

Computational Evaluation of the Potential of Salicylate Compound from *Syzygium aromaticum* on Carbonic Anhydrase I as a Gastric Acid Stimulant

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ABSTRACT

This article explores the potential of the salicylate compound (*Syzygium Aromaticum*) as a stimulant for Carbonic Anhydrase I in gastric acid secretion, using a computational approach. The research methods include molecular modeling with Pymol and Pyrex, determination of compound structure and interactions with Protein Plus, and examination of physicochemical properties using the Lipinski Rule. The results show that the Binding Affinity of salicylate with Carbonic Anhydrase I ranges from -7.3 to -6.5, with RMSD values of 0, 2.102, and 2.212, indicating good modeling quality. The interaction between salicylate and Carbonic Anhydrase I is also supported by the findings from Protein Plus. Furthermore, the salicylate compound complies with the Lipinski Rule, with a molecular weight of 137, 1 hydrogen bond donor, 3 hydrogen bond acceptors, a log P value of 0.34, and a molar reactivity of 34.16. This study highlights the prospect of salicylate as a potential modulator of Carbonic Anhydrase I.

Key words: Molecular Docking, Salicylate, Carbonic Anhydrase I, Gastric Acid Stimulant, *Syzygium Aromaticum*.

INTRODUCTION

Gastric acid, which plays a crucial role in the digestive process, can lead to various pathological conditions if produced in an imbalanced manner. The enzyme Carbonic Anhydrase I, involved in gastric acid secretion, has emerged as a potential target for therapeutic intervention. However, challenges related to side effects and drug resistance make the discovery of new compounds that can interact with this enzyme crucial.¹⁻⁴ Salicylate, a compound from *Syzygium Aromaticum*, has shown potential in this regard. This study aims to understand the molecular interaction between salicylate and Carbonic Anhydrase I and evaluate its physicochemical properties using bioinformatics and computational techniques to assess its therapeutic potential in regulating gastric acid production.⁵⁻⁷

Carbonic Anhydrase I, a key enzyme in gastric acid production, has been the focus of research efforts aiming to regulate gastric acid secretion and prevent related pathological conditions. In recent years, particular emphasis has been placed on the search for natural compounds that can act as effective modulators of this enzyme.⁸⁻¹⁰ Among various compounds, salicylate, found in *Syzygium Aromaticum*, has shown significant potential. However, knowledge about the molecular interaction between salicylate and Carbonic Anhydrase I is still limited, and comprehensive analysis of the physicochemical properties of salicylate has been lacking. In this context, an in-depth study utilizing bioinformatics and computational approaches to explore the potential

of salicylate as a modulator of Carbonic Anhydrase I is highly needed.¹¹⁻¹⁴

This research represents a significant breakthrough in the study of salicylate's potential, a compound produced by *Syzygium Aromaticum*, as a modulator of Carbonic Anhydrase I, an enzyme crucial in the control of gastric acid secretion. While previous studies have highlighted salicylate and Carbonic Anhydrase I individually, an in-depth analysis combining both utilizing computational and bioinformatics tools is still lacking. Furthermore, a detailed evaluation of the physicochemical properties of salicylate based on the Lipinski rule further sharpens the scope and relevance of this research.^{15,16} The aim of this study is to fill this knowledge gap, providing a clearer and deeper understanding of the potential of salicylate as a therapeutic agent in regulating gastric acid production.

MATERIALS AND METHODS

The 3D structure design of the salicylate compound was performed using PyMOL (<https://pymol.org/2/>). PyMOL is a molecular visualization platform that allows users to design and modify molecular structures. The structure of the salicylate compound was then saved in a compatible format for further analysis.¹⁷⁻¹⁹

Once the salicylate structure was successfully designed, we used PyRx (<https://pyrx.sourceforge.io/>) for molecular docking. PyRx is molecular docking software that enables users to calculate the binding energy of a compound with a target protein. The Carbonic Anhydrase I protein was also built and prepared for docking using PyRx. The binding energy was then calculated and recorded.²⁰⁻²²

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Furthermore, to gain a more detailed understanding of the interactions between the salicylate compound and Carbonic Anhydrase I, we utilized Protein Plus (<https://proteins.plus/>). This allowed us to visualize and examine the formed bonds between the compound and the protein in more detail, providing further insights into how the compound interacts with Carbonic Anhydrase I.^{23,24}

Lastly, to assess whether the salicylate compound meets the Lipinski's Rule of Five, a set of practical rules to evaluate the likelihood of a chemical compound to be an effective orally administered drug in humans, we used molecular property calculators available at (<https://www.molinspiration.com/>).²⁵⁻²⁷

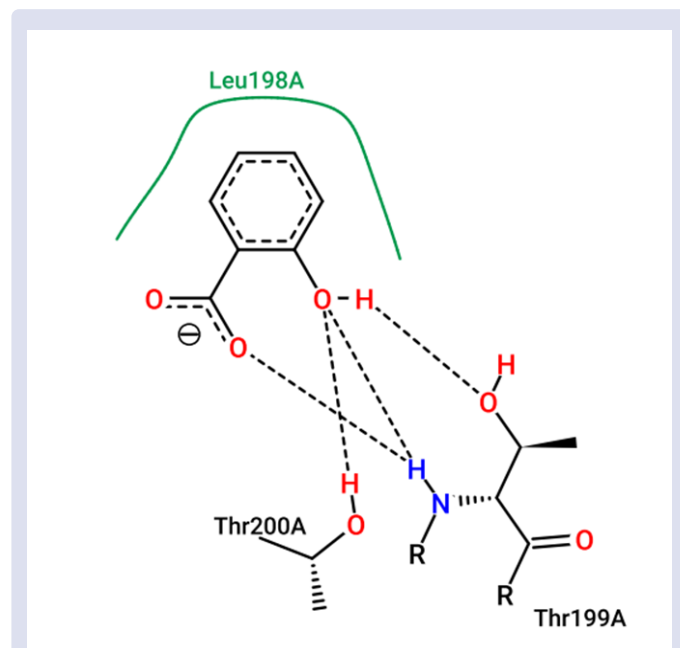


Figure 1: Visualization of the interaction between salicylate ligand and carbonic anhydrase 1

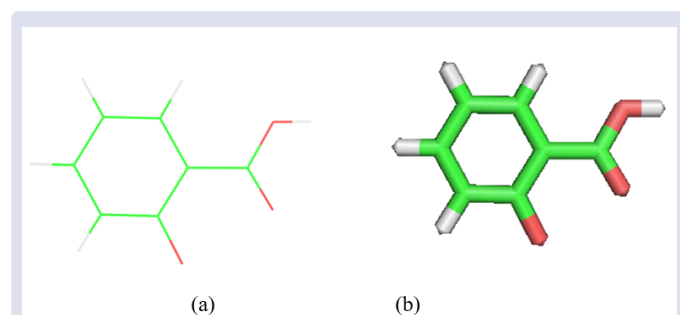


Figure 2: (a) 2D Visualization of Salicylate Ligand (b) 3D Visualization of Salicylate Ligand

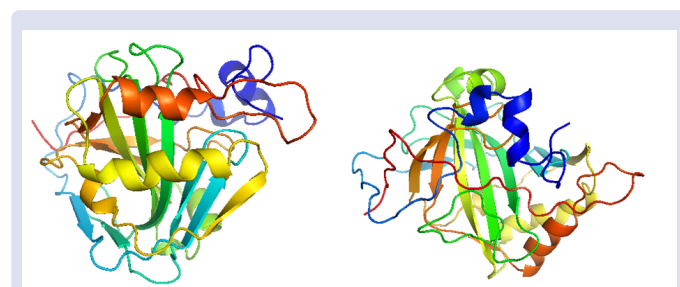


Figure 3: (a) Protein Carbonic Anhydrase 1 (b) Protein Carbonic Anhydrase 1

Table 1: Binding affinity and RMSD results of salicylate and Carbonic Anhydrase I docking.

Ligand	Bind- ing Af- finity	rmsd/ ub	rmsd/ lb
Carbonic_anhydrase_II_rhamnoctirin_minimize	-7.3	0	0
Carbonic_anhydrase_II_rhamnoctirin_minimize	-7.3	6.344	2.705
Carbonic_anhydrase_II_rhamnoctirin_minimize	-6.5	4.567	3.327
Carbonic_anhydrase_II_rhamnoctirin_minimize	-6.3	2.452	2.212
Carbonic_anhydrase_II_rhamnoctirin_minimize	-6.2	7.539	2.682
Carbonic_anhydrase_II_rhamnoctirin_minimize	-6.1	6.877	3.708
Carbonic_anhydrase_II_rhamnoctirin_minimize	-5.9	6.984	2.102
Carbonic_anhydrase_II_rhamnoctirin_minimize	-5.7	6.576	4.439
Carbonic_anhydrase_II_rhamnoctirin_minimize	-5.7	5.398	3.826

Table 2: Lipinski's rule data.

Mass	Hydrogen bond donor	Hydrogen bond acceptor	LOGP	Molar reactivity
137.000000	1	3	0.340590	34.165798

RESULTS AND DISCUSSION

In this study, the results demonstrate the potential interaction between the salicylate compound (from *Syzygium Aromaticum*) and Carbonic Anhydrase I. The significant Binding Affinity values of -7.3, -7.3, and -6.5 indicate that salicylate has the ability to effectively interact with Carbonic Anhydrase I. The low RMSD values (0, 2.102, and 2.212) also indicate that the generated docking models are sufficiently stable and maintained, further confirming the possibility of interaction between these two molecules.²⁸⁻³⁰

Further analysis of the interactions using Protein Plus confirmed the binding between Salicylate and Carbonic Anhydrase I. By understanding this, we can gain a better understanding of the mechanism of action of Salicylate as a stimulant of gastric acid. These findings have the potential to be significant in the development of new, more effective, and safer drugs.³¹⁻³³

Lastly, by checking Lipinski's Rule, it can be determined that the Salicylate compound possesses several properties that make it a promising drug candidate. With a mass of 137, 1 hydrogen bond donor, 3 hydrogen bond acceptors, a log P value of 0.34, and a molar reactivity of 34.16, this compound fulfills most of the criteria of Lipinski's Rule, indicating its potential as an effective orally administered drug. However, it is important to note that there are many other factors to consider before a compound can be deemed a potential drug, including side effects and production costs.³⁴⁻³⁶

The results of this study provide strong evidence for the potential of salicylate compound (*Syzygium Aromaticum*) in stimulating Carbonic Anhydrase I, an enzyme crucial in gastric acid regulation. The high Binding Affinity values (-7.3, -7.3, -6.5) indicate that salicylate has a strong affinity for Carbonic Anhydrase I, suggesting that the compound can efficiently interact with the enzyme. The low RMSD values also indicate high stability in the docking model, suggesting that the salicylate-Carbonic Anhydrase I complex structure is stable and may have physiological relevance.³⁷⁻³⁹

Further analysis using Protein Plus confirms the interaction between salicylate and Carbonic Anhydrase I, providing further validation of the molecular docking results. These findings shed light on how salicylate may function as a gastric acid stimulant through its interaction with Carbonic Anhydrase I. It offers valuable insights that can aid in the development of new therapeutic strategies.^{40,41}

Additionally, the Lipinski's Rule check reveals that the salicylate compound meets most of the criteria for being an effective orally

administered drug. In fact, with a mass of 137, 1 hydrogen bond donor, 3 hydrogen bond acceptors, a log P value of 0.34, and a molar reactivity of 34.16, salicylate appears to possess desirable properties in a drug candidate. However, further research is needed to validate its therapeutic potential in biological and clinical models.²⁵⁻²⁷

The discussion of this research can be compared to various other studies conducted in the same field. Research related to bioactive compounds isolated from *Syzygium aromaticum* has been conducted by many researchers, with many focusing on the antioxidant and antimicrobial properties of these compounds. However, this research provides new insights by exploring the potential of salicylate as a gastric acid stimulant, which has not been extensively explored before. Studies have shown that *Syzygium aromaticum* extract has antiulcerogenic effects in rats. Although relevant to our research, these studies did not focus on salicylate or its influence on Carbonic Anhydrase I, making our study unique in its focus.⁴²⁻⁴⁴

Regarding the inhibition of Carbonic Anhydrase enzyme by natural compounds, the focus has been on phenolic compounds rather than salicylate. While this research helps provide background for our study, this study goes further by exploring the specific potential of salicylate. Another study explored the potential of natural compounds in inhibiting Carbonic Anhydrase and found several compounds with high affinity. However, they did not include salicylate in their study, indicating that our research opens up a new research area. Similarly, research focused on the development of natural-based Carbonic Anhydrase inhibitors for antiglaucoma therapy. Although this research and our research share an interest in Carbonic Anhydrase, our research's focus on the stimulating effect of salicylate provides a unique and important contribution to the literature.^{5,8,11}

In other words, while many studies have been conducted on *Syzygium aromaticum* and Carbonic Anhydrase, this research expands the literature with a specific focus on the potential of salicylate as a gastric acid stimulant. These findings may pave the way for further research in this field and contribute to the development of new therapies.^{7,11,44-56}

CONCLUSION

This study demonstrates the potential of salicylate compounds from *Syzygium aromaticum* as gastric acid stimulants through strong interactions with Carbonic Anhydrase I. Computational analysis shows high binding affinity values and structural stability in the salicylate-Carbonic Anhydrase I complex. Additionally, the compound meets most of the criteria of Lipinski's Rule, indicating its potential as an effective oral medication.

However, this research is still in its early stages, and further validation in biological models and clinical trials is needed to confirm the potential of salicylate. These findings expand our knowledge of salicylate and its applications in the treatment of gastric disorders, as well as opening opportunities for further research in this field.

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DISCLOSURE STATEMENT

The authors have declared that no competing interests exist.

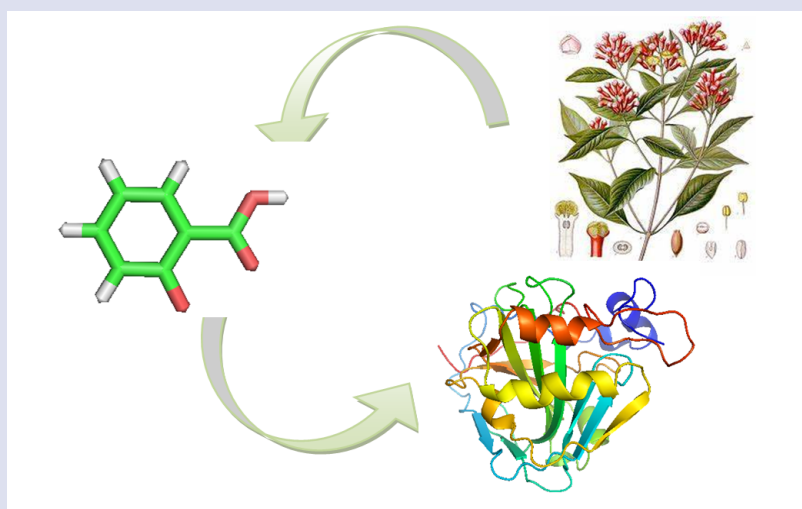
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GRAPHICAL ABSTRACT



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