GC-MS Profiling and In Silico Evaluation of the Analgesic, Anti-Inflammatory, Antioxidant, Antidiarrheal, and Hypoglycemic Potential of *Ixora cuneifolia* Leaf Extract

By

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A project submitted to the School of Pharmacy in partial fulfillment of the requirements of the degree of Bachelor of Pharmacy (Hons.)

School of Pharmacy

BRAC University

May 2026

Declaration

It is hereby declared that

1. The project submitted is our own original work while completing degree at BRAC University.
2. The project does not contain material previously published or written by a third party, except where this is appropriately cited through full and accurate references.
3. The project does not contain material which has been accepted, or submitted, for any other degree or diploma at a university or other institution.
4. We have acknowledged all main sources of help.

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Approval

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Ethics Statement

This study did not include any harm to humans or animals.

Abstract

Medicinal plants are an important source of bioactive compounds and play a significant role in the discovery of new therapeutic agents. *Ixora cuneifolia*, a member of the Rubiaceae family, is traditionally used for the treatment of various diseases including fever, pain, inflammation, and gastrointestinal disorders. In this study, the leaf of the plant *I. cuneifolia* were tested to explore its antioxidant, anti-inflammatory, anti-diabetes, anti-diarrheal, and analgesic activity using in silico approaches. Gas chromatography–mass spectrometry (GC–MS) analysis was performed to identify the chemical compounds present in the plant extract. Several bioactive phytochemicals were detected in the extract, indicating the presence of compounds that may contribute to its biological activities. To further understand the mechanism of action of these compounds, molecular docking analysis was conducted against selected target proteins. The docking results revealed that several identified compounds exhibited favorable binding affinities with the selected receptors through hydrogen bonding and hydrophobic interactions, suggesting strong ligand–protein interactions within the active sites of the target proteins. Among the detected compounds, certain molecules demonstrated particularly strong binding scores, indicating their potential as promising therapeutic candidates. The results suggested that several compounds possess acceptable pharmacokinetic characteristics and comply with standard drug-likeness criteria. Overall, the findings of this study support the traditional medicinal use of *I. cuneifolia* and suggest that its phytochemical constituents may serve as potential candidates for the development of novel anti-inflammatory, analgesic, antioxidant, hypoglycemic drugs. Further experimental and clinical studies are recommended to validate these findings and explore the therapeutic potential of the identified compounds.

Key words: GC-MS, Phytochemicals, Molecular docking, In silico study, Drug activity

Dedication

We would like to dedicate this to our parents and our well-wishers. They inspire us to do it properly and never forget to appreciate us.

Acknowledgement

In the name of Allah, firstly, we want to express my gratitude to my supervisor, Asef Raj Sir, for believing in us and allowing us to work with him. We greatly benefited from his advice while working on this project. Secondly, we want to thank our parents, who always recognized our little steps and gave us the freedom to achieve something for ourselves. Finally, we want to express my gratitude to all of my supportive friends who had faith in me.

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Chapter 1: Introduction

1.1Background of the study

Medicinal plants have been a valuable source of therapeutic agents, contributing significantly to modern drug development studies. In low-income regions especially, natural medicines are considered affordable and culturally acceptable, while in modern drug discovery, natural products remain important due to their structural diversity and novelty (Jamal Hossain et al., 2025). Species of the genus *Ixora* (family Rubiaceae) are widely recognized in ethnomedicine for their diverse pharmacological activities, including antimicrobial, antioxidant, anti-inflammatory, and central nervous system (CNS)-related effects (Gupta & Singh, 2018; Nadkarni, 2007). Among them, *Ixora cuneifolia*, a relatively less studied member, has been traditionally used in various regions to manage ailments such as fever, pain, and infections (Kadir, Sayeed, & Shams, 2013). Phytochemical analyses of its leaves and roots reveal the presence of flavonoids, tannins, alkaloids, glycosides, and phenolic compounds, which are likely responsible for these medicinal properties (Harborne, 1998; Tiwari et al., 2011). The family Rubiaceae, sometimes known as the Madder family, includes the genus *Ixora*. It is one of the most researched plants nowadays and includes 500 kinds. In Asia and other parts of the world, the genus *Ixora* is widely distributed in tropical and subtropical climes. ethnic groups from several Asian regions. Over centuries, the genus *Ixora* has been recognized for its extensive phytochemistry and pharmacological significance. Various species and plant parts, including leaves, stems, roots, and flowers, have not only been valued for ornamental purposes but also used traditionally in Sudanese medicine and Ayurveda to treat a wide range of ailments. Reported traditional uses include anti-inflammatory, hepatoprotective, antidiarrheal, wound-healing, anti-asthmatic, anticancer, antioxidant, and antiviral properties. For instance, *Ixora coccinea* extracts have been employed in the management of diarrhea, fever, headache, skin diseases, eye troubles, wounds, boils, and ulcers, while *Ixora Javanica* extracts have been used for ulcers, sores, stomach-related problems, and as an intestinal antiseptic and astringent. Despite increasing research in recent decades, only a handful of species have been studied in detail, and comprehensive investigations across the genus remain limited (Nadeem et al., 2025a). At the same time, the global reliance on herbal medicines continues to grow. While synthetic drugs are effective, they are often criticized for adverse side effects, driving interest toward plant-based alternatives that provide diverse bioactive compounds, are more ecofriendly,

and are less likely to cause harmful reactions. Historically, around 80,000 medicinal plants have been used in Indian traditional medicine, and nearly 80% of the world's population still relies on plant-based remedies. This study was designed to investigate the pharmacological activities of the methanolic extract of *I. cuneifolia* leaves and roots using in silico methods. The experimental protocols included analgesic evaluation, carrageenan-induced anti-inflammatory assay, antidiabetic assessment, CNS depressant activity, antioxidant and thrombolytic analyses, as well as in silico docking studies to support the observed pharmacological effects. These process allow assessment of not only biological activity but also systemic interactions, safety profiles, and therapeutic relevance in whole organisms (Khan et al., 2025). The plant is called Musea in Bangladesh, and its leaves are used in traditional medicine to treat fever and stomachaches (Huq et al., 2017). On the other hand, the roots are used to treat metorrhagia and as an antidiarrheal and antiemetic. We looked into the antioxidant, thrombolytic, analgesic, anti-inflammatory, and anti-diarrheal properties of the methanol extract of *I. cuneifolia* leaf because, to the best of our knowledge, there are no published reports regarding the pharmacological activity of this plant to confirm its medicinal properties.

1.2 Taxonomic Classification and Botanical Description

The plant selected for this study is *I. cuneifolia*, which belongs to the family Rubiaceae. This plant is a member of the genus *Ixora*, a group of flowering plants that are widely distributed in tropical and subtropical regions. The detailed taxonomic classification of the plant is presented below:

Kingdom: Plantae
Phylum: Streptophyta
Class: Equisetopsida
Subclass: Magnoliidae
Order: Gentianales
Family: Rubiaceae
Genus: *Ixora*
Species*: Ixora cuneifolia*

This classification helps scientists identify the plant accurately and understand its relationship with other plant species (Murugan et al., 2021).

I. cuneifolia is a flowering plant that typically grows as a small shrub or bush. It is often found in tropical areas and is known for its attractive clusters of flowers. Plants in the genus *Ixora* are frequently grown as ornamental plants due to their bright flowers and shiny leaves.

The plant usually has simple, green, and smooth leaves that grow opposite each other on the stem. The leaves tend to be thick and slightly leathery, which helps the plant thrive in warm climates. The shape of the leaves in *I. cuneifolia* is somewhat wedge-shaped, which is reflected in the species name cuneifolia. The plant produces small tubular flowers that grow in dense clusters at the ends of the branches. These flowers often have bright colors and attract insects like butterflies and bees, which aid in pollination. Like many plants in the family Rubiaceae, the plant has floral structures that help botanists identify it. The stem of the plant is usually woody and branched, allowing it to grow as a compact shrub. The roots are fibrous, helping the plant absorb water and nutrients from the soil (Huq et al., 2017; Murugan et al., 2021).

Researchers were forced to look into the phytochemical makeup of the many species of the Ixora genus because of its widespread usage in traditional medicine. Numerous investigations on the Rubiaceae family's genus *Ixora* have shown a wide variety of phenolic chemicals. Flavonoids, tannins, aromatic acrid oils, poly-sterols, saponins, carbohydrates, fatty acids, peptides, and terpenoids are among them (Nadeem et al., 2025b).

1.3 Justification of the study:

Previous studies on *I. cuneifolia* have reported several pharmacological activities of its methanolic leaf extract, including antioxidant, thrombolytic, analgesic, anti-inflammatory, anti-diarrheal, anxiolytic, and hypoglycemic effects in animal models. These findings suggest that the plant possesses significant therapeutic potential.

However, although these biological activities have been experimentally evaluated, the molecular mechanisms and target interactions responsible for these effects have not yet been explored through in silico molecular docking studies. Therefore, the present research aims to investigate the potential bioactive compounds of *I. Cuneifolia* and evaluate their interactions with relevant target proteins through in silico molecular docking analysis.

This study particularly focuses on the docking analysis related to analgesic, antidiabetic, anti-inflammatory, antidiarrheal, antioxidant, and hypoglycemic activities, which have not previously been examined using computational approaches.

1.4- Importance of GC-MS in phytochemical characterization:

Gas Chromatography–Mass Spectrometry (GC–MS) is a powerful analytical technique widely used for the separation, identification, and quantification of volatile and semi-volatile compounds in complex mixtures. It combines the separation capability of gas chromatography with the identification strength of mass spectrometry, making it a highly reliable tool in phytochemical analysis, GC–MS plays a crucial role in identifying bioactive compounds present in plant extracts. Many important phytochemicals, such as essential oils, terpenes, phenolics, aldehydes, and fatty acids, are volatile or semi-volatile in nature and can be effectively analyzed using this technique. The compounds are first separated based on their volatility and interaction with the stationary phase and then identified through their unique mass fragmentation patterns, which act as molecular fingerprints (Ezeokonkwo & Kabir, 2026).

One of the major advantages of GC–MS is its ability to accurately identify compounds by comparing their mass spectra with standard reference libraries such as NIST and Wiley databases. This enables the detection and characterization of numerous phytochemicals within a single analytical run, even at very low concentrations. As a result, GC–MS is extensively used in the identification of antimicrobial compounds from plant sources, contributing significantly to natural product research and drug discovery (Ezeokonkwo & Kabir, 2026). Ezeokonkwo and Kabir (2026) also argued that GC–MS provides high sensitivity, specificity, and reproducibility, making it an essential tool for comprehensive chemical profiling of plant metabolites.

It allows researchers to determine the composition of complex plant extracts and to associate specific compounds with biological activities such as antibacterial and antifungal effects. Despite this limitation, GC–MS remains one of the most widely used and effective techniques for phytochemical characterization in pharmaceutical and biomedical research (Ezeokonkwo & Kabir, 2026)

1.5 Importance of in silico in drug discovery:

In silico methods are typically utilized in conjunction with in vitro data gathering to develop and evaluate the model. Such models have been widely used in the identification and optimization of new compounds with affinity to a target, for the understanding of absorption, distribution, metabolism, excretion, and toxicity characteristics, and physicochemical study. For many years, in silico methods have been utilized in research to obtain more exact results by employing software to acquire, analyze, and integrate biological and medical data from a variety of sources. Furthermore, this data is utilized to create computational models or simulations that can be used to generate predictions, propose hypotheses, and eventually lead to discoveries or breakthroughs in medicine and therapeutics (Ekins et al., 2007).

The GC-MS analysis would provide us with a detailed profile of the chemical constituents in the form of a chromatogram and a table of identified compounds. Using molecular docking, we may evaluate the characteristics of the interaction between chemical molecules and biological targets (Paggi et al., 2024).

This study aims to comprehensively analyze the chemical constituents of *I. cuniferolia* using gas chromatography–mass spectrometry (GC–MS) and to evaluate the pharmacological properties of its methanolic extract and plant fractions. Furthermore, molecular docking was performed to assess the binding affinity of the active compounds, while in silico ADME (absorption, distribution, metabolism, and excretion) analyses were conducted to determine their pharmacokinetic and drug-like characteristics. In addition, both in vitro and in vivo approaches were employed to validate the biological activities. Collectively, this research seeks to provide valuable insights into the therapeutic potential of *I. cuniferolia* as a promising source of natural anti-inflammatory, analgesic, anti-oxidant, hypoglycemic and anti-diarrheal agents.

1.6 Research gap:

Existing studies on *I. cuneifolia* are limited and have primarily focused on its analgesic and anti-inflammatory activity. However, there is a lack of research exploring its phytochemical composition and other potential biological activities.

1.7 Aims and objectives of this study:

This study is guided by a set of clearly defined aims and objectives that establish its purpose and research focus. The aims and objectives are -

- To identify and characterize bioactive phytochemicals present in the plant's leaf extract.
- To predict the Analgesic, Anti-Inflammatory, Antioxidant, Antidiarrheal, and Hypoglycemic potential of the leaf extract by molecular docking.

Chapter 2. Plant Collection & Molecular Docking Study

2.1 Plant collection and authentication:

For this study, leaves of *I. cuneifolia* plants were used. The plants were collected from Chittagong hills, in Bangladesh. The experts from the Jahangirnagar University Herbarium (JUH), Savar, Dhaka identified the dried leaf sample. The leaves were separated from the plants, dried and crushed into powder.

2.2 Extract preparation:

After cleaning, the leaves were air-dried under sunlight for seven days in a semi-sheltered area to prepare them for further processing. The dried leaves were then ground into a coarse powder using a high-capacity grinding machine. Approximately 250 g of the powdered material was soaked in methanol in a clean round-bottom flask. The mixture was sealed with foil and kept for 15 days, with occasional shaking and stirring to facilitate extraction. Then the solvent from the extract was removed using a rotary evaporator (RE-52A) at 40°C at 7 kPa. The resulting concentrated extract was then collected and stored in a refrigerator to allow further drying until a stable residue was obtained.

2.3 Gas Chromatography and Mass Chromatography:

5 mg sample was taken in a small glass vial and sent to Bangladesh Council of Scientific and Industrial Research (BCSIR), Dhaka, Bangladesh. There, the sample was dissolved in methanol to perform GC-MS. The methanolic extract (ME) was analyzed using a Shimadzu GC–MS/MS TQ 8040 system equipped with electron impact ionization. Compound separation was carried out using a fused silica capillary column (Rxi-30 m, 0.25 mm internal diameter, 0.25 μm film thickness). The samples were injected at 250 °C, while the oven temperature was programmed to increase from 50 °C (held for 1 min) to 200 °C (held for 2 min), and finally to 300 °C (held for 7 min), with a total run time of 40 minutes. The analysis was performed under a pressure of 53.5 kPa with a flow rate of 11 mL/min. The ion source temperature was maintained at 230 °C, and the detector voltage was set at 0.5–0.6 kV. Data acquisition was carried out in Q3 scan mode over a mass range of m/z 25–600, with a solvent cut time of 3.5 minutes.

The detected compounds were tentatively identified by comparing their mass spectra with reference data available in the NIST and Wiley spectral libraries. The analyses were conducted in full scan (Q3 scan) mode, providing comprehensive spectral information. Further confirmation of the identified compounds is recommended through the use of authentic standards and calculation of retention indices to improve identification reliability in future studies (Nahar et al., 2025).

2.4 Molecular Docking Study:

The molecular docking study was performed to predict the binding affinity and interaction patterns of phytochemical compounds identified from *I. cuneifolia* through GC–MS analysis with selected target proteins associated with analgesic, anti-inflammatory, and antioxidant activities. Computational approaches were employed to evaluate the receptor–ligand interactions and to compare the binding efficiency of the identified compounds with standard drugs.

The three-dimensional (3D) structures of the ligands obtained from GC–MS analysis was prepared and optimized prior to docking. The in-silico docking study was carried out using PyRx for virtual screening and binding affinity calculation. Visualization and interaction analysis were performed using BIOVIA Discovery Studio 4.5. A semi-flexible docking approach was followed, where the ligands were treated as flexible and the receptor proteins were kept rigid, as commonly practiced in molecular docking studies (Munny et al., 2025).

2.4.1 Target Protein Selection

The potential pharmacological activities of the GC–MS identified compounds, including analgesic, anti-inflammatory, and antioxidant effects, were evaluated through molecular docking against selected target proteins. The choice of target proteins was based on their established roles in relevant biochemical and physiological pathways.

For antioxidant activity, Glutathione reductase (3GRS) was selected due to its critical role in maintaining cellular redox balance. For anti-inflammatory activity, Cyclooxygenase-2 (COX-2) (1CX2) was chosen as it is a key enzyme involved in prostaglandin synthesis. For analgesic activity, Mu-opioid receptor (5C1M) was selected because of its involvement in pain modulation. The 3D crystal structures of the selected proteins were retrieved from the RCSB Protein Data Bank in PDB format. The downloaded protein structures were then prepared using PyMOL 2.3 by removing water molecules, co-crystallized ligands, and other unwanted residues to obtain clean protein structures suitable for docking analysis (Munny et al., 2025).

To surround the active sites of receptors, grid boxes were set by resizing the center and dimension, ensuring optimal ligand binding to these receptors. Grid box coordinates for TNF-α (PDB ID: 2AZ5) was (Center: x= -10.2847, y= 68.2187, z= 19.3573) (Nahar et al., 2025), Urase oxidase (PDB ID: 1R4U) was (Center: x = 31.2863, y = 24.9787, z = 44.5625. Dimension: x = 20.6309, y = 28.8477, z = 27.7258) (Richi et al., 2026), Kappa opioid (PDB ID: 6VI4) was (Center: x = 54.1245, y = -50.4480, z = -16.2297. Dimension: x = 15.6710, y = 28.6679, z = 18.3413) (Richi et al., 2026), GLUT 3 (PDB ID: 4ZWB) was (Center: x = 106.7120, y = 10.9282, z = 61.9545. Dimension: x = 44.4237, y = 23.4932, z = 25.0000) (Munny et al., 2025), and hCOX-1 (PDB ID: 6Y3C) was (Center: x = -33.0157, y = -43.3105, z = 2.8379) (Miciaccia et al., 2021), COX-2 (PDB ID: 6COX) was (Center: x = 68.5740, y = 13.5052, z = 42.2488) (Nahar et al., 2025), μ-opioid (PDB ID: 5C1M) was (Center: x = -1.0089, y = 13.9161, z = -57.3965. Dimension: x = 19.3390, y = 19.0712, z = 21.3164) (Richi et al., 2026).

2.4.2 Protein Preparation

The three-dimensional arrangement of the target protein was acquired from the RCSB Protein Data Bank by using its specific PDB ID in Legacy PDB format. The downloaded structure was processed using PyMOL (version 3.1.8). All heteroatoms, such as co-crystallized ligands, unnecessary residues, and water molecules, were eliminated from the protein structure to create a clean receptor model. The refined protein structure was then saved in PDB format. Hydrogen atoms were later incorporated into the receptor using Swiss-PDB Viewer. Following the addition of hydrogen, energy minimization of the receptor structure was carried out to stabilize the protein conformation, and the minimized structure was saved for subsequent docking studies.

2.4.3 Ligand Preparation

The chemical structures of the selected ligands were obtained from the PubChem database. Each ligand was downloaded in 3D SDF format. The downloaded ligands were then imported into the docking platform for further processing, including energy minimization and format conversion prior to docking.

2.4.4 Molecular Docking

Molecular docking was performed using Pyrx, which integrates the Auto-Dock Vina engine.

The energy-minimized receptor structure was loaded into Pyrx and converted into a macromolecule (PDBQT format) using the Auto-Dock tool. The ligand molecules were imported through the Open Babel interface and individually minimized to obtain stable conformations. Subsequently, all ligands were converted into Auto-Dock ligand (PDBQT) format.

The docking process was carried out using the Vina Wizard. The receptor and selected ligands were chosen for docking, and the grid box was adjusted to cover the active binding site of the receptor. The grid dimensions defining the Vina search space were recorded for reproducibility. Docking simulations were then executed to predict the binding affinities between the receptor and ligands.

2.4.5 Docking Result Analysis

After completion of the docking simulation, the docking results were exported in CSV format. The binding affinities were analyzed using Microsoft Excel, and the top three ligands were selected based on their docking scores. Ligands showing the lowest (most negative) binding affinity values with acceptable mode, lower bound (LB), and upper bound (UB) values were considered the best-binding candidates.

2.4.6 Visualization of Docked Complex

The docked receptor–ligand complexes were visualized using PyMOL. The receptor structure and the corresponding ligand output files were loaded, and the docked complexes were exported in PDB format.

2.4.7 Interaction Analysis

The interaction analysis of the docked complexes was performed using BIOVIA Discovery Studio. The receptor–ligand complex file was opened, and visualization settings were adjusted for clarity. Hydrogen bond interactions and other non-bonded interactions were identified and analyzed. Amino acid residues involved in ligand binding were labeled using the three-letter amino acid code and residue ID.

Both 3D interaction images and 2D interaction diagrams were generated to illustrate the binding interactions between the receptor and the ligand. The interaction tables containing details such as

residue name, interaction type, distance, and interaction category were recorded for further interpretation.

Chapter 3. Results

3.1 Extract Yield Value:

Weight of raw material (leaf powder which was dissolved in methanol) = 250 gm
Weight of dried extract (root powder after extraction using rotary evaporator) = 6.445 gm
So, % Yield = (Weight of dried extract / Weight of raw material) × 100
= (6.445/ 250) × 100
= 2.578 %

3.2 GC MS:

GC-MS compounds identified from the methanolic extract of the methanolic leaf extract of *Ixora cuneifolia*.

Table 1: Phytochemicals detected in the methanolic leaf extract of *I. cuneifolia* by GC-MS.

Serial No	Component RT	Compound Name	Base Peak Area	Conc %
1	3.092996	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	5943987	0.5873
2	3.152045	1,1,1,2,2,3,3-Heptafluoro-3-(1,2,2,2-tetrafluoroethoxy)propane	3897042	0.3851
3	3.434593	Benzimidazol-5-amine, 1-(4-ethoxyphenyl)-	454480	0.0449
4	3.572132	Etilefrin, N-trifluoroacetyl, bis(trifluoroacetate)	555483.8	0.0549
5	3.65331	4-(2,7-Dihydroxy-6-methylheptan-2-yl)-3-hydroxybenzoic acid, 4Me derivative	38059760	3.7608

6	3.67001	3-Cyanopyrazolo[3,4-d]pyrimidine-4-one	144400.8	0.0143
7	4.316158	1,3-Benzenediol, 5-iodo-	38537.75	0.0038
8	4.543166	16-Methyl-octadecane-1,2-diol, isopropylidene derivative	624102.4	0.0617
9	5.009105	Heptane, 2,2,3,3,5,6,6-heptamethyl-	511428.8	0.0505
10	5.019037	2,2-Dimethyl-3-heptanone	2126225	0.2101
11	5.267538	phenol, 4-[[4-[(4-methoxyphenyl)amino]phenyl]amino]-	354649.2	0.035
12	5.326608	l-Leucine, N-allyloxycarbonyl-N-methyl-, pentadecyl ester	117629.8	0.0116
13	5.443986	1,3-Dioxolane, 2-hexyl-	7.21E+08	71.1951
14	5.517074	Valeric acid, 2-tetrahydrofurylmethyl ester	1021639	0.101
15	5.631504	1,1-Dimethylpropyl 2-ethylhexanoate	465017.6	0.0459
16	6.226881	1-Naphthamide, N-propyl-N-(2-ethylhexyl)-	144677.6	0.0143
17	6.720918	3-(4-Hydroxyphenyl)propionic acid, pentafluoropropionate	850766.9	0.0841
18	7.031217	4-Nitrobenzoic acid, 3-pentyl ester	524964	0.0519
19	7.061307	Benzofuran-5,6-diol-3-one, 2-benzylidene-	1787923	0.1767
20	7.079489	2,4-Diamino-8-hydroxy-5-propyl-5H-chromeno[2,3-b]pyridine-3-carbonitrile	1787923	0.1767
21	7.322055	4-Iodo-2H-pyrazole-3-carboxylic acid (4-nitro-benzylidene)-hydrazide	454878.2	0.0449
22	7.482508	2-Butanone, 1,1,1-trifluoro-	3785624	0.3741
23	7.491543	(1-Benzyl-1H-imidazol-2-yl) acetonitrile	346347	0.0342

24	7.497958	4,4'-(1,3-Dimethylbutylidene) bis phenol, bis(trifluoroacetate)	803306.2	0.0794
25	7.589897	Hexane, 3,3-dimethyl-	944204.5	0.0933
26	7.682988	2,4-Di-tert-butylphenol	49707251	4.9117
27	7.812395	1,5-Diphenyl-2H-1,2,4-triazoline-3-thione	1279641	0.1264
28	7.993802	Hexane, 3,3-dimethyl-	3774648	0.373
29	7.993923	c	3774648	0.373
30	8.114351	Acetamide, 2-thiophenyl-N-propyl-N-dodecyl-	658190.6	0.065
31	8.14908	Pyrrole, 2-methyl-5-phenyl-	201428.4	0.0199
32	8.343074	Phthalic acid, di(3,5-dimethylphenyl) ester	2604898	0.2574
33	8.346797	Phthalic acid, di(3-ethylphenyl) ester	2604898	0.2574
34	8.362255	L-Valine, N-(2-furoyl)-, undecyl ester	288077	0.0285
35	8.46901	Phthalic acid, di(3-ethylphenyl) ester	2171094	0.2145
36	8.544234	Hexadecanoic acid, (2-pentadecyl-1,3-dioxolan-4-yl)methyl ester	176483.4	0.0174
37	8.582317	Phthalic acid, di(3-ethylphenyl) ester	2657319	0.2626
38	8.591492	1,3-Isoindolinedione, 2-(4-methoxyphenyl)	2657319	0.2626
39	8.704953	Phthalic acid, di(3,5-dimethylphenyl) ester	310944.4	0.0307
40	8.764687	N-Cyclohexyl-1-(2-methoxyethyl)-2-methyl-5-oxopyrrolidine-2-carboxamide	547196.1	0.0541
41	9.104106	p-Octylacetophenone	375922.1	0.0371
42	9.104183	1-Methyl-2-allylthio-4(1H)-quinazolinone	375488	0.0371

43	9.295656	Pyrrole, 2-methyl-5-phenyl-	187590.6	0.0185
44	9.377067	R-1,2,3,4-Tetrahydroisoquinolin-1-phenylmethanol, 6,7-dimethoxy-	177426.9	0.0175
45	9.665341	7-Methoxy-2,3-diphenyl-4H-chromen-4-one	335791.3	0.0332
46	9.832076	Pyrrole, 2-methyl-5-phenyl-	431100.7	0.0426
47	9.853296	Pyrrole, 2-methyl-5-phenyl-	741323.2	0.0733
48	9.909985	Hexane, 3,3-dimethyl-	647731	0.064
49	10.37357	Decane, 3-ethyl-3-methyl-	677857.4	0.067
50	10.47074	Bis(dimethylamino)trifluorophosphorane	384735.7	0.038
51	11.13428	Cyclononasiloxane, octadecamethyl-	1.1E+08	10.9139
52	11.62398	(Phenylthio)acetic acid, heptyl ester	41947.8	0.0041
53	12.39045	Benzenepropanoic acid, 3,5-bis(1,1-dimethylethyl)-4-hydroxy-, methyl ester	1047160	0.1035
54	14.47924	Thiophen-2-methylamine, N-(2-fluorophenyl)-	89155.92	0.0088
55	14.76818	Methyl 3-nitro-cinnamate	219789.4	0.0217
56	15.83342	[3-(4-Methoxyphenyl)-4,5-dihydro-1,2-oxazol-5-yl]methanol	380531.7	0.0376
57	15.83346	Methyl 3-nitro-cinnamate	334822.5	0.0331
58	16.66183	3,4-Dihydropyridazin-6(1H)-one, 3-(2-butylpyrrol-5-yl)-	59660.65	0.0059
59	17.6401	Phthalic acid, octyl 2-propylpentyl ester (3D not present)	2215979	0.219
60	18.09651	1,2-Benzenediol, O-(2,6-difluorobenzoyl)-O'-(1-naphthoyl)-	364600.7	0.036
61	18.90177	1-Amino-2-methylnaphthalene	1115791	0.1103
62	19.20308	Ethane, iodo-	390953.6	0.0386

63	19.33013	2-[4-(Thiophene-2-carbonyl)-phenyl]-propionic acid, anthracen-9-ylmethyl ester	421739.8	0.0417
64	19.57781	Pyrrole, 2-methyl-5-phenyl-	595758.7	0.0589
65	19.68232	Pyrrole, 2-methyl-5-phenyl-	390343.6	0.0386
66	19.98856	Pyrrole, 2-methyl-5-phenyl-	1269107	0.1254
67	19.99906	Pyrrole, 2-methyl-5-phenyl-	1184480	0.117
68	20.12584	Quinoline, 2,7-dimethyl-	1020783	0.1009
69	20.22714	Terephthalic acid, 2,6-dimethoxyphenyl ethyl ester	326899.7	0.0323
70	20.40146	Bis(4-methylcyclohexyl) methylphosphonate	1614316	0.1595
71	20.64325	1-Methyl-5-(5-nitro-2-furyl)-3-(2-(5-nitro-2-furyl)vinyl)pyrazole	292043.7	0.0289
72	20.90264	2,5,8-Triphenyl benzotristriazole	231821.1	0.0229
73	20.98956	5-Acetyl-2-thioxo-dihydro-pyrimidine-4,6-dione	90580.35	0.009
74	21.06096	Cloroiodoacetylene	173014.7	0.0171
75	22.54305	Pyrrole, 2-methyl-5-phenyl-	2113910	0.2089
76	22.90386	4-Methoxybenzylamine, N,N-bis(pentafluoropropionyl)-	380858.2	0.0376
77	22.92364	L-Valine, N-(2-fluoro-3-trifluoromethylbenzoyl)-, undecyl ester	101497.5	0.01
78	23.14765	5-(4-Methoxy-phenyl)-[1,3,4]oxadiazole-2-thiol	1601125	0.1582
79	23.18189	Ethyl 4-methoxy-3,5-dimethylbenzoate	1662877	0.1643
80	23.22564	5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester	2219339	0.2193
81	23.55647	[1,1':4',1"-Terphenyl]-4-carbonitrile, 4"-pentyl-	614879.3	0.0608

82	24.04287	7-(2-Methylpropyl)amino-4-methylcoumarin	141552.7	0.014
83	24.34335	Cobalt, (.eta.5-2,4-cyclopentadien-1-yl)[[(2,3,4,5-.eta.)-2,4-cyclopentadien-1-yl]benzene]-	273006.7	0.027
84	24.40797	Succinic acid, 3,5-dinitrobenzyl 2-methylhex-3-yl ester	602432	0.0595
85	24.48895	Glutaric acid, 3-methylbut-2-yl pentafluorophenyl ester	1495025	0.1477
86	24.67042	Trimetozine	1512460	0.1494
87	24.68047	1,3-benzenedicarboxylic acid, 5-(dimethylamino)-	745109.4	0.0736
88	24.88483	10-Pentyl-10H-acridin-9-one	1160698	0.1147
89	24.96545	2-([(Dimethylamino)methylene]amino)-3-(3-chloro-4-ethyloxy-phenyl)propanoic acid, ethyl ester	804034.1	0.0794
90	25.23109	Benzene, 1-bromo-4-iodo-	151222.5	0.0149
91	25.36532	Benzenamine, 2,4-dibromo-	278760.9	0.0275
92	25.44887	Perhydrohistrionicotoxin, 2-depentyl-, methoxyformate(ester)	307369.7	0.0304
93	25.75922	Chroman-4-one, 2,3-dehydro-3-hydroxy-2-(4-dimethylaminophenyl)-	764065.5	0.0755
94	25.78872	5-Hydroxy-7-methoxy-2-methyl-3-phenyl-4-chromenone	282274	0.0279
95	26.04482	3(2H)-Benzofuranone, 6-methoxy-2-[(3-methoxyphenyl)methylene]-, (E)-	204457	0.0202
96	26.43984	Benzamide, 3-fluoro-4-trifluoromethyl-N-(2-phenylethyl)-N-dodecyl-	1651701	0.1632
97	26.45373	1,4-Benzenedicarboxylic acid, 2-nitro-, dimethyl ester	1570696	0.1552

98	26.54733	4-Butyl-N-(4-ethoxybenzylidene)aniline	922109.7	0.0911
99	26.77006	5-Amino-2-phenyl-1H-isoindole-1,3(2H)-dione	2133596	0.2108

3.3 Docking Score and Interaction type Table:

Table 2: Anti-inflammatory, Analgesic activites detected in the methanolic leaf extract of *I. cuneifolia* by molecular docking.

Docking score						
Serial No	**Compound Name**	**Pubchem ID**	**Anti-Inflammatory (2AZ5)**	**Analgesic (6COX)**	**Analgesic (6Y3C)**	**Analgesic (5CIM)**
1	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	5377779	-9.3	-8.9	-7.5	-6
2	1,1,1,2,2,3,3-Heptafluoro-3-(1,2,2,2-tetrafluoroethoxy)propane	94258	-6.4	-7.4	-6	-4.1
3	4-(2,7-Dihydroxy-6-methylheptan-2-yl)-3-hydroxybenzoic acid, 4Me derivative	23928030	-6.7	-7.1	-5.6	-5.3
4	2,2-Dimethyl-3-heptanone	140472	-5.1	-5.3	-4.6	-3.1
5	1,3-Dioxolane, 2-hexyl-	74360	-4.8	-5.4	-4.6	-3.7
6	2-Butanone, 1,1,1-trifluoro-	238288	-4.4	-4.9	-4.2	-3.5
7	2,4-Di-tert-butylphenol	7311	-6.4	-6.2	-5.3	-4.6
8	Hexane, 3,3-dimethyl-	11233	-4.4	-5	-4.1	-2.8

9	Nonane, 4,5-dimethyl-	86541	-5.3	-5.6	-4.5	-3.5
10	Phthalic acid, di(3,5-dimethylphenyl) ester	6425844	-9	-10.5	-7.5	-5.2
11	Phthalic acid, di(3-ethylphenyl) ester	91738752	-8.7	-9.2	-8.1	-6.7
12	1,3-Isoindolinedione, 2-(4-methoxyphenyl)	250687	-7	-7.8	-5.9	-5.4
13	5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester	91730924	-7.6	-8.9	-6.4	-5.5

Table 3: Hypoglycemic, Anti-oxidant, Anti-diarrheal activities detected in the methanolic leaf extract of *I. cuneifolia* by molecular docking.

Docking score table					
Serial No	**Compound Name**	**Pubchem ID**	**Hypoglycemic (4ZWB)**	**Anti-oxidant (1R4U)**	**Anti-diarrheal (6VI4)**
1	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	5377779	-9.8	-8.6	-8.2
2	1,1,1,2,2,3,3-Heptafluoro-3-(1,2,2,2-tetrafluoroethoxy)propane	94258	-7.1	-5.4	-5.7
3	4-(2,7-Dihydroxy-6-methylheptan-2-yl)-3-hydroxybenzoic acid, 4Me derivative	23928030	-6.7	-5.3	-5.6
4	2,2-Dimethyl-3-heptanone	140472	-5.6	-3.8	-4.6
5	1,3-Dioxolane, 2-hexyl-	74360	-5.5	-4.3	-4.5
6	2-Butanone, 1,1,1-trifluoro-	238288	-4.8	-3.9	-4
7	2,4-Di-tert-butylphenol	7311	-7.3	-6.1	-6.6
8	Hexane, 3,3-dimethyl-	11233	-4.8	-3.6	-4.4

9	Nonane, 4,5-dimethyl-	86541	-5.4	-4.1	-5.2
10	Phthalic acid, di(3,5-dimethylphenyl) ester	6425844	-10.5	-7.9	-7.6
11	Phthalic acid, di(3-ethylphenyl) ester	91738752	-10.2	-7.1	-7.2
12	1,3-Isoindolinedione, 2-(4-methoxyphenyl)	250687	-8.2	-6.6	-6.9
13	5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester	91730924	-9.5	-7.7	-7.7

Table 4: Interaction type of Analgesic and Anti-inflammatory activites detected in the methanolic leaf extract of *I. cuneifolia* by molecular docking with the selected receptor.

Serial No.	PDB ID	Compound Name	Binding affinity	Interaction Type	Amino Acid Residues
1	6COX	Phthalic acid, di(3,5-dimethylphenyl) ester	-10.5	Carbon Hydrogen Bond	HIS388(2)
				Pi–Sigma	LEU391(2)
				Pi–Pi Stacked	HIS386
				Pi–Pi T-shaped	HIS207
				Amide–Pi Stacked	ALA202, GLN203
				Alkyl	VAL295, LEU391, LEU408, VAL444

				Pi–Alkyl	PHE200, HIS207, PHE210, HIS386(2), HIS388, PHE395, ALA202, VAL295
2	6COX	Phthalic acid, di(3-ethylphenyl) este	-9.2	Conventional Hydrogen Bond	ARG120, TYR355
				Carbon Hydrogen Bond	SER353
				Pi–Cation	ARG120
				Pi–Sigma	LEU352, VAL523(2)
				Amide–Pi Stacked	GLY526, ALA527
				Alkyl	ALA527, VAL349, LEU531, LEU384
				Pi–Alkyl	TYR385, TRP387, VAL349(2), LEU359, ALA527, LEU531

3	6COX	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	-8.9	Conventional Hydrogen Bond	HIS388
				Pi-Sigma Hydrophobic Interaction	LEU294
				Pi-Sigma Hydrophobic Interaction	LEU391
				Pi-Sigma Hydrophobic Interaction	LEU391
				Alkyl Hydrophobic Interaction	VAL447
				Pi-Alkyl Interaction	HIS388
				Pi-Alkyl Interaction	LEU408
				Pi-Alkyl Interaction	VAL295
				Pi-Alkyl Interaction	LEU408
4	6Y3C	Phthalic acid, di(3-ethylphenyl) ester	-8.1	Pi–Sigma	LEU43, LEU40
				Alkyl	LEU40, LEU44(2), VAL69(2), LEU43

				Pi–Alkyl	VAL69(2), LEU44, LEU40, LEU43
5	6Y3C	Phthalic acid, di(3,5-dimethylphenyl) ester	-7.5	Pi–Sigma	LEU43, LEU44
				Alkyl	VAL69(2), LEU40(2), LEU44, LEU43(2), ILE47
				Pi–Alkyl	PHE72(2), LEU40(2), LEU44
6	6Y3C	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	-7.5	Pi–Sigma	LEU40, LEU43
				Alkyl	LEU44
				Pi–Alkyl	LEU40, LEU44, VAL69
7	5C1M	Phthalic acid, di(3-ethylphenyl) ester	-6.7	Conventional Hydrogen Bond	HIS597
				Pi–Sigma	TRP634
				Pi–Pi Stacked	HIS597
				Amide–Pi Stacked	HIS596, HIS597

				Alkyl	LEU604
				Pi–Alkyl	PHE595, TRP634(2)
8	5C1M	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	-6	Conventional Hydrogen Bond	HIS597(2)
				Pi–Pi Stacked	TRP634(2)
				Pi–Pi T-shaped	—
9	5C1M	5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester	-5.5	Conventional Hydrogen Bond	HIS597, GLN663
				Halogen (Fluorine)	GLN663, LEU635
				Pi–Pi Stacked	TRP634(2)
10	2AZ5	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	-9.3	Conventional Hydrogen Bond	GLY121
				Pi–Pi Stacked	TYR59(2)
				Pi–Pi T-shaped	—
11	2AZ5	Phthalic acid, di(3,5-dimethylphenyl) ester	-9	Conventional Hydrogen Bond	LEU120, GLY121
				Pi–Sigma	TYR59
				Pi–Pi Stacked	TYR119, TYR59
				Alkyl	LEU57(3)

				Pi–Alkyl	TYR59
12	2AZ5	Phthalic acid, di(3-ethylphenyl) ester	-8.7	Conventional Hydrogen Bond	GLY121
				Pi–Pi Stacked	TYR59, TYR119
				Alkyl	LEU57(2)
				Pi–Alkyl	TYR59, LEU57

Table 5: Interaction type of Hypoglygemic, Anti-diarrheal, and Anti-oxidant activites detected in the methanolic leaf extract of *I. cuneifolia* by molecular docking with the selected receptor.

Serial No.	PDB ID	Compound name	Binding Affinity	Interaction Types	Amino Acids Residues
1	1R4U	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	-8.5	Conventional Hydrogen Bond	GLU259
				Pi-Cation	ARG176
				Pi-Pi Stacked	PHE258
				Alkyl	LYS171
2	1R4U	Phthalic acid, di(3,5-dimethylphenyl) ester	-7.9	Pi-Pi Stacked	PHE258
				Alkyl	LEU170
					LYS171
				Pi-Alkyl	PHE258 (2)
					ARG176
					LYS171

3	1R4U	5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester	-7.7	Conventional Hydrogen Bond	ARG176
					ASN254
					GLU259
				Carbon Hydrogen Bond	HIS256
				Halogen (Fluorine)	TYR257 (2)
				Pi-Anion	GLU259
				Alkyl	ARG176
				Pi-Alkyl	PHE278
					ARG176
4	6VI4	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	-8.2	Pi-Pi Stacked	TRP222 (2)
				Pi-Alkyl	PRO215
5	6VI4	5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester	-7.7	Conventional Hydrogen Bond	TRP222
				Carbon Hydrogen Bond	PRO215 (2)
				Pi-Pi Stacked	TRP222 (2)
				Alkyl	PRO215
				Pi-Alkyl	PHE214

					TRP222 (2)
					PRO215
					LYS174
					ILE177 (2)
6	6VI4	Phthalic acid, di(3,5-dimethylphenyl) ester	-7.6	Conventional Hydrogen Bond	TRP222
				Pi-Pi Stacked	TRP222 (2)
				Alkyl	LYS174
					ILE178 (2)
				Pi-Alkyl	PHE169
					PRO215
					ILE177
					LYS174
7	4ZWB	Phthalic acid, di(3,5-dimethylphenyl) ester	-10.5	Conventional Hydrogen Bond	ASN413 (2)
				Pi-Sigma	TRP410
				Pi-Pi Stacked	PHE289
				Pi-Pi T-shaped	PHE24
					PHE377
					TRP410
				Alkyl	ILE166
				Pi-Alkyl	PHE24
					PHE70
					PHE289
					TRP410 (2)
					ILE166
					ILE285
8	4ZWB		-10.2		GLN281

		Phthalic acid, di(3-ethylphenyl) ester		Conventional Hydrogen Bond	ASN413 (2)
				Pi-Pi Stacked	PHE289
				Pi-Alkyl	ILE166
					ILE285
9	4ZWB	Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-	-9.8	Conventional Hydrogen Bond	THR28
					ASN413
				Carbon Hydrogen Bond	GLY29
				Pi-Pi Stacked	PHE289
				Alkyl	VAL67
				Pi-Alkyl	ILE166
					ILE285 (2)

3.4 Molecular Docking study for Analgesic, Anti-inflammatory, Hypoglycemic, Anti-oxidant, Anti-diarrheal Activities:

Molecular docking for Analgesic activity

Regarding their analgesic properties, all compounds demonstrated affinity for the human cyclooxygenase-2 inhibitor (PDB: 6COX). Phthalic acid, di(3,5-dimethylphenyl) ester exhibited the highest binding affinity (−10.5 kcal/mol), surpassing even the reference drug Diclofenac (−8.4 kcal/mol). The next most potent compounds were Phthalic acid, di(3-ethylphenyl) ester (−9.2 kcal/mol) and Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- (−8.9 kcal/mol). A detailed docking analysis revealed that). Phthalic acid, di(3,5-dimethylphenyl) ester formed six Alkyl bonds at short intermolecular distances with residues VAL444, PHE395, VAL295, LEU408, PHE200, PHE210. These interactions indicate that Phthalic acid, di(3,5-dimethylphenyl) ester binds strongly to the active site of the human cyclooxygenase-2 inhibitor, underscoring its high affinity and potential as a potent analgesic agent.

Regarding their analgesic properties, all compounds demonstrated affinity for the human cyclooxygenase-1 inhibitor (PDB: 6Y3C). Phthalic acid, di(3-ethylphenyl) ester exhibited the highest binding affinity (−8.1 kcal/mol). The next most potent compounds were Phthalic acid, di(3,5-dimethylphenyl) ester (−7.5 kcal/mol) and Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- (−7.5 kcal/mol). A detailed docking analysis revealed that Phthalic acid, di(3-ethylphenyl) formed six Alkyl bonds at short intermolecular distances with residues LEU44 (2), LEU43, LEU40, VAL69(2), and 4 pi-Alkyl bonds with VAL69 (2), LEU44, LEU40, LEU43. These interactions indicate that Phthalic acid, di(3,5-dimethylphenyl) ester binds strongly to the active site of the human cyclooxygenase-1 inhibitor, underscoring its high affinity and potential as a potent analgesic agent.

Regarding their analgesic properties, all compounds demonstrated affinity for the human μ-opioid receptor (PDB:5CIM). Phthalic acid, di(3-ethylphenyl) ester exhibited the highest binding affinity (−6.7 kcal/mol). The next most potent compounds were Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- (−6 kcal/mol) and 5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester (−5.5 kcal/mol). A detailed docking analysis revealed that Phthalic acid, di(3-ethylphenyl) formed one Alkyl bonds at short intermolecular distances with residues LEU604, and three pi-Alkyl bonds with PHE595, TRP634(2). These interactions indicate that Phthalic acid, di(3,5-dimethylphenyl) ester binds strongly to the active site of the human μ-opioid receptor, underscoring its high affinity and potential as a potent analgesic agent.

Molecular Docking for Anti-Inflammatory Activity

The anti-inflammatory efficacy of the selected bioactive compounds from the plant was evaluated by analyzing their interactions with TNF-alpha (PDB: 2AZ5). Each compound demonstrated significant binding affinity to the target receptor. Among them, Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- exhibited the highest binding affinity (−9.3 kcal/mol), followed by Phthalic acid, di(3,5-dimethylphenyl) ester (-9 kcal/mol) and Phthalic acid, di(3-ethylphenyl) ester (−8.7 kcal/mol). The docking study revealed that Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- formed two Pi–Pi stacking interactions with the amino acid residue TYR59 (2) and a conventional hydrogen bond with GLY121, with short intermolecular

distances. These interactions indicate a strong binding affinity within the active site of TNF-α. Since hydrophobic interactions play a crucial role in drug–receptor binding, shorter bond distances (less than 5 Å) generally lead to stronger binding stability and improved docking scores. Therefore, these results suggest that Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- may serve as a potential candidate for anti-inflammatory drug development.

Molecular docking for Antioxidant activity

In case of their antioxidant properties, all compounds showed affinity for the Urase Oxidase (URO) receptor (PDB: 1R4U). Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- exhibited the highest affinity (-8.6 kcal/mol). The next most potent compound was Phthalic acid, di(3,5-dimethylphenyl) ester (-7.9 kcal/mol), and 5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester (-7.7 kcal/mol). A detailed docking analysis revealed that Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- formed one alkyl bond with LYS171, one Pi-Alkyl bond with ARG176, and one conventional hydrogen bond with GLU259 with short intermolecular distance. These interactions indicate a strong binding affinity within the active site of Urase Oxidase (URO). Since hydrophobic interactions play a crucial role in drug-receptor binding, shorter bond distance (less than 5 Å) generally lead to stronger binding stability and improved docking scores. Therefore, these results suggest that Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- may serve as potential candidate for antioxidant drug development.

Molecular docking for Anti-diarrheal activity

In case of their anti-diarrheal properties, all compounds showed affinity for the Kappa Opioid Receptor (KOR) receptor (PDB: 6VI4). Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- exhibited the highest affinity (-8.2 kcal/mol). The next most potent compound was 5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester (-7.7 kcal/mol), and Phthalic acid, di(3,5-dimethylphenyl) ester (-7.6 kcal/mol). A detailed docking analysis revealed that Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- formed one Pi-alkyl bond with PRO215, two Pi-Stacked bonds with TRP222 with short intermolecular distance. These interactions indicate a strong binding affinity within the active site of Kappa Opioid Receptor (KOR) receptor. Since hydrophobic interactions play a crucial role in drug-receptor binding, shorter bond distance (less

than 5 Å) generally lead to stronger binding stability and improved docking scores. Therefore, these results suggest that Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- may serve as potential candidate for antioxidant drug development.

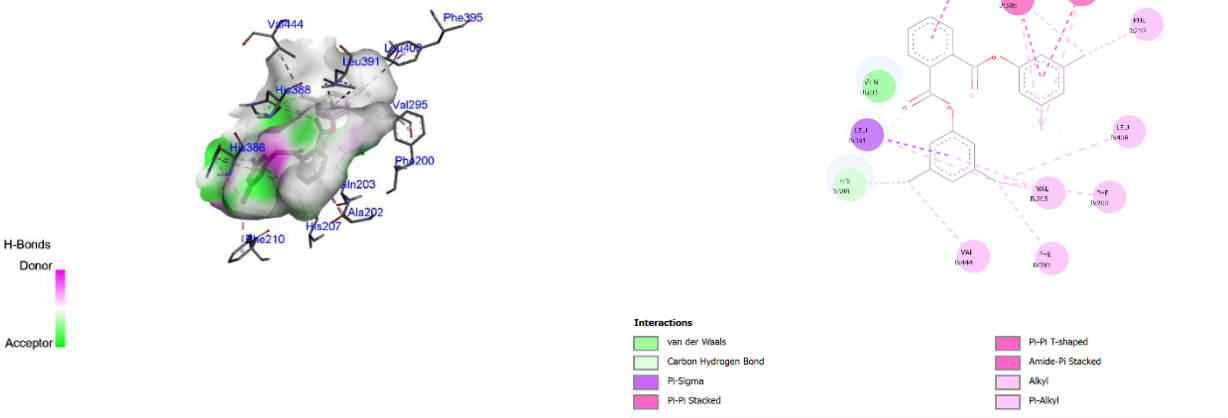
Molecular docking for Hypoglycemic activity

In case of their hypoglycemic properties, all compounds showed affinity for the GLUT 3 receptor (PDB: 4ZWB). Phthalic acid, di(3,5-dimethylphenyl) ester exhibited the highest affinity (-10.5 kcal/mol). The next most potent compound was Phthalic acid, di(3-ethylphenyl) ester (-10.2 kcal/mol), and Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- (-9.8 kcal/mol). A detailed docking analysis revealed that Phthalic acid, di(3,5-dimethylphenyl) ester has formed one alkyl bond with ILE166, two Pi-alkyl bond with TRP410, one Pi-alkyl bond with PHE24, one Pi-alkyl bond with PHE70, one Pi-alkyl bond with PHE289, one Pi-alkyl bond with ILE285 and one Pi-alkyl bond with ILE166. It has also formed one Pi-Pi stacked bond with PHE289 and two conventional hydrogen bonds with ASN413. It also formed a Pi-sigma bond with TRP410. It has formed these bonds with short intermolecular distance. These interactions indicate a strong binding affinity within the active site of GLUT3 receptor. Since hydrophobic interactions play a crucial role in drug-receptor binding, shorter bond distance (less than 5 Å) generally lead to stronger binding stability and improved docking scores. Therefore, these results suggest that Phthalic acid, di(3,5-dimethylphenyl) ester may serve as potential candidate for antioxidant drug development.

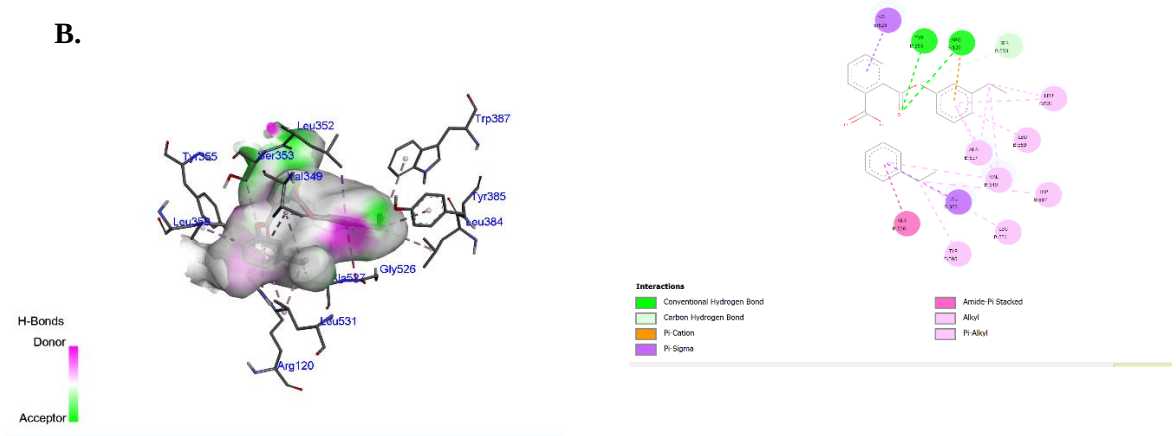
3.5 In silico Analysis

Molecular docking interaction of compounds against the **human cyclooxygenase-2 inhibitor** (PDB: 6COX): A. Phthalic acid, di(3,5-dimethylphenyl) ester B. Phthalic acid, di(3-ethylphenyl) ester C. Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl-

A.



B.



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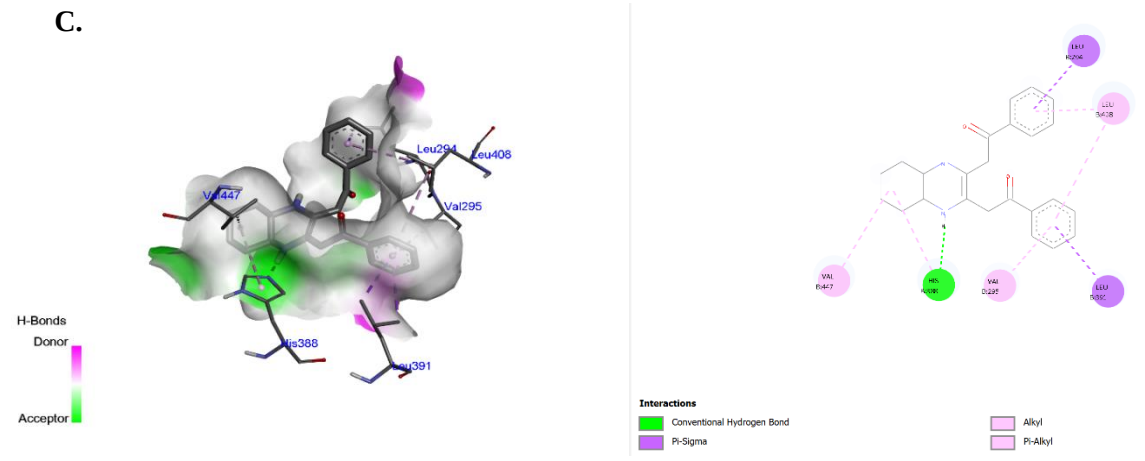
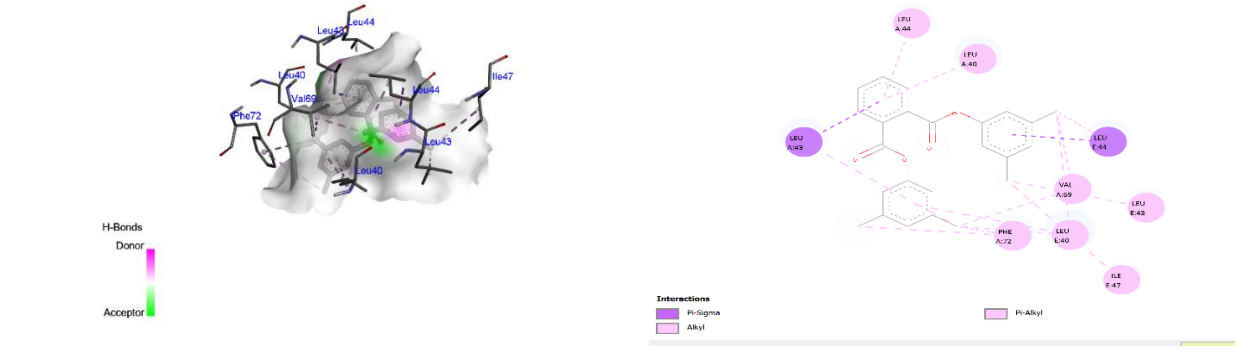


Molecular docking interaction of compounds against **the human cyclooxygenase-1 inhibitor** (PDB: 6Y3C): A. Phthalic acid, di(3-ethylphenyl) ester B. Phthalic acid, di(3,5-dimethylphenyl) ester C. Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl-

A.

B.



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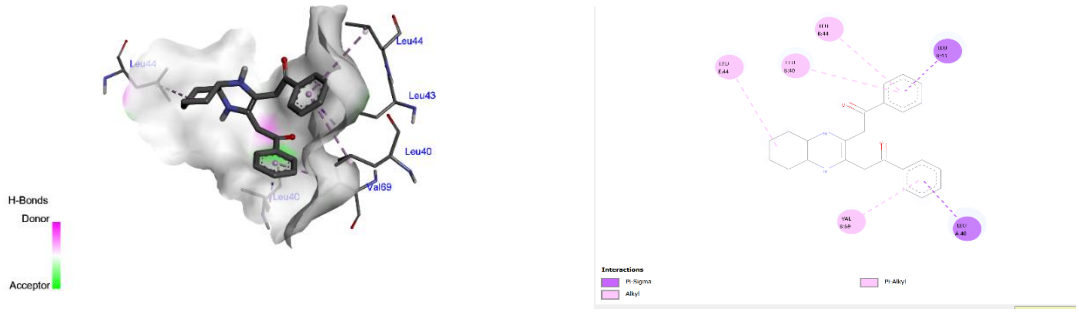
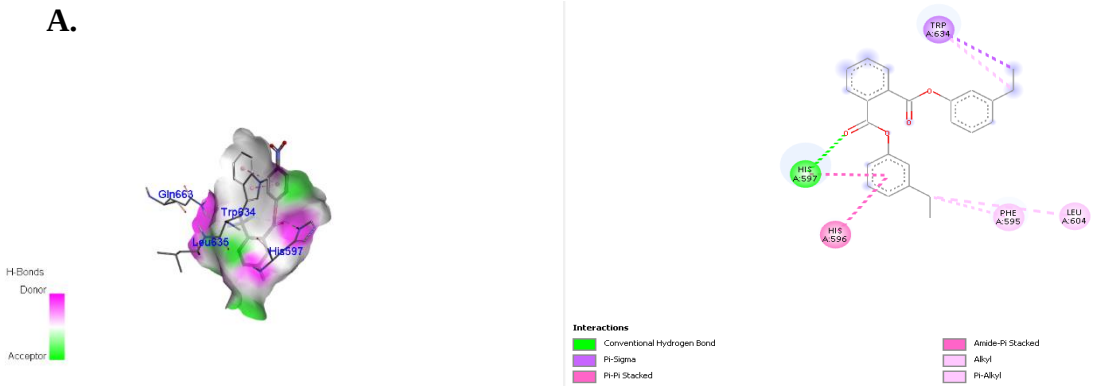


Molecular docking interaction of compounds against the **human μ-opioid receptor** (PDB: 5CIM): A.Phthalic acid, di(3-ethylphenyl) ester B. Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl- C. 5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester

A.

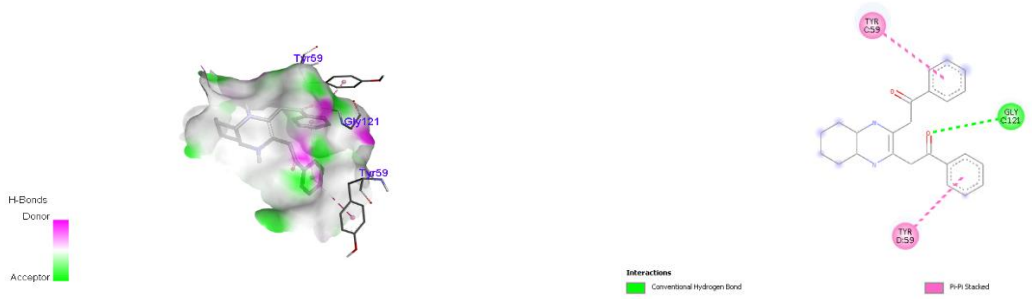


B.

C.

Molecular docking interaction of compounds against the human **TNF Alpha receptor** (PDB: 2AZ5): A. Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- B. Phthalic acid, di(3,5-dimethylphenyl) ester C. Phthalic acid, di(3-ethylphenyl) ester

A.

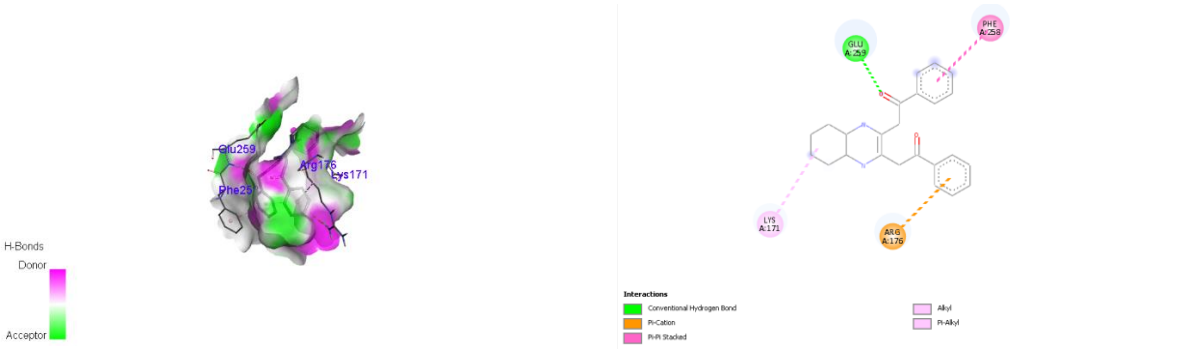


B.

C.

Molecular docking interaction of compounds against the human **Urase Oxidase (URO) receptor** (PDB: 1R4U): A. Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- B. Phthalic acid, di(3,5-dimethylphenyl) ester C. Phthalic acid, di(3-ethylphenyl) ester

A.



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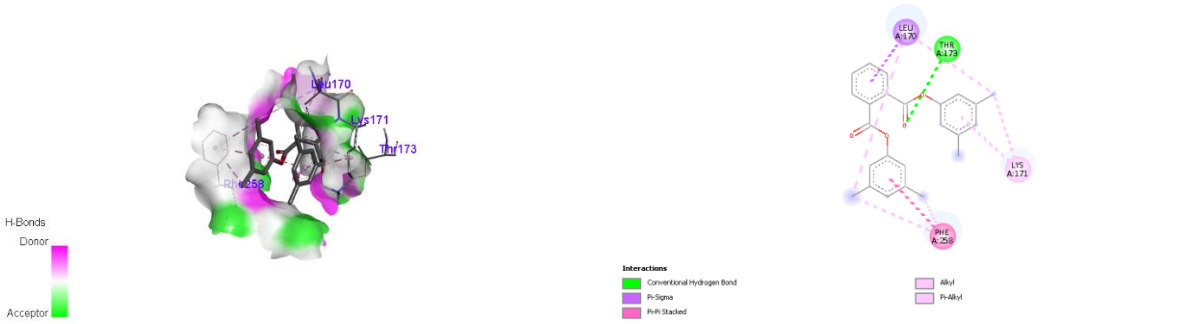

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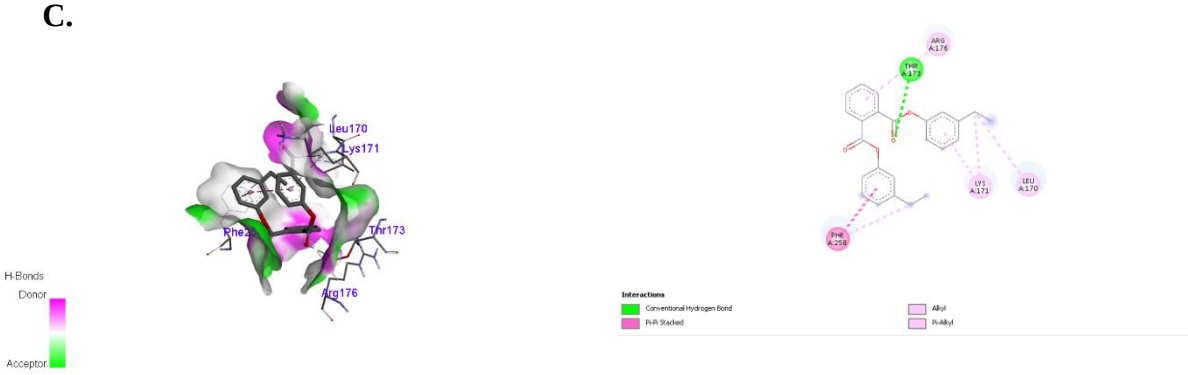
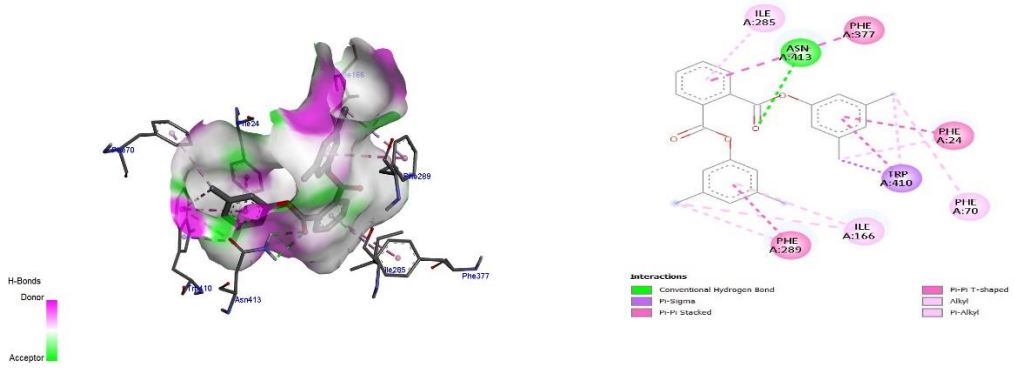


Molecular docking interaction of compounds against the **human GLUT 3 receptor hypoglysemic** (PDB: 4ZWB): A. Phthalic acid, di(3,5-dimethylphenyl) ester B. Phthalic acid, di(3-ethylphenyl) ester C. Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl-

A.



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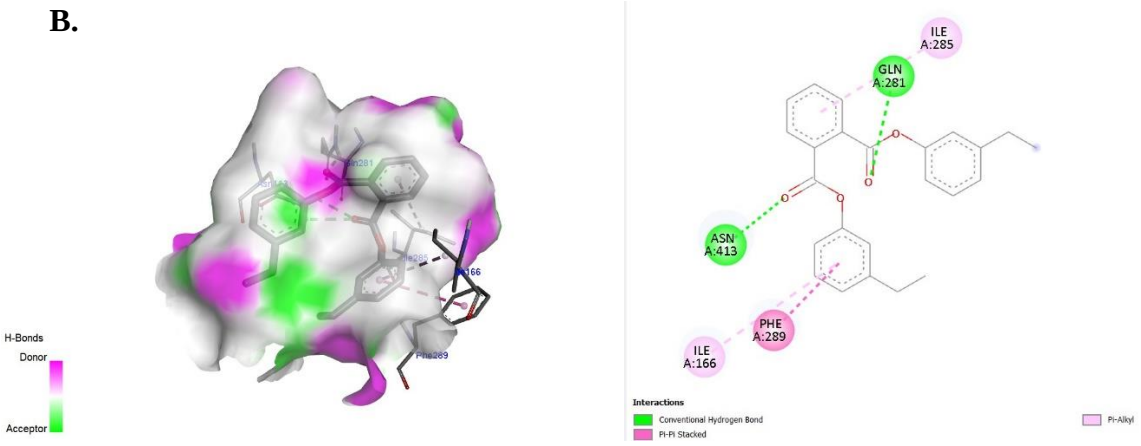

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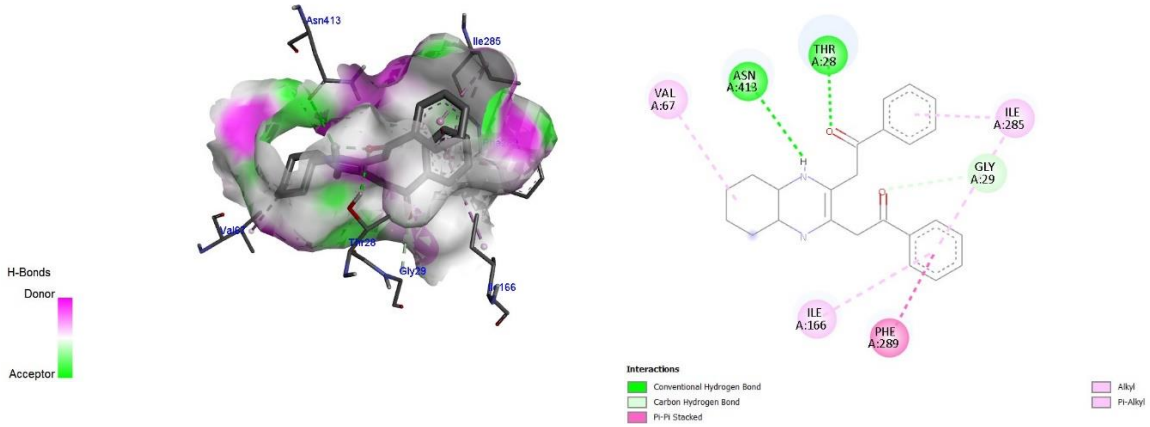
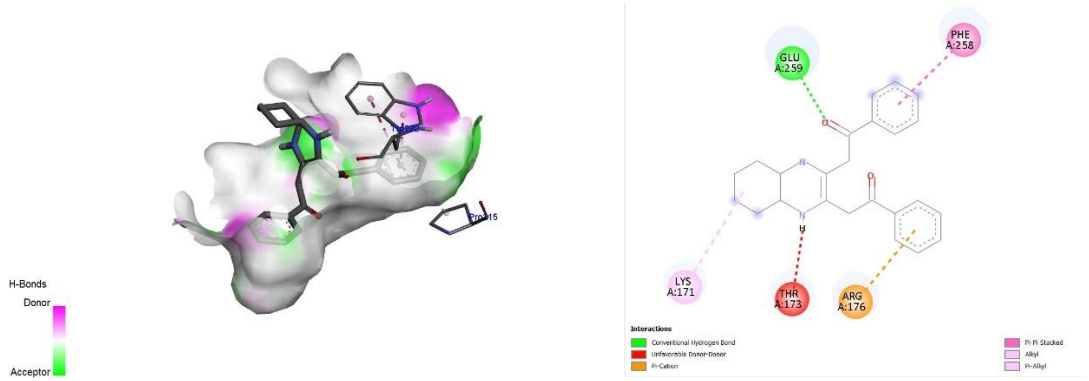


Molecular docking interaction of compounds against the **human Kappa Opioid Receptor (KOR)** receptor (Anti diarrheal) (PDB: 6VI4): A. Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- B. 5-Fluoro-2-trifluoromethylbenzoic acid, 4-nitrophenyl ester C. Phthalic acid, di(3,5-dimethylphenyl) ester

A.



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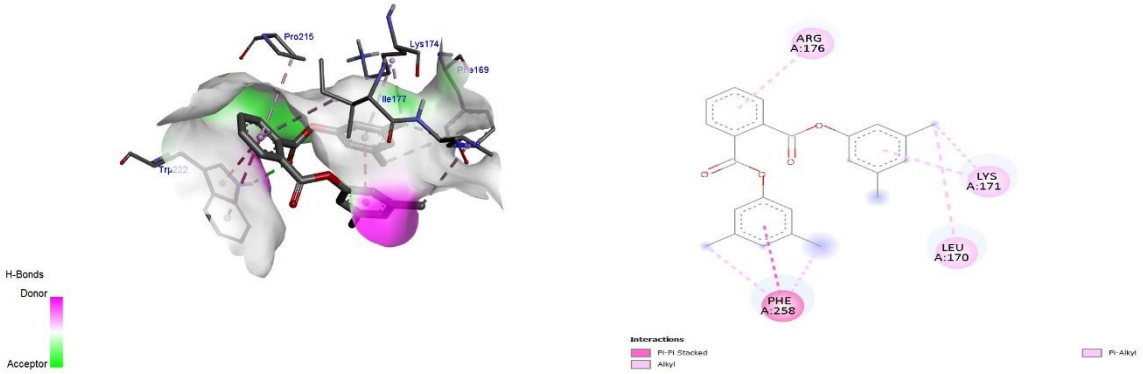

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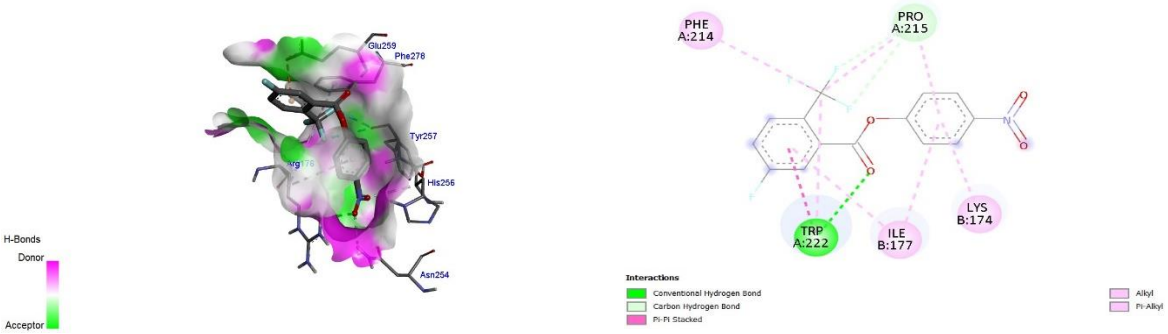

Chapter 4: Discussion

4.1 Gas Chromatography and Mass Chromatography Analysis

The ME was examined utilizing a Shimadzu GC-MS/MS TQ 8040 system with electron impact ionization. Separation was performed on a fused silica capillary column (Rxi-30 m, 0.25 mm ID, and 0.25 μm film thickness). Samples were introduced at a temperature of 250 °C, and the oven temperature was programmed to rise from 50 °C (for 1 minute) to 200 °C (for 2 minutes) and then to 300 °C (for 7 minutes). The overall run duration was 40 minutes at a pressure of 53.5 kPa, with a flow rate of 11 mL/min. The ion source was maintained at a temperature of 230 °C, and the detector voltage ranged from 0.5 to 0.6 kV, employing Q3 scan mode (m/z 25–600), with a solvent cut time set to 3.5 minutes. Compounds were tentatively identified by matching their mass spectra against reference spectra from the NIST and Wiley mass spectral databases (Ezeokonkwo & Kabir, 2026).

4.2 Molecular Docking

Molecular docking analyses are commonly used to anticipate ligand-target interactions and improve our comprehension of the bioactivities of natural compounds. These investigations also offer perspectives on possible binding mechanisms in protein binding sites (Nahar et al.,2025). In this study, molecular docking has elucidated and reinforced the biological outcomes, providing a better understanding of the effects observed. Twenty-three chosen compounds identified via GC-MS/MS analysis of ME, along with reference drugs, were analyzed through docking studies using target proteins such as TNF-alpha (PDB: 2AZ5), human COX-2 inhibitor (PDB: 6COX), COX-1 Inhibitor (PDB: 6Y3C), Mu-Opioid receptor (PDB: 5CIM). The molecular docking study was carried out using three target proteins, including Urase oxidase (PDB: 1R4U), kappa opioid receptor (PDB: 6VI4), and GLUT3 receptor (PDB: 4ZWB), to predict possible antioxidant, anti-diarrheal, and hypoglycemic activities. The results showed that the selected compounds had good binding affinity with all the receptors, with docking scores ranging from around −7.6 to −10.5 kcal/mol. Among them, Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene) bis [1-phenyl- and Phthalic acid derivatives showed comparatively better interactions. These strong binding interactions suggest

that the identified compounds may have potential biological activities and could be considered as possible candidates for further drug development. The objective was to forecast possible biological modes of action, such as anti-inflammatory, analgesic, anti-oxidant, anti-diarrheal and hypoglycemic effects. The findings showed that the bioactive compounds of *I. Cuneifolia* displayed outstanding binding affinities (−10.5 to 6 kcal/mol) toward the chosen receptors. This strong binding affinity indicates that these compounds are more likely to be viewed as promising drug candidates because of their enhanced interactions with the target receptors.

Nonetheless, additional study is advised to establish if these compounds exhibit superior receptor interactions relative to other bioactive compounds. Consequently, further experimental confirmation is required to verify the pharmacological impacts of these isolated compounds and to investigate their therapeutic potential in more depth (Nahar et al., 2025).

Chapter 5: Conclusion

The current investigation showed that the methanolic extract of *I. Cunifolia* and many of its fractions, Ethanone, 2,2'-(octahydro-2,3-quinoxalinediylidene)bis[1-phenyl-, Phthalic acid, di(3,5-dimethylphenyl) ester, Phthalic acid, di(3-ethylphenyl) ester had notable analgesic and anti-inflammatory, anti-diarrheal, anti-oxidant and hypoglycemic properties. GC-MS analysis and phytochemical screening revealed a number of secondary metabolites that could be in charge of these pharmacological effects. Additionally, the reported biological activities were supported by in silico molecular docking studies that corroborated the experimental results. To identify and describe the precise substances causing these effects and to clarify their underlying mechanisms of action, however, more sophisticated study is required. These studies may lead to the creation of new medicinal substances derived from *I. Cunifolia*.

Chapter 6: Limitation and Future opportunities

6.1 Limitations:

Only GC–MS analysis and molecular docking were carried out in this study. No in vivo experiments or molecular dynamics simulations were performed, so the findings cannot fully show how the phytochemical compounds would behave in a real biological system, as factors like metabolism, bioavailability, and toxicity in living organisms were not considered.

6.2 Future Research Opportunities:

In future studies, in vivo experiments and clinical trials should be conducted to evaluate toxicity, pharmacokinetics, and real therapeutic effectiveness, as well as to confirm the safety and biological activity of these compounds. Additionally, molecular dynamics simulations can be performed to better understand the stability and interactions of the compound–receptor complexes. Studying possible synergistic effects would also be useful to determine whether a combination of compounds works better than individual ones alone.

Chapter 7: Reference

1. Bhuiyan, M. A., Galdes, N., Cuschieri, S., & Hu, P. (2024). A comparative systematic review of risk factors, prevalence, and challenges contributing to non-communicable diseases in South Asia, Africa, and Caribbeans. *Journal of Health, Population and Nutrition*, *43*(1), 140. https://doi.org/10.1186/s41043-024-00607-2
2. Pham, J. V., Yilma, M. A., Feliz, A., Majid, M. T., Maffetone, N., Walker, J. R., Kim, E., Cho, H. J., Reynolds, J. M., Song, M. C., Park, S. R., & Yoon, Y. J. (2019). A Review of the Microbial Production of Bioactive Natural Products and Biologics. *Frontiers in Microbiology*, *10*, 1404. https://doi.org/10.3389/fmicb.2019.01404
3. Ekins, S., Mestres, J., & Testa, B. (2007). *In silico* pharmacology for drug discovery: Methods for virtual ligand screening and profiling. *British Journal of Pharmacology*, *152*(1), 9–20. https://doi.org/10.1038/sj.bjp.0707305
4. Huq, T. B., Rahman, M. S., Nure, M. A., Hossain, M. S., Sarwar, A., Islam, A., Das, M., Haque, M. E., Malik, T., Reza, M. W., Adhikary, B. C., Rahman, M., Begum, T., & Begum, M. M. (2017). Evaluation of pharmacological activities of methanol extract of Ixora cuneifolia leaves. *Clinical Phytoscience*, *2*(1), 22. https://doi.org/10.1186/s40816-016-0036-1
5. Jamal Hossain, Md., Abdus Samadd, Md., Akter, S., Shohel Hossen, Md., Kuddus, A., Azizur Rahman Tamim, Md., Mitu, M. M., & Rashid, M. A. (2025). Unveiling Phytochemicals and Antioxidant, Cytotoxic, Antithrombotic, Anti-Inflammatory, Analgesic, Hypoglycemic and Antidiarrheal Activities from the Leaves Extract of *Zanthoxylum rhetsa* (Roxb.) DC. *Natural Product Communications*, *20*(2), 1934578X251319206. https://doi.org/10.1177/1934578X251319206
6. Khan, I. A., Anwar, M., Arshad, S. F., Hussain, A., Usman, M., Ansari, M. N., Arshad, H. J., Rukh, A. S., Ain, Q. U., & Khan, M. K. (2025). Biochemical validation for the therapeutic use of Plumeria rubra in coagulation disorders: A study combining in silico, in vitro, and in vivo approaches. *Protoplasma*, *262*(5), 1319–1336. https://doi.org/10.1007/s00709-025-02055-z
7. Munny, F. A., Islam, M., Akter, M., Ferdousi, M., Asif, Md. M. A., Hossain, Md. S., Sharmin, S., Zahidul Islam, M., Hossain, Md. A., & Islam, Md. R. (2025). Phenolic Compounds of *Justicia gendarussa* Show Pharmacological Potentials Against Pain,

Oxidation, Hyperglycemia, Diarrhea, and Microbes: Phytopharmacological and Computational Approaches. *BioMed Research International*, *2025*(1), 2561508. https://doi.org/10.1155/bmri/2561508

8. Murugan, P., Murugan, C., & Karthigeyan, K. (2021). Notes on the identity and taxonomy of Ixora cuneifolia and I. notoniana and typification of three names in Ixora. *Gardens' Bulletin Singapore*, *73*(2), 481–487. https://doi.org/10.26492/gbs73(2).2021-18
9. Nadeem, R., Imran, M., Saeed, Z., Pervaiz, M., & Younas, U. (2025). Exploring the therapeutic potential of Ixora extract: A comprehensive review of mediated studies. *Advances in Traditional Medicine*, *25*(1), 107–144. https://doi.org/10.1007/s13596-024-00797-4
10. Nahar, A., Khandakar, Md. J., Mamun, Md. J. I., Rasel, Md. H., Ihsan, A. B., Raj, A., Ahmed, S., Hossain, M. K., Hasan, M. R., & Saito, T. (2025). Investigation of Analgesic, Anti-Inflammatory, and Thrombolytic Effects of Methanolic Extract and Its Fractions of Dischidia bengalensis: In Vitro and In Vivo Studies with In Silico Interventions. *Molecules*, *30*(18), 3724. https://doi.org/10.3390/molecules30183724
11. Paggi, J. M., Pandit, A., & Dror, R. O. (2024). The Art and Science of Molecular Docking. *Annual Review of Biochemistry*, *93*(1), 389–410. https://doi.org/10.1146/annurev-biochem-030222-120000
12. Pham, J. V., Yilma, M. A., Feliz, A., Majid, M. T., Maffetone, N., Walker, J. R., Kim, E., Cho, H. J., Reynolds, J. M., Song, M. C., Park, S. R., & Yoon, Y. J. (2019). A Review of the Microbial Production of Bioactive Natural Products and Biologics. *Frontiers in Microbiology*, *10*, 1404. https://doi.org/10.3389/fmicb.2019.01404
13. Ekins, S., Mestres, J., & Testa, B. (2007). *In silico* pharmacology for drug discovery: Methods for virtual ligand screening and profiling. *British Journal of Pharmacology*, *152*(1), 9–20. https://doi.org/10.1038/sj.bjp.0707305
14. Ezeokonkwo, M. A., & Kabir, D. (2026). Applications of FTIR, GC-MS, and LC-MS in the Identification of Antimicrobial Phytochemicals. *Arabian Journal of Chemical and Environmental Research*, *13*(2), 194–216.

15. Huq, T. B., Rahman, M. S., Nure, M. A., Hossain, M. S., Sarwar, A., Islam, A., Das, M., Haque, M. E., Malik, T., Reza, M. W., Adhikary, B. C., Rahman, M., Begum, T., & Begum, M. M. (2017). Evaluation of pharmacological activities of methanol extract of Ixora cuneifolia leaves. *Clinical Phytoscience*, *2*(1), 22. https://doi.org/10.1186/s40816-016-0036-1
16. Jamal Hossain, Md., Abdus Samadd, Md., Akter, S., Shohel Hossen, Md., Kuddus, A., Azizur Rahman Tamim, Md., Mitu, M. M., & Rashid, M. A. (2025). Unveiling Phytochemicals and Antioxidant, Cytotoxic, Antithrombotic, Anti-Inflammatory, Analgesic, Hypoglycemic and Antidiarrheal Activities from the Leaves Extract of *Zanthoxylum rhetsa* (Roxb.) DC. *Natural Product Communications*, *20*(2), 1934578X251319206. https://doi.org/10.1177/1934578X251319206
17. Khan, I. A., Anwar, M., Arshad, S. F., Hussain, A., Usman, M., Ansari, M. N., Arshad, H. J., Rukh, A. S., Ain, Q. U., & Khan, M. K. (2025). Biochemical validation for the therapeutic use of Plumeria rubra in coagulation disorders: A study combining in silico, in vitro, and in vivo approaches. *Protoplasma*, *262*(5), 1319–1336. https://doi.org/10.1007/s00709-025-02055-z
18. Munny, F. A., Islam, M., Akter, M., Ferdousi, M., Asif, Md. M. A., Hossain, Md. S., Sharmin, S., Zahidul Islam, M., Hossain, Md. A., & Islam, Md. R. (2025). Phenolic Compounds of *Justicia gendarussa* Show Pharmacological Potentials Against Pain, Oxidation, Hyperglycemia, Diarrhea, and Microbes: Phytopharmacological and Computational Approaches. *BioMed Research International*, *2025*(1), 2561508. https://doi.org/10.1155/bmri/2561508

19. Murugan, P., Murugan, C., & Karthigeyan, K. (2021). Notes on the identity and taxonomy of Ixora cuneifolia and I. notoniana and typification of three names in Ixora. *Gardens' Bulletin Singapore*, *73*(2), 481–487. https://doi.org/10.26492/gbs73(2).2021-18
20. Nadeem, R., Imran, M., Saeed, Z., Pervaiz, M., & Younas, U. (2025b). Exploring the therapeutic potential of Ixora extract: A comprehensive review of mediated studies. *Advances in Traditional Medicine*, *25*(1), 107–144. https://doi.org/10.1007/s13596-024-00797-4
21. Nahar, A., Khandakar, Md. J., Mamun, Md. J. I., Rasel, Md. H., Ihsan, A. B., Raj, A., Ahmed, S., Hossain, M. K., Hasan, M. R., & Saito, T. (2025). Investigation of Analgesic, Anti-Inflammatory, and Thrombolytic Effects of Methanolic Extract and Its Fractions of Dischidia bengalensis: In Vitro and In Vivo Studies with In Silico Interventions. *Molecules*, *30*(18), 3724. https://doi.org/10.3390/molecules30183724
22. Paggi, J. M., Pandit, A., & Dror, R. O. (2024). The Art and Science of Molecular Docking. *Annual Review of Biochemistry*, *93*(1), 389–410. https://doi.org/10.1146/annurev-biochem-030222-120000

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