proliferation [5-7]. The molecular docking program utilized in this study was Moe software. Which is a computer method for predicting the binding mechanism and affinity of small molecules for a certain target protein. The process involves determining the optimal ligand orientation and conformation within the receptor's binding pocket [8].

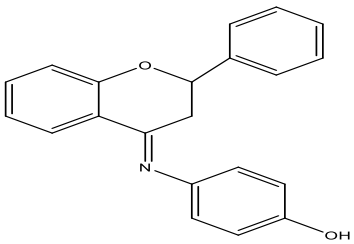

Figure 1: Chemical structure of N-(hydroxyl-Phenyl)4-iminoflavan.

2. Experimental

In order to obtain the structure of the compound N-(hydroxyl-Phenyl)4-iminoflavan, a ChemDraw software was used and the PDB database was used to obtain the complete structure of the MAPK 1 protein. The initial step in molecular docking analysis is to prepare the ligand and receptor structures. the 4-iminoflavan derivative, is prepared by adding hydrogen atoms to the structure then minimizing the Energy. MAPK 1, a protein, is generated by removing all attached ligands and crystallographic water molecules. The crystallographic structure or homology model is used to identify MAPK1's active site and the necessary residues are selected for docking analysis. The docking simulations are run using the MOE docking

DOI: 10.21467/abstracts.169 ISBN: 978-81-970666-4-1 (eBook)

program, and a large number of docking poses are generated. positions represent the various orientations and binding processes of the N-(hydroxyl-Phenyl) 4-iminoflavan in MAPK1's active site.

3. Results and Discussion

Molecular docking studies demonstrated that N-(hydroxyl-Phenyl) 4-iminoflavan interacts to MAPK1's active site, generating a stable complex. The visualization of the results showed the optimum binding position, with a binding energy of -5.5 kcal/mol, the interaction study indicated that the ligand formed backbone donor interactions with a key MAPK1 residue (Met108), Besides the second bond which is defined by an arene-H interaction with (Asp167). The interaction within the complex can be seen in (Figure 2).

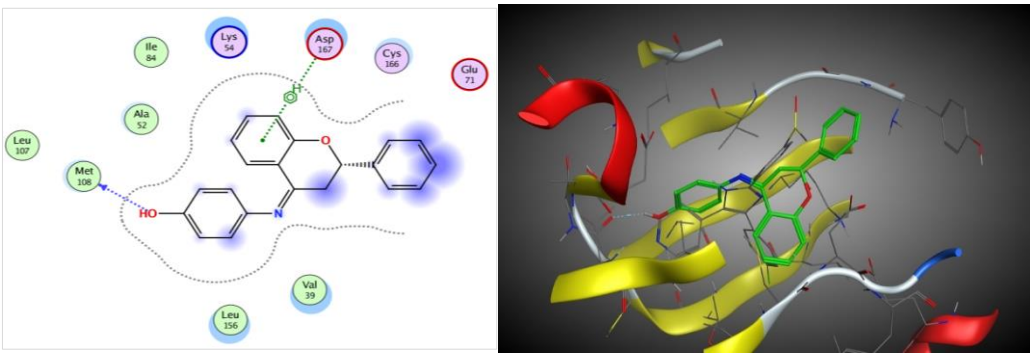

Figure 2: Ligand interactions of N-(hydroxyl-Phenyl) 4-iminoflavan with Mitogen-activated protein kinase1 (MAPK1) by using Moe software.

4. Conclusions

Finally, a molecular docking studies gives light on the potential chemical interactions between N-(hydroxyl-Phenyl) 4-iminoflavan and MAPK1. The interpretation of such analyses contributes to understanding the structural basis of ligand-protein interactions and has the potential to find innovative treatment candidates targeting MAPK1 signaling pathways.

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ISBN: 978-81-970666-4-1

Series: AIJR Abstracts

DOI: 10.21467/abstracts.169