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Exploring the Potential of Azaflavanones in Annexin A5 Inhibition: A Molecular Docking Study for Anti-inflammatory Therapy

Djawhara Haddad [1] *, Nasser Belboukhari [1], Khaled Sekkoum[1], Meriem Bouanini[1]

[1] Bioactive Molecules and Chiral Separation Laboratory, Faculty of exact sciences, Tahri Mohammed University, Istiklal street PO 417 Bechar, 08000, Algeria

*Corresponding author's email: haddad.djawhara@univ-bechar.dz

ABSTRACT

Azaflavanones, a class of flavonoids have been extensively studied for their diverse biological activities, including their anti-inflammatory properties. In this study, molecular docking was employed to investigate the potential of azaflavanones as anti-inflammatory agents by docking them with Annexin A5, a protein involved in various cellular processes and implicated in inflammation. The results revealed that azaflavanones forms stable interactions with Annexin A5, suggesting its potential as a novel anti-inflammatory agent. The findings of this study provide valuable insights into the molecular mechanisms underlying the anti-inflammatory activity of azaflavanone and pave the way for further exploration of its therapeutic potential.

Keywords: Azalavanones, Annexin A5, inflammation, Molecular Docking.

1. Introduction

Inflammation is a vital immune response that helps the body fight against harmful stimuli. However, chronic inflammation can lead to various diseases, including cancer, diabetes, and cardiovascular disorders [1,2]. The discovery of new anti-inflammatory agents is essential to develop effective treatments for these diseases. In recent years, molecular docking studies have emerged as a valuable tool to identify potential drug candidates [3]. Molecular docking analysis of azaflavanones for targeting Annexin A5 in anti-inflammatory therapy involves the use of computational techniques to study the interaction between azaflavanones and Annexin A5, a protein involved in the regulation of inflammation [4]. Azaflavanones are a class of natural compounds found in various fruits and vegetables, known for their potential anti-inflammatory properties [5]. Annexin A5, on the other hand, plays a crucial role in modulating the inflammatory response by regulating the release of pro-inflammatory mediators and controlling cell membrane repair processes [4,6].

2. Experimental

Three azalavanones derivatives were chosen from literature which were recreated with ChemDraw, converted to MOE compatible mol format, and subjected to 3D protonation and energy minimization. the crystal structure of Annexin A5 was obtained from the Protein Data Bank (PDB). The docking simulations were performed using the default settings of the MOE software, with the binding site defined as the active site of Annexin A5.

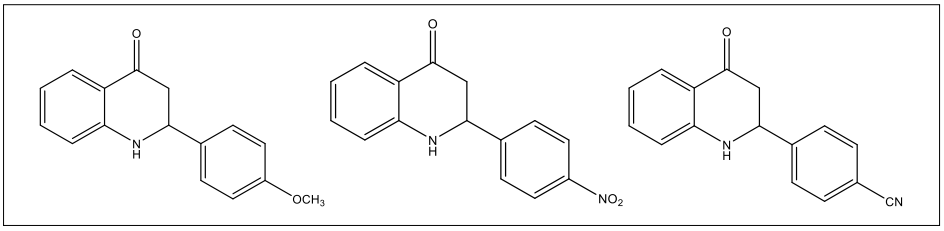

Figure 1: chemical structures of azaflavanones derivative

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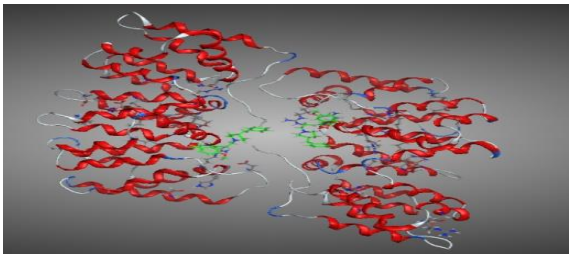

Figure 2: Crystal structure of Annexin A5

3. Results and Discussion

The results of the molecular docking study revealed that azaflavanone showed favorable binding interactions with Annexin A5 and the results obtained for the azaflavanone derivatives were shown to be better than the standard compounds, it was observed these molecules exhibit interactions with the enzyme across two distinct binding sites show figure 01.

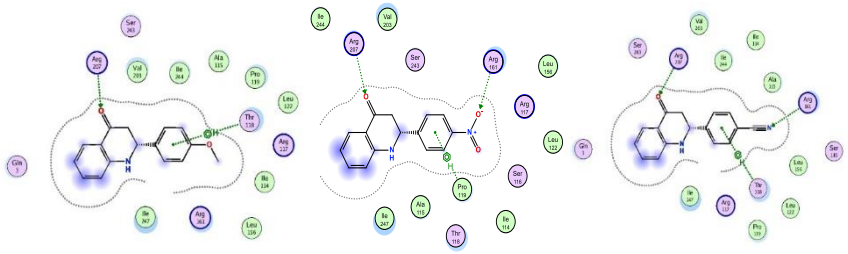

Figure 3: ligands interactions of Azaflavanones with Annexin A5 by using Moe software

The first interaction involves a sidechain acceptor bond with Arg 207 and Arg 161, while the second bond are characterized by an arene-H interaction with Thr 118 highlighting the importance of these interactions for the inhibition of Anx5. The binding energies of these azaflavanones were found to be in the range of -4 to -5 kcal/mol, indicating their potential to modulate the anti-inflammatory properties of Anx5. These findings suggest that azaflavanones has the potential to modulate the activity of Annexin A5, thereby exerting anti-inflammatory effects.

4. Conclusions

In conclusion, the molecular docking study provides a strong basis for the potential anti-inflammatory properties of azaflavanone. However, further experimental validation, such as in vitro and in vivo studies, is necessary to confirm the results and determine the therapeutic potential of azaflavanone as a novel anti-inflammatory agent.

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