Docking Analysis of Omeprazole Against *Neisseria gonorrhoeae*

This study was performed to investigate whether Omeprazole can interact with important membrane-associated resistance proteins of *Neisseria gonorrhoeae*. The results were compared with Ceftriaxone, which is a clinically used antibiotic against gonorrhea.

Two important proteins were selected for the docking study:

- PorB membrane porin (PDB ID: 4AUI)
- MtrD efflux pump (PDB ID: 4MT1)

Docking was carried out using AutoDock Vina after receptor cleaning and ligand preparation.

Docking Against PorB Membrane Porin (4AUI)

The PorB protein is a membrane porin channel involved in molecular transport across the bacterial outer membrane. Docking was focused on the lumen region of the porin channel.

Omeprazole Results

Omeprazole showed a best binding affinity of:

$$-5.448 \text{ kcal/mol}$$

This indicates a moderate interaction with the pore region of the membrane channel.

Ceftriaxone Results

Ceftriaxone showed a stronger binding affinity of:

$$-6.339 \text{ kcal/mol}$$

This stronger interaction is expected because ceftriaxone is an active antibacterial drug against *N. gonorrhoeae*.

Interpretation

The docking results suggest that omeprazole can interact with the PorB channel region, but the interaction is weaker than ceftriaxone. The findings support possible transient membrane-associated interaction rather than strong channel inhibition or confirmed transport through the porin.

Supporting docking logs:

Docking Against MtrD Efflux Pump (4MT1)

The MtrD protein is a multidrug efflux transporter associated with antimicrobial resistance in *N. gonorrhoeae*. Docking was focused on the periplasmic substrate-binding cleft of the transporter.

Omeprazole Results

Omeprazole demonstrated a best binding affinity of:

$$\mathbf{-5.770 \text{ kcal/mol}}$$

This indicates moderate interaction with the transporter-associated region.

Ceftriaxone Results

Ceftriaxone showed a stronger affinity of:

$$\mathbf{-6.805\ kcal/mol}$$

This suggests stronger interaction with the substrate-associated cavity of the efflux pump.

Interpretation

The docking results indicate that omeprazole can interact with the MtrD transporter region, although less strongly than ceftriaxone. The interaction may suggest weak-to-moderate transporter-associated behavior, but the results are insufficient to prove direct efflux inhibition.

Overall Comparison

The computational analysis showed that ceftriaxone consistently produced stronger docking affinities against both the PorB membrane channel and the MtrD efflux transporter. This was biologically expected because ceftriaxone is an established antibacterial drug.

Omeprazole demonstrated moderate interaction with both proteins. Although the docking scores were weaker than ceftriaxone, the results still suggest that omeprazole may possess membrane-associated or transporter-associated interaction potential.

The study does not prove that omeprazole directly kills *N. gonorrhoeae*, blocks membrane channels, or inhibits efflux transporters. However, the findings support the possibility that omeprazole may influence membrane-associated resistance mechanisms indirectly.

Conclusion

This docking study demonstrated that Omeprazole interacts moderately with both the PorB membrane porin and the MtrD efflux pump of *Neisseria gonorrhoeae*.

Compared with Ceftriaxone, omeprazole showed weaker but reproducible interactions under identical docking conditions.

The results provide preliminary computational evidence supporting possible membrane-associated and transporter-associated interaction behavior of omeprazole. Further studies such as molecular dynamics simulations, efflux inhibition assays, and antibiotic synergy experiments are required to determine whether these interactions could contribute to antimicrobial resistance modulation.

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