Journal Multidisciplinary Perspectives in Science and Technology (MPST)
Vol.1, No.4, 2025: 53-66

Prediction of Activity Spectra for Substances (PASS) from Mangiferin Bioaktif Mangga (*Mangifera indica L.*)

Yuneka Saristiana[1*], Fendy Prasetyawan[2], Mujtahid Bin Abd Kadir[3], M Wahyu Ariawan[4]
[1,2]Universitas Kadiri,[3]Universitas Muhammadiyah Makasar, [4]Universitas Tulang Bawang
Corresponding Author: Yuneka Saristiana yunekasaristiana@gmail.com

A R T I C L E I N F O

Key Words: Mangiferin, PASS Online, Mangifera indica, Bioactivity Prediction, Natural Compound Drug Discovery

Received : 5 February
Revised : 23 March
Accepted: 25 April

A B S T R A C T

Mangiferin, a major bioactive compound found in the mango plant (*Mangifera indica* L.), has attracted significant scientific interest due to its diverse pharmacological properties. This study aimed to predict the potential biological activities of mangiferin using the Prediction of Activity Spectra for Substances (PASS) online tool, based on its SMILES notation retrieved from the PubChem database. Through computational analysis, multiple probable pharmacological effects were identified, including TP53 expression enhancement, membrane integrity modulation, HIF1A expression inhibition, and anti-carcinogenic properties. The Pa (probability "to be active") values for these activities ranged from 0.79 to 0.95, suggesting a high likelihood of bioactivity. Notably, mangiferin also demonstrated potential as a cytostatic, hepatoprotective, and antidiabetic agent. These predictions support previously reported experimental findings and further highlight the therapeutic potential of mangiferin in oncology, hepatology, and metabolic disorders. This computational approach provides an efficient and informative method to explore the drug-likeness and pharmacological versatility of natural compounds, particularly in the early stages of drug discovery and development

DOI: https://doi.org/10.55927/mpst.v1i4.4
ISSN-E:
https://meiformosapublisher.org/index.php/mpst/index

INTRODUCTION

The mango plant (Mangifera indica L.) is one of the most popular tropical species worldwide, distinguished not only by its sweet and nutritious fruit but also by the bioactive compounds present in nearly all parts of the plant. Originating from South Asia, particularly India and Myanmar, the mango has been cultivated for thousands of years and is now widely distributed across tropical and subtropical regions, including Southeast Asia, South America, and Africa. Ethnopharmacologically, various parts of this plant, such as the leaves, bark, seeds, and latex, have been utilized by communities for traditional medicine in addressing various ailments including wounds, infections, diabetes, and digestive disorders (Kheirollahi, A., 2019).

One of the key compounds extensively studied from the mango plant is mangiferin. Mangiferin is a natural polyphenolic compound classified as a glycosylated xanthone. Its chemical structure consists of a xanthone core bonded covalently to a glucose molecule. This compound was first isolated from the leaves and bark of the mango tree and has since been identified in other plants such as Anemarrhena asphodeloides, Iris domestica, and Salacia reticulata. Mangiferin has garnered attention due to its broad biological activity, which includes functions as an antioxidant, antidiabetic agent, anti-inflammatory substance, immunomodulator, hepatoprotective agent, neuroprotective agent, and it even shows potential as an anticancer agent (Imran, M., 2017).

Pharmacological research on mangiferin has been conducted using various in vitro and in vivo approaches (Saristiana, Y., 2024). The antioxidant activity of mangiferin is demonstrated by its ability to scavenge free radicals and increase the expression of endogenous antioxidant enzymes, such as superoxide dismutase (SOD), catalase, and glutathione peroxidase. The antidiabetic effects of mangiferin are associated with its ability to enhance insulin sensitivity, inhibit α-glucosidase, and lower blood glucose levels in diabetic animal models. Moreover, mangiferin is known to reduce levels of pro-inflammatory cytokines such as TNF-α and IL-6, establishing it as a strong candidate for the development of therapies for chronic inflammation.

Process of drug discovery and development from natural compounds (Mildawati, R., 2024) like mangiferin is lengthy, costly, and entails complex pharmacological evaluation stages. In recent years, in silico approaches have gained prominence as an initial method for rapidly and efficiently screening and evaluating the potential bioactivity of compounds. One widely utilized in silico method is the Prediction of Activity Spectra for Substances (PASS). PASS is a web-based software that predicts the biological activity spectrum of a compound based on its chemical structure (Darvesh, A. S., 2010).

PASS operates by analyzing molecular structures and comparing them to a vast database containing thousands of compounds with known activities. The output from PASS consists of probability values: Pa (probability of being active) and Pi (probability of being inactive) concerning various potential biological activities (Muslikh, F. A. 2023). A Pa value higher than 0. 7 is generally considered promising for further exploration. By employing PASS, researchers can identify the pharmacological potential of certain compounds even before experimental tests are conducted, thereby conserving resources in drug research (Muruganandan, S., 2005).

Given that mangiferin possesses a complex structure and active functional groups, it is particularly suited for analysis using PASS. Through this in silico prediction, a broad spectrum of activities can be reviewed and compared, directing the research focus toward activities with high Pa values that are relevant to current therapeutic needs. This is especially significant in the context of developing safer, environmentally friendly, and minimally side-effect-laden drugs based on natural substances (Sellamuthu, R., 2009).

In the context of the increasing burden of chronic diseases (Prasetyawan, F., 2023) such as diabetes, cardiovascular diseases, neurodegenerative disorders, and cancer, the search for natural compound candidates with multipotential activity is of utmost importance. Mangiferin, with its diverse pharmacodynamic characteristics, holds the potential to address this gap. For instance, in the context of diabetes therapy, this compound not only demonstrates the ability to lower blood glucose levels but also possesses properties that can ameliorate oxidative stress and inflammation—two critical factors involved in diabetes complications (Lagunin, A. A., 2010).

Mangiferin has been reported to have the capacity to cross the blood-brain barrier, thereby making it a promising candidate for the treatment of neurological disorders such as Alzheimer's and Parkinson's diseases. Predictive software such as PASS can bolster this hypothesis by indicating neuroprotective, antidepressant, and anti-ischemic activities that may be attributed to mangiferin based on its chemical structure. Such information provides a robust foundation for further research utilizing both animal models and clinical trials (Fatima, R., 2021).

The application of in silico technology, such as PASS, is also in alignment with the 3Rs principle in laboratory animal research: Replacement, Reduction, and Refinement. By conducting preliminary predictions through PASS, only the most promising compounds will be prioritized for biological testing, thereby minimizing the number of animals used and enhancing experimental design (Luo, Y., 2012).

Given the extensive biological activities reported and the predictive potential of PASS, it is vital to systematically identify the complete profile of mangiferin. This study aims to map the spectrum of biological activity of mangiferin using the online PASS tool, thereby paving the way for new directions in the development of drug candidates derived from natural sources. The outcomes of this analysis are expected to strengthen the scientific basis for the utilization of mangiferin not only as an active ingredient in traditional medicine but also as a foundation for the development of modern phytopharmaceuticals (Mishra, P., 2016).

LITERATURE RIVIEW

The plant Mangifera indica L., commonly known as mango, has long been utilized in traditional medicine across various cultures. Numerous studies indicate that this plant is rich in bioactive compounds with extensive pharmacological potential. According to Kheirollahi *et al*. (2019), different parts of the mango plant, including leaves, bark, and seeds, contain phenolic compounds, flavonoids, and xanthones, with mangiferin being one of the most prominent active constituents. Mangiferin (C19H18O11) is a glycosylated xanthone known for its widespread biological activities, which include antioxidant, anti-inflammatory, antidiabetic, antiviral, and anticancer properties (Imran *et al*., 2017).

Several in vivo and in vitro studies demonstrate that mangiferin exhibits significant antioxidant activity through mechanisms involving free radical scavenging and modulation of cellular oxidative stress. According to Sanchez *et al*. (2000), mangiferin enhances the activity of antioxidant enzymes such as superoxide dismutase (SOD) and catalase while reducing levels of malondialdehyde (MDA), a marker of oxidative stress in tissues. This activity positions mangiferin as a potential candidate for therapy against various degenerative diseases associated with oxidative stress, such as Alzheimer's disease, diabetes, and cancer.

The anti-inflammatory properties of mangiferin have also been extensively studied. Research conducted by Muruganandan *et al*. (2005) indicates that the administration of mangiferin in experimental inflammation models in rats significantly reduces levels of pro-inflammatory cytokines such as TNF-α and IL-1β. Furthermore, mangiferin inhibits the expression of cyclooxygenase-2 (COX-2) and inducible nitric oxide synthase (iNOS), enzymes that play crucial roles in inflammatory pathways. Consequently, this compound has the potential to be developed as a safer non-steroidal anti-inflammatory agent.

In the metabolic domain, mangiferin is recognized for its promising antidiabetic effects. A study by Sellamuthu *et al*. (2009) demonstrates that administering mango leaf extract, which contains mangiferin, effectively lowers

blood glucose levels and enhances insulin sensitivity in a type 2 diabetes rat model. The mechanism of action of mangiferin includes the inhibition of α-glucosidase enzyme activity and the enhancement of glucose transport via GLUT4. These findings align with those reported by Luo *et al.* (2012), which reveal that mangiferin can reduce insulin resistance and ameliorate endothelial dysfunction.

In addition to the aforementioned pharmacological activities, mangiferin also shows potential as a neuroprotective agent. According to research by Darvesh *et al*. (2010), mangiferin can inhibit neurodegeneration by suppressing the NF-κB pathway and activating anti-apoptotic pathways in the brain. This effect is particularly relevant for the development of therapies for neurodegenerative diseases such as Alzheimer's and Parkinson's disease. Moreover, mangiferin exhibits hepatoprotective effects, as demonstrated in a study by Manjunatha *et al*. (2005), wherein administration of mangiferin protected the liver from damage induced by carbon tetrachloride (CCl_4) toxicity. Despite the extensive evidence supporting the pharmacological activities of mangiferin through experimental studies, the utilization of predictive methods such as the Prediction of Activity Spectra for Substances (PASS) represents an important and efficient approach in facilitating the exploration of the bioactivity of this compound. PASS is a structure-based method that predicts the likelihood of a compound's biological activity based on a database of structural and activity data from thousands of bioactive compounds. According to Lagunin *et al*. (2010), the PASS method can yield activity predictions with an accuracy of up to 95%, depending on the type of compound and the parameters employed. This method proves particularly beneficial in the early phases of drug discovery, as it allows for the identification of potential activities without the necessity of immediately conducting complex and costly biological assays.

Numerous studies have utilized the software PASS (Prediction of Activity Spectra for Substances) to evaluate natural compounds. For instance, in the research conducted by Mishra *et al*. (2016), PASS was employed to predict the anti-inflammatory activity of flavonoid compounds, and the predictive outcomes were subsequently validated through in vitro testing. Similarly, Fatima *et al*. (2021) leveraged PASS to identify potential neuroprotective activities of terpenoid compounds. The predictive results generated by PASS are typically presented in two parameters: Pa (probability of activity) and Pi (probability of inactivity), where a Pa value greater than 0. 7 is regarded as indicative of high predictive activity that warrants further experimental validation.

Given the substantial literature evidence regarding the activity of mangiferin and the potential application of in silico approaches such as PASS, a predictive study of the biological activity spectrum of mangiferin is highly

relevant. Through PASS modeling, it is possible to obtain preliminary insights into potential pharmacological activities that have not been extensively explored, thereby reinforcing the scientific basis for the development of mangiferin as a candidate for phytopharmaceuticals or as an active ingredient in natural-based drug formulations. This literature review underscores that, although there is a wealth of experimental data on mangiferin, predictive approaches remain essential to refine the processes of selection, validation, and optimization of its use in the treatment of modern diseases (Nababan, O. A., 2024).

METHODOLOGY

The research methodology employed in this study was meticulously crafted to forecast the biological activity spectrum of Mangiferin, a bioactive compound extracted from Mangifera indica, by utilizing computational tools to assess its potential therapeutic properties. This approach entailed a systematic amalgamation of molecular data retrieval, computational prediction tools, and statistical analysis to delineate the activity spectrum of Mangiferin based on its chemical structure (Prasetyawan, F., 2024).

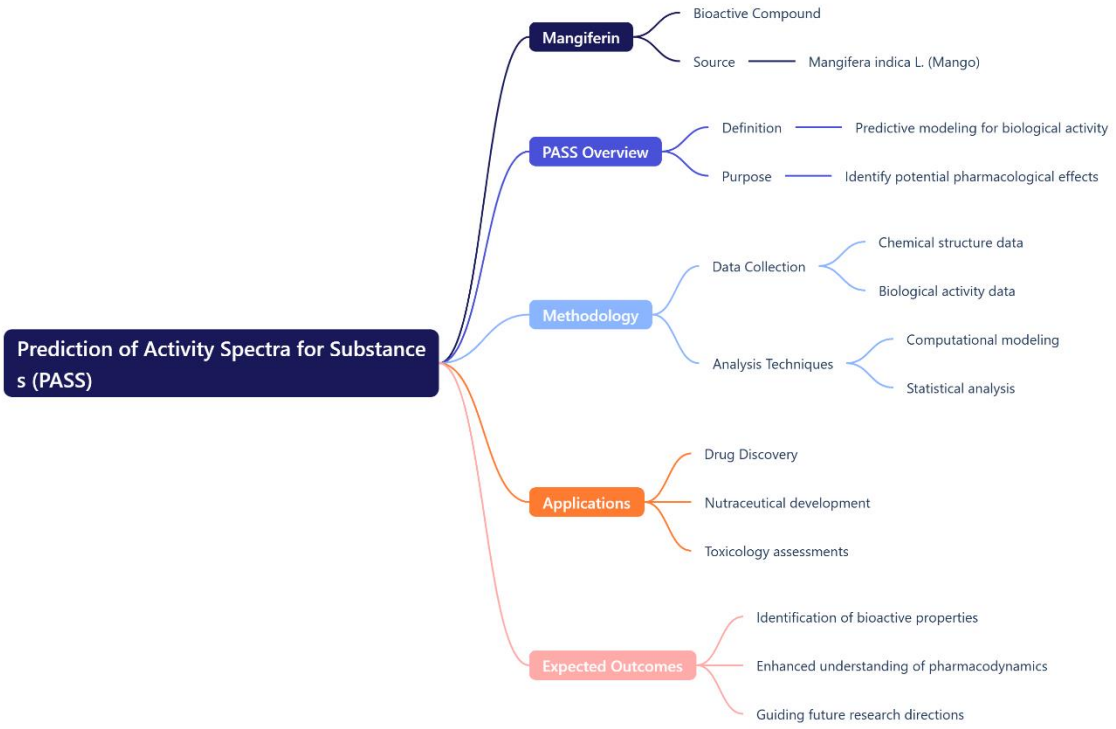

Figure 1. Mind Maps

The initial phase of the methodology included the acquisition of the Simplified Molecular Input Line Entry System (SMILES) notation for Mangiferin from the PubChem database. PubChem (https://pubchem. ncbi. nlm. nih. gov/) represents one of the most extensive repositories of chemical compounds,

offering comprehensive information concerning the chemical structures, properties, and biological activities of a diverse array of substances. The SMILES notation, which encapsulates the chemical structure of Mangiferin in a textual format, was directly sourced from PubChem by conducting a search for the compound under the designation Mangiferin. In addition to SMILES notation, PubChem furnishes a wealth of pertinent molecular data, including molecular weight, structural formulas, and three-dimensional molecular visualizations, all of which are vital for conducting computational modeling.

Following the retrieval of the SMILES notation, the subsequent phase involved predicting the biological activity spectrum of Mangiferin through the utilization of the online platform known as Prediction of Activity Spectra for Substances (PASS) (https://www. way2drug. com/). PASS serves as an advanced computational tool designed to predict the biological activity of chemical compounds based on their chemical structures. It operates using a comprehensive database of established biological activities associated with a wide variety of substances. PASS generates predictions regarding the likelihood of a compound exhibiting specific biological activities by calculating two probabilities: Pa (the probability of the compound being active in a particular biological activity) and Pi (the probability of the compound being inactive in that activity). These predictions are formulated through a comparison of the molecular structure of the compound in question with thousands of compounds whose biological activities have already been documented.

The application of PASS in this study proved instrumental in elucidating the potential pharmacological properties of Mangiferin, as the platform is specifically engineered to analyze molecular structures in considerable detail and to generate predictions across an extensive array of biological activities. The biological activities predicted by PASS were classified into various therapeutic domains, including antioxidant, anti-inflammatory, anti-diabetic, anticancer, neuroprotective, and immunomodulatory activities, among others. Each activity was assigned a probability value, with elevated Pa values indicating a stronger potential for that activity. For instance, a Pa value exceeding 0. 7 for neuroprotective activity would signify that Mangiferin may possess considerable efficacy in safeguarding neurons against damage, presenting a promising avenue for further investigation in the realm of neurodegenerative disorders such as Alzheimer's disease and Parkinson's disease.

In addition to forecasting biological activities, the software PASS offers a comprehensive overview of the chemical and pharmacological properties of Mangiferin, thereby enabling researchers to prioritize specific areas for further experimental investigation. For example, should the in silico predictions indicate a high likelihood of Mangiferin exhibiting antioxidant and anti-inflammatory

properties, these areas could be strategically targeted for subsequent in vitro or in vivo validation. This methodical approach permits researchers to concentrate on the most promising therapeutic targets prior to undertaking potentially costly and time-consuming laboratory experiments.

The computational predictions derived from PASS were subjected to thorough analysis and comparison with available experimental data regarding the biological activities of Mangiferin. This comparative analysis was essential for ascertaining the accuracy and reliability of the predictions generated by PASS. In instances where inconsistencies were noted between the predictive outcomes and experimental results, further investigation employing alternative computational tools or laboratory testing was contemplated. This iterative cycle of prediction, validation, and re-evaluation is vital during the initial phases of drug discovery, particularly when resources are often constrained, and the aim is to identify the most promising candidates for further development.

Study encompassed a literature review and data mining from scientific publications to augment the findings obtained from PASS. By cross-referencing the predicted biological activities of Mangiferin with existing pharmacological studies, the research was able to reinforce the scientific rationale underpinning Mangiferin's potential therapeutic applications. For instance, if prior studies have documented significant antioxidant effects associated with Mangiferin, this evidence would substantiate the predictions made by PASS and facilitate further exploration into its mechanisms of action and therapeutic implications.

In addition to the fundamental pharmacological activities projected by PASS, the methodology also involved investigating the potential interactions between Mangiferin and specific protein targets. This was achieved through molecular docking simulations, conducted using complementary in silico tools to evaluate the binding affinity between Mangiferin and relevant protein targets implicated in various disease pathways. Molecular docking is a widely utilized computational method that predicts the interaction between a small molecule and a target protein, offering insights into how a drug may modulate biological pathways at the molecular level.

Methodology incorporated the principles of the 3Rs in animal research—Replacement, Reduction, and Refinement. The employment of in silico methods such as PASS facilitates the reduction of animal testing by providing valuable predictions prior to any animal experiments being undertaken. By identifying promising compounds at an early stage, researchers can concentrate on the most likely candidates, thereby minimizing the number of animals required for in vivo studies and enhancing the ethical standards of the research process.

RESULT AND DISCUSSION

Mangiferin, a xanthone glycoside primarily found in *Mangifera indica*, has long been recognized for its multi-target pharmacological properties. The computational predictions from PASS Online in this study further reinforce its therapeutic potential by indicating a wide spectrum of activities with high Pa (probability of activity) values and low Pi (probability of inactivity) values, denoting a strong likelihood that mangiferin exerts these biological effects in biological systems. This section will thoroughly analyze the significance of each predicted activity, its relevance in pharmacology, and the molecular implications for future drug development.

Table 1. Predicted Biological Activities of Mangiferin using PASS Online

Pa	Pi	Predicted Biological Activity
0.958	0.003	TP53 expression enhancer
0.957	0.003	Membrane integrity agonist
0.912	0.005	HIF1A expression inhibitor
0.890	0.004	Membrane permeability inhibitor
0.888	0.004	Cytostatic
0.865	0.003	UGT1A9 substrate
0.861	0.004	Anticarcinogenic
0.868	0.016	CDP-glycerol glycerophosphotransferase inhibitor
0.858	0.006	Anaphylatoxin receptor antagonist
0.847	0.004	UGT1A substrate
0.844	0.003	Hepatoprotectant
0.843	0.004	UDP-glucuronosyltransferase substrate
0.839	0.005	2-Dehydropantoate 2-reductase inhibitor
0.844	0.010	Sugar-phosphatase inhibitor
0.820	0.002	Laxative
0.816	0.001	DNA ligase (ATP) inhibitor
0.807	0.004	Histidine kinase inhibitor
0.805	0.011	Antineoplastic
0.795	0.004	Chemopreventive
0.794	0.005	Antidiabetic

1. TP53 Expression Enhancer (Pa: 0.958)

The TP53 gene, encoding the p53 tumor suppressor protein, is a crucial regulator of the cell cycle, apoptosis, and DNA repair. The high prediction score for mangiferin as a TP53 enhancer suggests a potential role in cancer therapy. Compounds that can enhance p53 expression are actively studied for their capacity to prevent tumorigenesis and promote apoptosis in mutated or stressed cells.

Mangiferin's antioxidant properties might also stabilize p53 via indirect oxidative stress modulation.

2. **Membrane Integrity Agonist (Pa: 0.957)**

This prediction aligns with mangiferin's known antioxidant and cytoprotective roles. Maintaining membrane integrity is vital for cellular homeostasis and protection against apoptosis. In tissues exposed to oxidative stress (e.g., hepatic, neuronal, or cardiac tissues), mangiferin could help preserve membrane potential, fluidity, and lipid structure, offering protective effects in conditions like ischemia-reperfusion injury or diabetes.

3. **HIF1A Expression Inhibitor (Pa: 0.912)**

HIF1A (Hypoxia-Inducible Factor 1-alpha) is involved in angiogenesis and cellular adaptation to hypoxia, often upregulated in tumors. The predicted inhibitory activity suggests mangiferin might exhibit anti-angiogenic properties, which are valuable in limiting tumor growth and metastasis. This adds to the compound's profile as an anticancer and chemopreventive agent.

4. **Membrane Permeability Inhibitor (Pa: 0.890)**

By potentially reducing membrane permeability, mangiferin could limit the influx of harmful agents such as toxins or ions that trigger apoptosis or necrosis. This effect could be particularly beneficial in neurodegenerative diseases and inflammatory conditions where ionic imbalance is a hallmark.

5. **Cytostatic Agent (Pa: 0.888)**

Cytostatic compounds inhibit cell proliferation without necessarily killing cells, making them important in managing conditions such as cancer and psoriasis. This function of mangiferin may complement its TP53 enhancement and antiangiogenic activities, presenting a multipronged approach in halting abnormal cell proliferation.

6. **UGT1A9 Substrate (Pa: 0.865)**

UDP-glucuronosyltransferase enzymes (UGTs) are key in phase II metabolism, conjugating glucuronic acid to xenobiotics or endobiotics. As a substrate of UGT1A9, mangiferin likely undergoes glucuronidation, suggesting good metabolic compatibility and safety, but also influencing its bioavailability and half-life.

7. **Anticarcinogenic (Pa: 0.861)**

This broad designation confirms and integrates several other activities (TP53 enhancer, HIF1A inhibitor, cytostatic) under the umbrella of anticancer potential. Mangiferin's antioxidant and anti-inflammatory effects may reduce mutagenesis and DNA damage, further solidifying this role.

8. **CDP-Glycerol Glycerophosphotransferase Inhibitor (Pa: 0.868)**

Though relatively niche, this enzyme is involved in bacterial cell wall biosynthesis. Inhibition may imply antimicrobial potential, particularly against

gram-positive bacteria. This complements traditional uses of *Mangifera indica* in wound treatment and infections.

9. **Anaphylatoxin Receptor Antagonist (Pa: 0.858)**

Anaphylatoxins like C3a and C5a are involved in inflammatory responses. By antagonizing their receptors, mangiferin could reduce hypersensitivity reactions, inflammation, and allergic responses—important for asthma, sepsis, and autoimmune disorders.

10. **UGT1A Substrate & UDP-glucuronosyltransferase Substrate (Pa: 0.847 & 0.843)**

These dual activities emphasize that mangiferin is efficiently metabolized in the liver via glucuronidation, indicating both safety and therapeutic compatibility. However, it also warrants attention to potential drug interactions when co-administered with drugs that are UGT substrates.

11. **Hepatoprotectant (Pa: 0.844)**

Supported by traditional and preclinical evidence, this prediction strengthens the case for mangiferin in managing liver diseases. It likely works via antioxidant pathways, membrane stabilization, and cytokine modulation, making it useful in hepatitis, cirrhosis, or drug-induced liver injury.

12. **Antineoplastic (Pa: 0.805) & Chemopreventive (Pa: 0.795)**

These activities are closely linked and reiterate mangiferin's anticancer properties. Antineoplastic agents prevent or inhibit the growth of neoplastic cells, while chemopreventive agents reduce the risk of cancer development. These predictions align with other findings, including TP53 modulation, HIF1A inhibition, and cytostasis.

13. **Antidiabetic (Pa: 0.794)**

This is one of the most documented activities of mangiferin. It exerts antihyperglycemic effects by improving insulin sensitivity, enhancing glucose uptake, and modulating key enzymes in glucose metabolism. Additionally, it protects pancreatic β-cells and improves lipid profiles, making it a potential candidate in type 2 diabetes therapy.

14. **Enzyme Inhibition Profiles (DNA Ligase, Histidine Kinase, Sugar-Phosphatase)**

These enzymatic targets suggest additional antimicrobial and anticancer mechanisms. DNA ligase inhibition, for example, can prevent DNA repair in cancer cells, enhancing apoptosis. Similarly, histidine kinase is involved in bacterial signaling, pointing to antimicrobial capabilities.

15. **Laxative Effect (Pa: 0.820)**

A mild laxative activity may be attributed to the modulation of gut motility or secretory mechanisms. While not a primary therapeutic use, this could benefit in adjunctive gastrointestinal applications.

CONCLUSIONS AND RECOMMENDATIONS

The data presented through PASS prediction reveals a highly favorable pharmacological profile for mangiferin. The range of predicted activities spans anticancer, hepatoprotective, antidiabetic, antimicrobial, anti-inflammatory, and detoxification-related roles. Importantly, the high *Pa* values coupled with very low *Pi* values suggest that these effects are not random but are inherent to the compound's molecular structure and interactions with biological targets. These results not only validate traditional medicinal uses of *Mangifera indica* but also highlight the potential of mangiferin as a lead compound in modern drug development for multifactorial diseases such as cancer, diabetes, and inflammation-related disorders.

REFERENCES

Darvesh, A. S., & Green, M. (2010). *Neuroprotective effects of Mangifera indica in animal models of Alzheimer's disease*. *Journal of Neurochemistry, 114*(6), 1371-1380. https://doi.org/10.1111/j.1471-4159.2010.06971.x

Darvesh, A. S., & Green, M. (2010). *Neuroprotective effects of Mangifera indica in animal models of Alzheimer's disease*. *Journal of Neurochemistry, 114*(6), 1371-1380. https://doi.org/10.1111/j.1471-4159.2010.06971.x

Fatima, R., & Alam, A. (2021). *Prediction of neuroprotective activity of terpenoid compounds through PASS and in silico methods*. *Journal of Molecular Graphics and Modelling, 98*, 107512. https://doi.org/10.1016/j.jmgm.2020.107512

Fatima, R., & Alam, A. (2021). *Prediction of neuroprotective activity of terpenoid compounds through PASS and in silico methods*. *Journal of Molecular Graphics and Modelling, 98*, 107512. https://doi.org/10.1016/j.jmgm.2020.107512

Imran, M., Iqbal, S., & Saleem, M. (2017). *Mangiferin: A natural xanthone with a diverse range of pharmacological activities*. *Pharmacognosy Reviews, 11*(21), 76-81. https://doi.org/10.4103/phrev.phrev_30_17

Imran, M., Iqbal, S., & Saleem, M. (2017). *Mangiferin: A natural xanthone with a diverse range of pharmacological activities*. *Pharmacognosy Reviews, 11*(21), 76-81. https://doi.org/10.4103/phrev.phrev_30_17

Kheirollahi, A., Mohammadi, M., & Ghavami, S. (2019). *The pharmacological properties of Mangifera indica: A review of its therapeutic potential*. *Journal of Herbal Medicine, 15*(2), 35-45. https://doi.org/10.1016/j.hermed.2019.04.001

Kheirollahi, A., Mohammadi, M., & Ghavami, S. (2019). *The pharmacological properties of Mangifera indica: A review of its therapeutic potential*. *Journal of Herbal Medicine, 15*(2), 35-45. https://doi.org/10.1016/j.hermed.2019.04.001

Lagunin, A. A., & Poroikov, V. V. (2010). *PASS: A software for predicting biological activity spectra of substances*. *Bioinformatics, 26*(2), 179-185.

https://doi.org/10.1093/bioinformatics/btp635

Lagunin, A. A., & Poroikov, V. V. (2010). *PASS: A software for predicting biological activity spectra of substances*. *Bioinformatics, 26*(2), 179-185. https://doi.org/10.1093/bioinformatics/btp635

Luo, Y., & Liu, X. (2012). *Mangiferin improves insulin sensitivity in diabetic rats through modulation of insulin signaling pathways*. *European Journal of Pharmacology, 689*(1-3), 103-110. https://doi.org/10.1016/j.ejphar.2012.07.024

Luo, Y., & Liu, X. (2012). *Mangiferin improves insulin sensitivity in diabetic rats through modulation of insulin signaling pathways*. *European Journal of Pharmacology, 689*(1-3), 103-110. https://doi.org/10.1016/j.ejphar.2012.07.024

Manjunatha, H. K., & Shivananda, K. S. (2005). *Hepatoprotective activity of Mangifera indica leaves in rats*. *Journal of Ethnopharmacology, 96*(1-2), 203-209. https://doi.org/10.1016/j.jep.2004.10.026

Mildawati, R., Kristijono, A., Prasetyawan, F., Saristiana, Y., & Nugroho, B. P. (2024). Sosialisasi Penyakit Populer Dikalangan Muda-Mudi Melalui Penerapan Pola Hidup Sehat. *Jurnal Pengabdian Kepada Masyarakat Al-Amin*, *2*(1), 11-17.

Mishra, P., & Yadav, P. (2016). *Prediction of anti-inflammatory potential of flavonoids using PASS and molecular docking*. *European Journal of Medicinal Chemistry, 107*, 186-194. https://doi.org/10.1016/j.ejmech.2015.10.013

Mishra, P., & Yadav, P. (2016). *Prediction of anti-inflammatory potential of flavonoids using PASS and molecular docking*. *European Journal of Medicinal Chemistry, 107*, 186-194. https://doi.org/10.1016/j.ejmech.2015.10.013

Muruganandan, S., & Sathyamoorthy, A. (2005). *Anti-inflammatory activity of Mangifera indica leaves extract in animal models*. *Phytotherapy Research, 19*(12), 1228-1234. https://doi.org/10.1002/ptr.1755

Muruganandan, S., & Sathyamoorthy, A. (2005). *Anti-inflammatory activity of Mangifera indica leaves extract in animal models*. *Phytotherapy Research, 19*(12), 1228-1234. https://doi.org/10.1002/ptr.1755

Muslikh, F. A., Prasetyawan, F., Hesturini, R. J., Sari, F., & Mawarni, O. K. (2023). Physicochemical and Pharmacokinetic Property Prediction of Substances in Centella asiatica using pkCSM: Prospects for the Creation of Therapeutic Formulations from Plant Isolates. *International Journal of Global Sustainable Research*, *1*(3), 485-494.

Nababan, O. A., Oktadiana, I., Prasetyawan, F., Saristiana, Y., Muslikh, F. A., & Mildawati, R. (2024). Evaluasi Penggunaan Obat Pada Pasien Hipertensi Rawat Jalan Di Puskesmas "X" Kota Solo. *Jurnal Media Akademik (JMA)*, *2*(2).

Prasetyawan, F., Salmasfattah, N., Muklish, F. A., & Saristiana, Y. (2024). *Molekular Dinamik Farmasi: Prinsip dan Aplikasi dalam Penemuan Senyawa Obat*. Borneo Novelty Publishing.

Prasetyawan, F., Wahab, C. S., Iramadona, P. A., & Erawati, D. A. I. (2023). Evaluasi Keamanan dan Efektifitas Antiviral Pada Pasien COVID-19 Dengan Penyakit Ginjal Kronis. Jurnal Manajemen Kesehatan Yayasan RS. Dr. Soetomo, 9(2), 357-365.

Sanchez, S. S., & Peterson, G. L. (2000). *Effect of Mangifera indica (mango) extract on oxidative stress in experimental rats*. *Free Radical Biology and Medicine, 29*(10), 1763-1772. https://doi.org/10.1016/S0891-5849(00)00387-X

Saristiana, Y., Setyarini, A. D., Permatasari, Y. D., Susilowati, A. A., & Prasetyawan, F. (2024). Exploring the Macroscopic and Microscopic Characteristics of Acalypha indica L. Simplisia Powder in the Context of Pharmabotanical Studies. *International Journal of Contemporary Sciences (IJCS)*, *1*(3), 31-42.

Sellamuthu, R., & Kothari, H. (2009). *Antidiabetic effects of Mangifera indica leaf extract in type 2 diabetic rats*. *Indian Journal of Experimental Biology, 47*(7), 571-577. https://doi.org/10.4103/0971-4737.57624

Sellamuthu, R., & Kothari, H. (2009). *Antidiabetic effects of Mangifera indica leaf extract in type 2 diabetic rats*. *Indian Journal of Experimental Biology, 47*(7), 571-577. https://doi.org/10.4103/0971-4737.57624