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MOLECULAR DOCKING STUDIES OF OZENOXACIN

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Abstract –

In recent years, research aimed at predicting the binding of small compounds to their target proteins has become more dependent on the use of bioinformatics techniques, such as molecular docking. With the integration of several commonly used pieces of software in computational chemistry, Docking Server provides a web-based, user-friendly interface that handles all facets of molecular docking, from ligand and protein setup to results presenting. While Docking Server's user-friendly interface makes docking calculations and results evaluation possible for researchers from all areas of biochemistry, it also gives more experienced users full control over setting particular parameters for ligand and protein setup and docking calculations. The programme can be used for high throughput docking of ligand libraries to target proteins as well as for the study and docking of single ligands.. In a molecular docking study, the inhibitory potential of the Ozenoxacin was evaluated against the Streptococcus pyogenes

Key Words: **Molecular docking**, ozenoxacin**,**

1. INTRODUCTION

A quinolone antibacterial medication is ozenoxacin. Additionally, ozenoxacin, like the majority of quinolones, primarily carries out its mechanism of action by entering bacterial cells and acting to inhibit the bacterial DNA replication enzymes. Topoisomerase IV and The main mechanism of ozenoxacin action is to inhibit DNA gyrase A and topoisomeraseIV, which are necessary for bacterial DNA replication processes like supercoiling, supercoil relaxation, chromosomal condensation, chromosomal decatenation , and more. This drug has been shown to be bactericidal against S. aureus and S. pyogenes organisms Label.A brand-new non-fluorinated quinolone is ozenoxacin. As of May 2019, 12 nations with in the European Union (EU) had approved the topical use of ozenoxacin 1% cream for the treatment of non-bullous impetigo in patients 6 months of age and older[1]. Ozenoxacin[2,3] 1%cream is approved for the topical treatment of bullous impetigo in the USA and Canada, despite the fact that relatively few patients under the age of six months and/or with bullous impetigo were involved in pivotal phase III clinical trials of the drug . Ozenoxacin1% cream is approved for use in the USA and Canada for the topical treatment of non-bullous and bullous impetigo in patients 2 months of age and older, despite the fact that relatively few infants younger than 6 months of age and/or those with bullous impetigo were enrolled in pivotal phase III clinical trials of the drug. Ozenoxacin has significant antibiotic action against streptococci and staphylococci, the two main bacteria responsible for impetigo[4], according to comparative in vitro studies. Additionally, ozenoxacin exhibits a wide spectrum of efficacy against S. aureus strains that are resistant to methicillin, mupirocin, and ciprofloxacin. The main mechanism of ozenoxacin action is to inhibit DNA gyrase A and topoisomeraseIV, which are necessary for bacterial DNA replication processes like supercoiling, supercoil relaxation, chromosomal condensation, chromosomal decatenation, and more. This drug has been shown to be bactericidal against S. aureus[5,6] and S. pyogenes organisms Label. The dual inhibitory activity of ozenoxacin against DNA gyrase and topoisomerase IV, two enzymes involved in bacterial replication, guards against the emergence of resistance,and the lack of a fluorine atom in its molecular structure confers a safer profile than that of fluorinated quinolones, including the absence of quinolone-induced chondrotoxicity.Ozenoxacin is barely absorbed when applied topically, and phase I investigations revealed great skin tolerability . All together, these characteristics imply that ozenoxacin would be a good choice for empirical therapy of localised impetigo. Ozenoxacin 1% cream (used twice daily for 5 days) has been shown in clinical tests to be efficient and well tolerated in treating impetigo in both children and adults . We retrieved and analysed data for children and adolescents who had participated in ozenoxacin clinical trials and were between the ages of 6 months and 18 years in order to better understand the profile of the drug specifically in the paediatric population.

2. MATERIALS AND METHODS

Molecular docking[7] is a technique for computationally determining the architecture of compounds made up of two or more different molecules. Predicting intended three-dimensional structures is the goal of docking investigations. Only appropriate incentive structures are generated by docking in and of themselves. The structures that are most likely to exist in nature are sorted using scoring functions from among these possibilities. In recent years, research aimed at predicting the binding of small compounds to their target proteins has become more dependent on the use of bioinformatics techniques, such as molecular docking. With the integration of several commonly used pieces of software in computational chemistry, Docking Server provides a web-based, user-friendly interface that handles all facets of molecular docking, from ligand and protein setup to results presenting. While Docking Server's user-friendly interface makes docking calculations and results evaluation possible for researchers from all areas of biochemistry, it also gives more experienced users full control over setting particular

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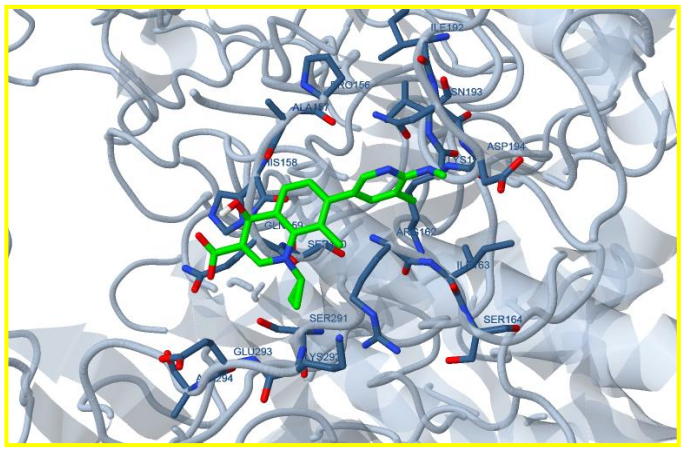
ligand and protein setup and docking calculations. The programme can be used for high throughput docking of ligand libraries to target proteins as well as for the study and docking of single ligands.

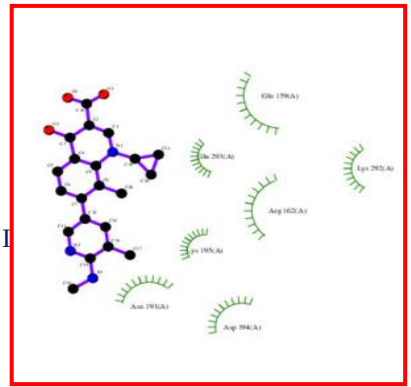
3. MOLECULAR DOCKING OF OZENOXACIN

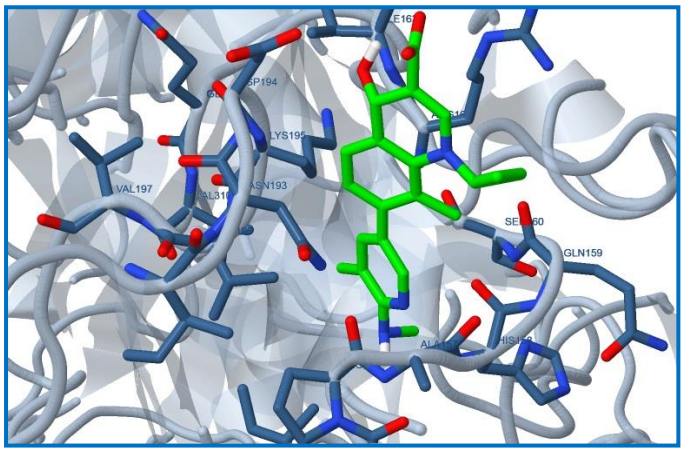
Impetigo is a bacterial skin infection mostly brought on by S aureus and S pyogenes, with highly contagious sores that can spread quickly through contact. To minimise outbreaks and possibly avoid problems, rapid, efficient treatment is essential for reducing the transmission of illness and the spread of pathogens. Ozenoxacin is a significant potential therapy option with an enlarged spectrum against bacterial infections, particularly those resistant to mupirocin, ciprofloxacin, and methicillin (including MRSA), raising worries about the prevalence of antibiotic resistance. The topical antibiotic ozenoxacin, which has very little skin absorption, has the potential to significantly enhance the treatment of impetigo, as well as slow the spread of pathogens and infection. Clinical medicine benefits from ozenoxacin's capacity to destroy both drug-resistant and drug-susceptible organisms. We have performed a molecular modeling study to investigate the possible binding conformation for the ozenoxacin by inhibiting Streptococcus pyogenes enzyme binding site which may be give an idea about mechanism of action. The crystal structure (PDB code: 5XXZ,5XYA,5XYR) was downloaded directly from the Protein Data Bank (www.rcsb.org). All the computations were performed using the Online docking server[8] . The 3D and 2D interaction between the protein and ligands were SHOWN in Fig . In silico studies revealed ozenoxacin showed good



binding energy toward the target protein ranging from −7.85 to −5.34 kJ mol^{-1}.

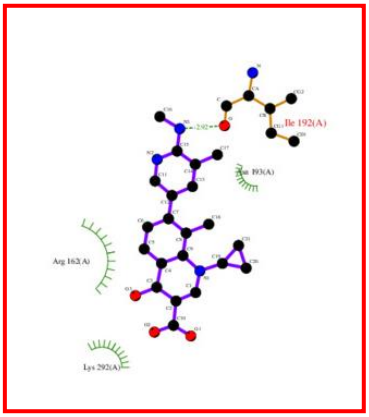
(A)





(B)

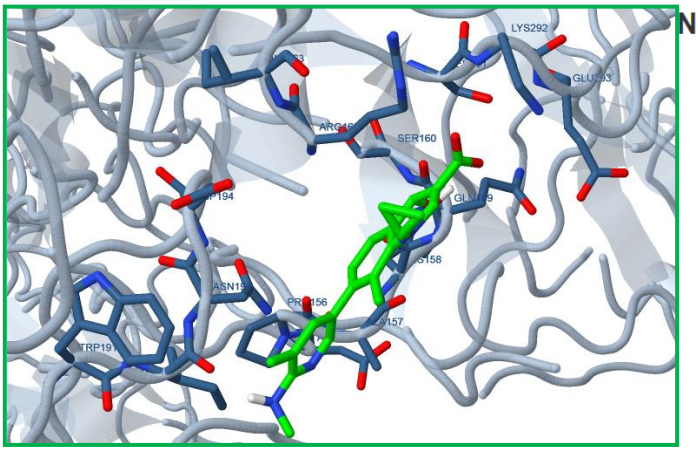
Fig -1: (A) 3D and (B) 2D interaction of 5XXZ with ozenoxacin



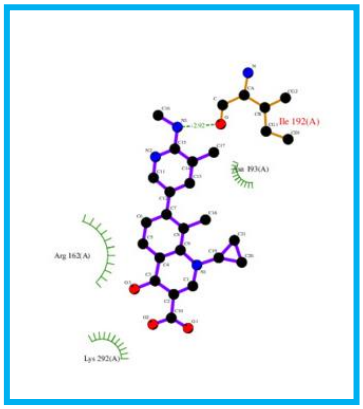
(A)

(B)

Fig -2: (A) 3D and (B) 2D interaction of 5XYA with ozenoxacin



(A)



(B)

Fig -2: (A) 3D and (B) 2D interaction of 5XYR with ozenoxacin

Table -1:

LIGAND	PROTEIN	BINDING ENERGY
ozenoxacin	**5XXZ**	-5.99 kcal/mol
ozenoxacin	**5XYA**	-7.85 kcal/mol
ozenoxacin	**5XYR**	-5.34 kcal/mol

3. CONCLUSIONS

The molecular docking study of ozenoxacin was carried out and the results of such studies were reported. *In silico* studies revealed that all the target protein have relatively lesser binding energy and may be considered as a good inhibitor of Streptococcus pyogenes.

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BIOGRAPHIES (Optional not mandatory)

1'st Author Photo

Description about the author1 (in 5-6 lines)

Dr.C.M.MAHALAKSHMI working as an Assistant professor and she has known the knowledge of synthetic organic chemistry ,DFT and Molecular docking studies.