BUKTI KORESPONDENSI

ARTIKEL JURNAL NASIONAL TERAKREDITASI SINTA 2

Judul Artikel : Multi-Target Potential of Moringa oleifera-Derived Compounds against cariogenic and Endodontic Virulence Proteins by Molecular Docking Analysis Reveals

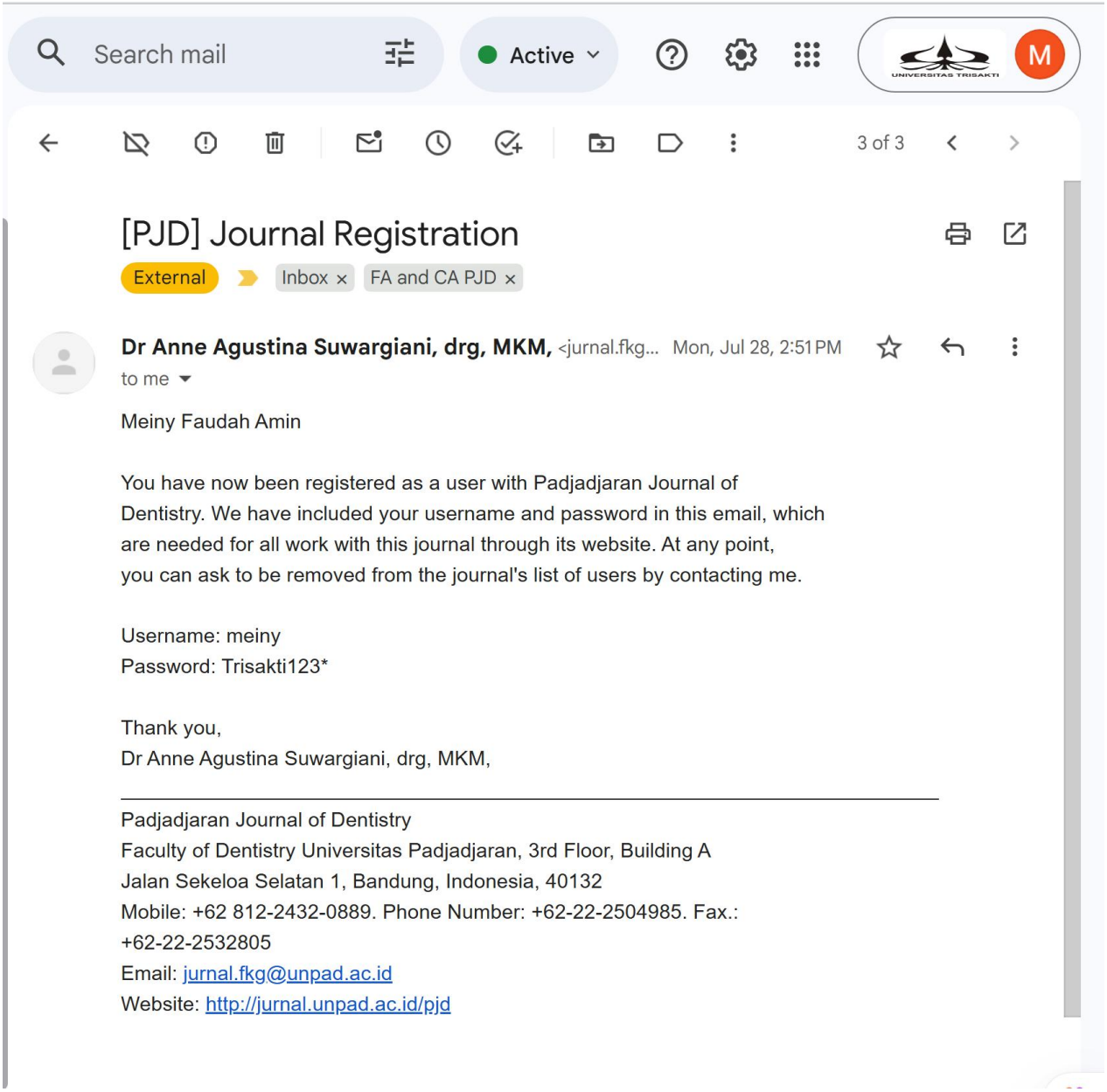
Jurnal : Padjadjaran Journal of Dentistry

Penulis : **Meiny Faudah Amin**, Dikdik Kurnia, Taufiq Ariwibowo, Dicky Hardy

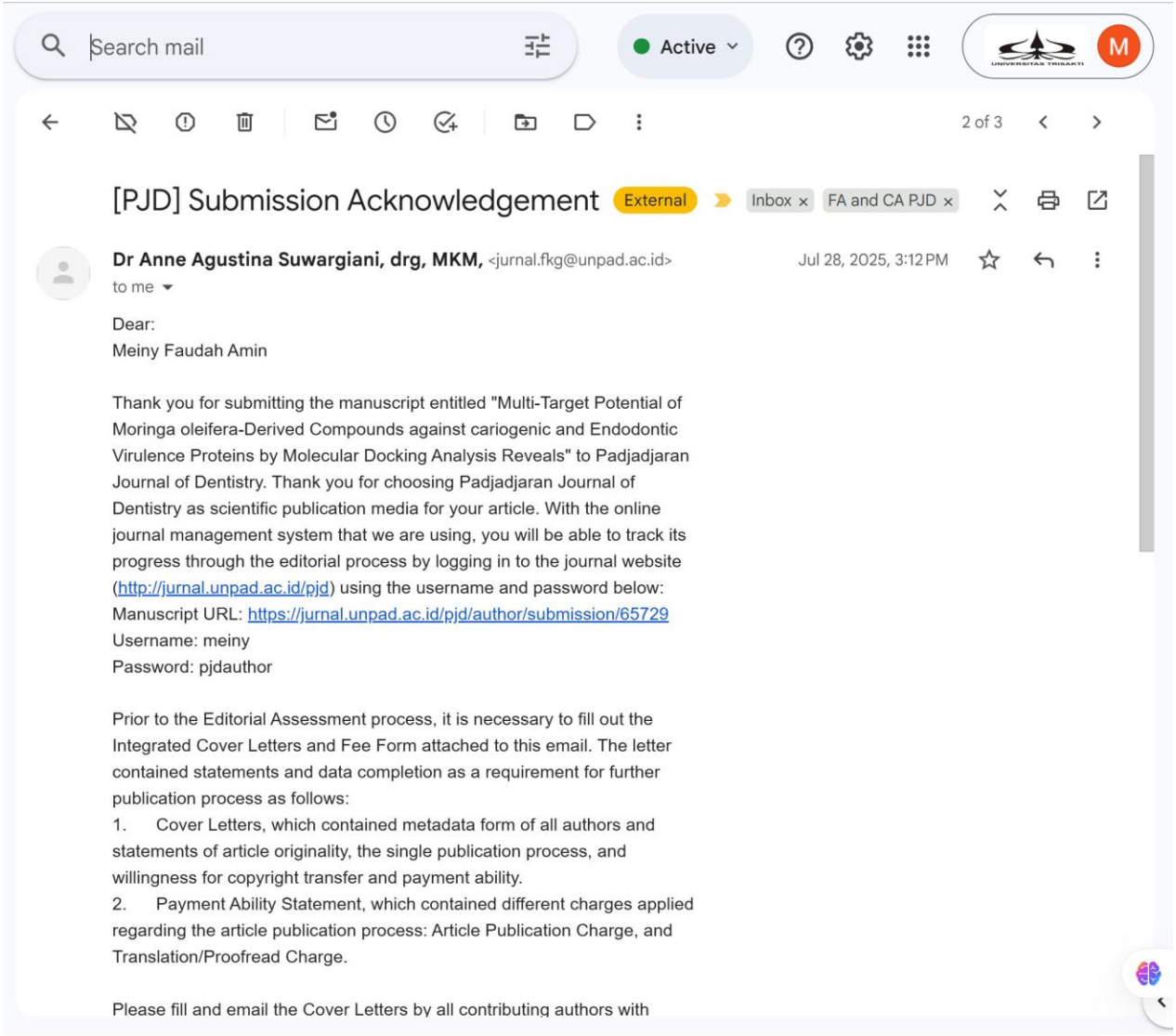
No	Perihal	Tanggal
1	Bukti registrasi sebagai penulis	28 Juli 2025
2	Bukti konfirmasi submit manuskrip diterima	28 Juli 2025
3	Bukti manuskrip dalam status review oleh reviewer	02 Desember 2025
4	Bukti komunikasi pertanyaan dan jawaban dengan reviewer	02 Desember 2025
5	Bukti surat manuskrip diterima	30 Maret 2026
6	Bukti publikasi	31 Maret 2026

1. Bukti registrasi sebagai penulis

28 Juli 2025


Search mail
Active
3 of 3
[PJD] Journal Registration
External
Inbox ×
FA and CA PJD ×
Dr Anne Agustina Suwargiani, drg, MKM, <jurnal.fkg... Mon, Jul 28, 2:51 PM
to me
Meiny Faudah Amin
You have now been registered as a user with Padjadjaran Journal of Dentistry. We have included your username and password in this email, which are needed for all work with this journal through its website. At any point, you can ask to be removed from the journal's list of users by contacting me.
Username: meiny
Password: Trisakti123*
Thank you,
Dr Anne Agustina Suwargiani, drg, MKM,
Padjadjaran Journal of Dentistry
Faculty of Dentistry Universitas Padjadjaran, 3rd Floor, Building A
Jalan Sekeloa Selatan 1, Bandung, Indonesia, 40132
Mobile: +62 812-2432-0889. Phone Number: +62-22-2504985. Fax.: +62-22-2532805
Email: jurnal.fkg@unpad.ac.id
Website: http://jurnal.unpad.ac.id/pjd

2. Bukti konfirmasi submit manuskrip diterima 28 Juli 2025


Search mail
Active
2 of 3
[PJD] Submission Acknowledgement
External
Inbox ×
FA and CA PJD ×
Dr Anne Agustina Suwargiani, drg, MKM, <jurnal.fkg@unpad.ac.id>
Jul 28, 2025, 3:12 PM
to me
Dear:
Meiny Faudah Amin
Thank you for submitting the manuscript entitled "Multi-Target Potential of Moringa oleifera-Derived Compounds against cariogenic and Endodontic Virulence Proteins by Molecular Docking Analysis Reveals" to Padjadjaran Journal of Dentistry. Thank you for choosing Padjadjaran Journal of Dentistry as scientific publication media for your article. With the online journal management system that we are using, you will be able to track its progress through the editorial process by logging in to the journal website (http://jurnal.unpad.ac.id/pjd) using the username and password below:
Manuscript URL: https://jurnal.unpad.ac.id/pjd/author/submission/65729
Username: meiny
Password: pjdauthor
Prior to the Editorial Assessment process, it is necessary to fill out the Integrated Cover Letters and Fee Form attached to this email. The letter contained statements and data completion as a requirement for further publication process as follows:
1. Cover Letters, which contained metadata form of all authors and statements of article originality, the single publication process, and willingness for copyright transfer and payment ability.
2. Payment Ability Statement, which contained different charges applied regarding the article publication process: Article Publication Charge, and Translation/Proofread Charge.
Please fill and email the Cover Letters by all contributing authors with

3. Bukti manuskrip dalam status review
02 Desember 2025

PADJADJARAN JOURNAL OF DENTISTRY
p-ISSN : 1979-0201 e-ISSN : 2549-6212
In affiliation with Indonesia Dental Association
Published by Universitas Padjadjaran Faculty of Dentistry

#65729 Review

Submission

Authors	Meiny Faudah Amin, Dikdik Kurnia, Taufiq Ariwibowo, Dicky Hardi
Title	Multi-Target Potential of Moringa oleifera-Derived Compounds against cariogenic and Endodontic Virulence Proteins by Molecular Docking Analysis Reveals
Section	Articles
Editor	Felisha Balafif, drg., M.Kes. Indah Wahyuni, drg., Sp.PM(K) Prof.Dr Dudi Aripin, drg, SpKG, SubspKR(K) Dr Anne Suwargiani, drg, MKM Prof. Dr. Nina Djustiana, drg, MKes drg. Muhammad Firdausy, M.Sc (DMS)

Peer Review

Round 1

Review Version	65729-259032-1-RV.DOCX 2025-07-28
Initiated	2025-11-06
Last modified	2025-12-02
Uploaded file	None

Editor Decision

Decision	Revisions Required 2025-12-02
Notify Editor	Editor/Author Email Record 2025-12-02
Editor Version	65729-262642-1-ED.DOCX 2025-08-25 65729-262642-2-ED.DOCX 2025-12-02
Author Version	None
Upload Author Version	Choose File No file chosen Upload

4. Bukti komunikasi pertanyaan dan jawaban dengan reviewer 02 Desember 2025

ORIGINAL ARTICLE

Multi-Target Potential of *Moringa oleifera*-Derived Compounds against cariogenic and Endodontic Virulence Proteins by Molecular Docking Analysis Reveals: Research Article

Meiny Faudah Amin[1]
Okdi Kurnia[2]
Taufiq Ariwibowo[1]
Dicky Hardi[1]

[1] Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti, Jakarta Barat, Indonesia
[2] Department of Chemistry, Faculty of Mathematics, and Natural Sciences, Universitas Padjadjaran, Sumedang, Indonesia

* Correspondence:
meiny.faudah@trisakti.ac.id

Received: ** month 20**
Revised: ** month 20 **
Accepted: ** month 20**;
Published: ** month 20**
DOI: 10.4***/ojd.***

p-ISSN 1979-0201
e-ISSN 2549-6212

Citation:
Last Name, First Names, Last Name, First Names, Article Title. Padj. J Dent, March. 20**; 35(*): 1-7.

ABSTRACT

Introduction: Dental infections, including cariogenic and endodontic conditions, are multifactorial diseases, including bacterial adherence, biofilm formation, and tissue damage. Furthermore, genetics, as well as environmental and behavioral factors, influence disease onset, susceptibility, and progression rate. The progression of the disease and its clinical manifestations are caused by the interaction between the host immune system and the bacteria found in dental plaque. Potential substitutes for current antibiotics are being studied, including natural compounds with broad-spectrum antibacterial properties. *Moringa oleifera*, a medicinal plant that has long been used to treat systemic and oral diseases, is one of the natural sources. This study aimed to systematically evaluate the interaction profiles of four Moringa oleifera–derived compounds against multiple virulence-associated proteins of cariogenic and endodontic pathogens using in silico molecular docking. **Methods**: This study was conducted by molecular docking simulations to assess the binding energy of four *M. oleifera*-derived compounds-eugenol, trans-anethole, arachidonic acid, and phytosphingosine-to five important virulence-associated proteins from key cariogenic and endodontic pathogens of Cystalysin, SrpA, FimA, RadD, and DdI. AutoDock 4.0 was utilized in docking simulations. **Results**: Phytosphingosine-DdI exhibited the lowest binding energy of -7.42 kcal/mol, followed by eugenol with three different receptors-Cystalysin, SrpA, and FimA-and arachidonic acid-RadD. The lowest inhibition constant was shown by the phytosphingosine-DdI complex of 3.61 µM. Each compound interacted with various targets, but phytosphingosine exhibited the most consistent and widespread predicted binding via hydrogen bonds of Glu222, Arg291, Glu306, Asp293, Lys251, and hydrophobic interactions of Phe295, Phe245, Phe175, and Leu145. **Conclusion:** These findings demonstrate that phytosphingosine can disrupt multiple virulence processes, highlighting its potential as a supplementary therapeutic agent in conservative dentistry.

KEYWORDS

Molecular Docking, *Moringa oleifera*, Periodontitis, Cariogenic pathogens, Virulence factors

INTRODUCTION

An inflammatory condition caused by infection that affects the hard and soft tissues of the tooth—such as enamel, dentin, pulp, and periapical tissues—is characteristic of various dental diseases in the field of conservative dentistry, including cariogenic and endodontic infections[1]. Furthermore, the development of

Reviewer
The manuscript addresses a relevant topic and presents a clear multi-target molecular docking screen of four Moringa oleifera–derived compounds against five oral pathogen virulence proteins. The idea is sound and the docking
Meiny F Amin
Thank you for your helpful comments. We have revised the manuscript accordingly. Technical errors have been corrected, and additional methodological details—including docking parameters, validation steps, and
Reply

Reviewer
Add type of research
Meiny F Amin
Thank you for the suggestion. We have added the type of research
Reply

Reviewer
state the research objectives here;
Meiny F Amin
Thank you for the helpful comment. We have added a clear statement of the research objectives
Reply

Reviewer
Please make sure, this is for periodontitis or cariogenic or endodontics
Meiny F Amin
Thank you for the comment. We have clarified the disease focus in the revised manuscript. While most virulence proteins (Cystalysin, FimA, RadD, and SrpA) are derived from periodontitis-related pathogens, DdI
Reply

Reviewer

the disease, the exposure of vulnerable individuals to its onset, and the rate of advancement are all influenced by genetics as well as environmental and behavioral variables. Multiple factors contribute to the aetiology of periodontitis[2]. In a vulnerable host, subgingival dental biofilm triggers an inflammatory and immunological reaction that ultimately results in the irreversible destruction from dental tissue to the periodontium, which includes the alveolar bone and periodontal ligament[3]. Subgingival bacteria, their virulence factors, and host immunological responses combine intricately to cause irreversible damage, pulp necrosis and periodontitis, a multifactorial inflammatory disease. The formation of organized, multispecies biofilms and the coordination of diverse bacterial tactics to colonize, persist, and harm periodontal tissues are important aspects of disease progression[4].

These various virulence mechanisms are demonstrated by a number of proteins from common oral pathogens: RadD, an adhesin necessary for interspecies coaggregation and expressed by *Fusobacterium nucleatum*, links early and late colonizers in the dental plaque matrix to promote the production of complex biofilms[5]. The serine-rich repeat adhesin SrpA, which is produced by *Streptococcus sanguinis*, binds salivary glycoproteins and facilitates early bacterial adhesion to tooth surfaces and other microorganisms, starting the formation of biofilms[6]. To adhere to host epithelial cells, invade oral tissues, and co-aggregate with other pathogenic bacteria to sustain mature biofilms, *Porphyromonas gingivalis* utilizes FimA, a key fimbrial protein[7]. *Streptococcus mutans*' D-alanine: D-alanine ligase (Ddl) is a key enzyme in the biosynthesis of peptidoglycans, preserving the integrity of the bacterial cell wall, allowing for survival in the oral cavity's acidic and immunologically demanding environment, and indirectly promoting biofilm stability by preserving bacterial viability[8]. Finally, the PLP-dependent L-cysteine desulfhydrase Cystalysin, which is secreted by *Treponema denticola*, breaks down host cysteine to produce hydrogen sulfide and ammonia. These substances harm epithelial cells, disrupt tissue barriers, and trigger inflammatory responses that contribute to the degradation of dental and surrounding oral tissues[9].

More research is being conducted on natural substances with broad-spectrum antimicrobial activities as potential substitutes for existing antibiotics, particularly those that target bacterial virulence rather than viability. Promising candidates include phytosphingosine, arachidonic acid, trans-anethole, and eugenol-bioactive compounds that have been shown to have antibacterial, anti-inflammatory, and biofilm-disrupting qualities[10-13]. The structures of the compound were presented in **Figures 1**. However, *Moringa oleifera*, a medicinal plant that has long been used to treat systemic and oral infections, contains all four of these compounds[14, 15]. All the compounds were found in the extract based on the data of the extract's LC-MS analysis. The application of compounds produced from *M. oleifera* is consistent with new approaches to managing periodontitis, which seek to reduce the development of antibiotic resistance while interfering with bacterial virulence factors and biofilm formation[16, 17].

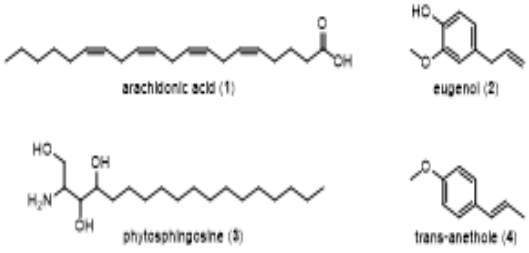


Figure 1. Structure of *Moringa oleifera* derived compounds

Reviewer

Please complete it, for an example you can see the previous PJD publication

Mainy F Amin

Thank you, we have added it

Comprehensive studies assessing the efficacy of natural compounds against key virulence factors involved in cariogenic and endodontic infections remain limited, despite growing interest in these compounds as alternative antimicrobial agents. Four compounds derived from *M. oleifera*, eugenol, *trans*-anethole, arachidonic acid, and phytosphingosine, are evaluated simultaneously against a selected group of five virulence-associated proteins from major oral bacteria. These proteins of Cystalysin, FimA, Ddl, SrpA, and RadD represent various mechanisms of adhesion, biofilm formation, cell survival, and tissue destruction.

The novelty of this study lies in the simultaneous multi-target evaluation of these four natural compounds against virulence-related proteins, an approach that has not been reported previously. This study aims to ascertain the binding affinities and predict the interaction profiles of these natural compounds, identify the compounds with the strongest potential to inhibit multiple virulence targets, and provide computational evidence supporting further exploration of M. oleifera constituents as adjuvant agents in the prevention and treatment of periodontitis using molecular docking simulations.

METHODS

The *in silico* method was employed to conduct the research, which involved molecular docking simulations to determine the molecular activity of each compound towards specified receptors. The three-dimensional structures of each receptor were obtained from the RCSB Protein Data Bank website (https://www.rcsb.org/). This study used five receptors: Cystalysin (PDB ID: 1C7O), SrpA (PDB ID: 5EQ3), FimA (PDB ID: 6JZK), RadD (PDB ID: 7R7J), and Ddl (PDB ID: 7U9K). Two reference ligands were used for each target protein: the native ligand and a positive control. The native ligand refers to the biological ligand that was crystallized together with the protein in the PDB structure, representing the natural binding conformation within the active site. The positive control refers to an inhibitor or compound that has been previously reported to interact with the corresponding target protein, and is included to provide a reference for comparison with the docking performance of the tested phytochemical compounds. L-arginine for RadD, D-glycoserine for Cystalisin and Ddl, Neu5Gc for SrpA and GalNAc for FimA were the three positive controls utilized in this study. All of the structures were obtained from PubChem with CIDs 67427, 440001, 6234, and 35717. Four compounds-arachidonic acid, eugenol, phytosphingosine, and *trans*-anethole-found in *M. oleifera* were examined for their capacity to interfere with virulence factors of periodontitis. The structures of arachidonic acid, eugenol, phytosphingosine, and *trans*-anethole were obtained from the PubChem website (https://pubchem.ncbi.nlm.nih.gov/) with CIDs of 444899, 3314, 122121, and 637563, respectively. After downloading each ligand structure in SDF format, they were all converted to pdb format and optimized using Chem3D Ultra 12.0's MM2 energy minimizer. To validate the docking protocol, we re-docked each original ligand to its respective protein binding site after removing it from the original crystal structure. The root mean square deviation (RMSD) between the docking pose and the crystallographic pose was calculated to assess the reliability of the docking setup. An RMSD value < 3.0 Å was considered acceptable, indicating that the selected docking parameters were able to accurately reproduce the experimentally observed binding conformation. The RMSD re-docking values are obtained in **Tabel 1 and Figure 2**.

Table 1. Grid center coordinates for each receptor

Receptor's name	PDB ID	Positive Control	Grid Center (coordinates)			RMSD
			x	y	z	
Cystalysin	1C7O	D-glycoserine	14.561	-4.847	20.75	2.167
SrpA	5EQ3	Neu5Gc	15.260	11.538	0.568	2.436
FimA	6JZK	GalNAc	1.287	-3.755	93.097	3.102

Reviewer
The Introduction should clearly identify the novelty of this research (e.g., "The novelty of this research lies in..."), explaining how it contributes new insights or
Mainy F Amin
Thank you for the valuable feedback. We have revised the Introduction accordingly. The updated version now clearly states the novelty of this research by explicitly describing how our multi-target molecular docking
Reply

Reviewer
The manuscript mixes "native ligand" and "positive control" terms. Define each and explain selection (e.g., D-cycloserine for Ddl, GalNAc for FimA). Show reDocking RMSD of native ligand to validate docking setup and report
Mainy F Amin
Thank you for this valuable comment. We have performed the re-docking validation for all native ligands. Most ligands produced RMSD values below 2.0 Å, indicating good agreement with the
Reply

Reviewer
Please add the positive control for SrpA.
Mainy F Amin
Thank you for the comment. The positive control for SrpA has been added.
Reply

Reviewer
Please check again. The grid center for Cystalysin lists y = -4847 which is almost certainly a typographical or copy paste error. Verify and correct all grid center coordinates and units (Å). Report the grid box origin consistently with

RadD	7R7J	L-Arginine	-6.627	-37.876	107.279	3.097
Ddl	7U9K	D-alvcoserine	7.923	20.387	27.732	1.159

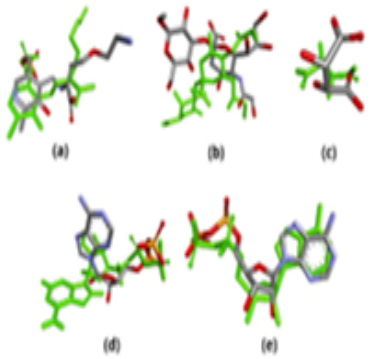


Figure 2. Re-docking conformation for (a) Cystalysin, (b) SrpA, (c) FimA, (d) RadD, and (e) Ddl.

The AutoDock 4.0 application was used to carry out the molecular docking simulations. Every receptor and ligand in PDB format was converted to pdbqt format before the simulations commenced. For every receptor, a 40 Å x 40 Å x 40 Å grid box was applied, featuring specific x, y, and z coordinates of the grid center. Each receptor's coordinates were provided in **Table 1**. All of the receptors were subjected to a 0.375 Å spacing. The binding energy and inhibition constant for every receptor-ligand complex were analyzed. Using Discovery Studio 2020, each receptor-ligand complex's interaction was examined and illustrated. A graphic was created to illustrate the hydrophobic and hydrogen bonding interactions of receptor-ligand interactions.

RESULTS

The four compounds derived from *M. oleifera* showed different affinities for the five target proteins according to molecular docking simulations. The lowest (i.e., strongest) binding energies were typically displayed by the native ligands, with RadD (-8.27 kcal/mol) and Ddl (-8.94 kcal/mol) being especially remarkable. Eugenol showed consistently favorable binding energies across the majority of targets among the investigated natural compounds (-5.64 to -3.46 kcal/mol), followed by *trans*-anethole (-5.17 to -3.61 kcal/mol) and arachidonic acid (-5.13 to -1.73 kcal/mol). The most deprived binding was found for phytosphingosine, particularly with FimA (-1.74 kcal/mol) and SrpA (-2.68 kcal/mol). Positive controls demonstrated varied binding, with RadD (-2.78 kcal/mol) performing least favorably and Ddl (-6.09 kcal/mol) performing the best. Similar patterns were seen in calculated inhibition constants. Across all targets, the compounds showed Ki values in the nanomolar to millimolar range; native ligand binding to RadD (0.89 $x10^{-3}$ µM or 890 nM) and Ddl (0.28 $x10^{-3}$ µM) had the lowest (strongest) Ki. However, the Ki values of the compounds were higher (weaker) than those of their respective positive controls for a number of targets, particularly SrpA and FimA. $54.29x10^{3}$ µM or 54.29 mM for arachidonic acid binding to SrpA and $53.30x10^{3}$ µM for phytosphingosine binding to FimA. The inhibition constants of each complex ligand and receptor were presented in **Table 2**.

Table 2. Molecular docking summary for all ligand–target pairs

Target	Ligand	ΔG	Ki	hydrogen bonds	hydrophobic interactions
Cystalysin	Native	-6.78	10.76	Val88, Ala243, Tyr123, Ser237, Cys171, Lys238	-
	Positive control	-5.21	150.55	Arg369, Tyr124, Asp355, Ala39	-

Reviewer
Please add information in detail:
• State AutoDock Vina version and exact command / exhaustiveness used.
• Describe receptor preparation steps: how were missing

Mainy F Amin
Thank you for the comment
- In our study, we did not use AutoDock Vina; instead, the docking simulations were performed using AutoDock 4.0. Therefore, the Vina version and

Reply

Missing content
This comment thread contains content that's not yet supported. Select it to view it in the Revisions pane.

Reviewer
Please Reformat Tables 2–5 to include one line per ligand–target pair with columns: ΔG (kcal·mol⁻¹), computed Ki (nM or µM), number H bonds, key interacting residues, and whether interactions overlap native ligand

Mainy F Amin
Thank you for the suggestion. Tables 2–5 have been reformatted as requested.

Reply

	Comp. (1)	-5.13	174.80	Lys238, Tyr123	Cys171, Val99, Val98, Ala39, His206, Ile205, Val38, Ala243
	Comp. (2)	-5.64	72.98	Lys238, Tyr123, His206	Ala39, Ile205
	Comp. (3)	-3.81	1620	Ala39, Tyr123, Tyr124	Val99, Val98, Ile205, His206, Lys238, Ala235
	Comp. (4)	-5.17	161.76	Ala39, Tyr123, Asp355, Tyr124	Ala39, Cys171, Ile205, His206
SrpA	Native	-6.36	21.70	Thr346, Gln344, Pro335, Tyr368, Arg367	Pro337, Arg342
	Positive control	-5.82	53.74	Arg342, Arg347, Thr346, Gln344, Tyr368, Ala343	-
	Comp. (1)	-1.73	54.20×10^3	Arg342	Pro337, Phe294
	Comp. (2)	-4.22	802.41	Arg347, Thr346	Phe345, Gln344
	Comp. (3)	-3.18	4.663×10^3	Gln344, Arg347,Thr346	Phe348, Pro347, Arg342
	Comp. (4)	-3.78	1.69×10^3	Thr346	Arg342, Gln344
FimA	Native	-4.96	230.57	Lys59, Thr61, Ser75, Met103	-
	Positive control	-4.73	343.084	Gly101, Ala102, Met103, Leu105, Val106	-
	Comp. (1)	-3.97	1230	Lys59, Ser75	Lys108, Val106, Leu105
	Comp. (2)	-4.19	843.62	Met103	Ile73, Leu105
	Comp. (3)	-1.74	53.30×10^3	Glu104. Val106	Ile73. Leu105
	Comp. (4)	-4.04	1090	Ser75	Leu105, Val106, Ile73
RadD	Native	-8.27	0.89×10^{-3}	Arg343, Arg6, Tyr105, Gly36, Gly34, Ala35, Thr33	Arg343, Leu344
	Positive control	-2.78	9230	Asp315, Tyr105, Gly34, Arg6	-
	Comp. (1)	-4.65	390.63	Lys37, Thr33	Lys68, Arg6, Leu39, Leu72
	Comp. (2)	-4.00	1170	Gly36, Lys37	Ala35
	Comp. (3)	-2.67	11.12×10^3	Gly36, Arg6, Tyr105, Leu344	Leu39, Leu72, Ala71, Lys37, Lys68
	Comp. (4)	-4.42	579.42	Gly34, Pro32	Leu39, Leu72, Lys68, Lys37, Ala35
Ddl	Native	-8.94	0.28×10^{-3}	Lys130, Asn305, Glu213, Val216, Gln214, Glu220, Tyr246, Ser184, Gly182, Asn308, Ser183, Lys251	-
	Positive control	-6.09	34.60	Ile221, Phe294, Asn305, Glu222	-
	Comp. (1)	-6.52	16.49	Asn305	Leu143, Val216, Phe295, Phe175, Phe245, Ile187
	Comp. (2)	-5.40	109.80	Ala218, Ala244, Glu220	Phe295, Phe175, Leu145
	Comp. (3)	-7.42	3.61	Glu222, Arg291, Glu306, Asn293. Lys251	Phe295, Phe245, Phe175. Leu145
	Comp. (4)	-5.25	142.83	Phe245, Tyr246	Phe175, Phe295, Leu145

The *M. oleifera* compounds formed multiple hydrogen bonds across several targets, stabilizing their binding in active or binding sites. The native ligand-Ddl complex showed the most hydrogen bonds among other complexes, consisting of Lys130, Asn305, Glu213, Val216, Gln214, Glu220, Tyr246, Ser184, Gly182, Asn308, Ser183, and Lys251. Among the compounds, phytosphingosine formed strong hydrogen bonds, with phytosphingosine-Ddl presenting the most hydrogen bonds compared to other receptors, with residues Glu222, Arg291, Glu306, Asp293, and Lys251. Hydrophobic interactions were most abundant for arachidonic acid and phytosphingosine, which engaged numerous hydrophobic residues across targets, including Cys171, Val99, Val98, Ala39, His206, Ile205, Val38, Ala243 for arachidonic acid binding to Cystalysin and Val99, Val98, Ile205, His206, Lys238, and Ala235 for phytosphingosine binding to Cystalysin.

DISCUSSION

This study explores *Moringa oleifera*-derived compounds as potential multi-target inhibitors of key proteins involved in various stages of cariogenic and endodontic pathogenesis. Molecular docking and in-depth study of hydrogen bonding and hydrophobic interactions to determine how these compounds might interfere with adhesion-related receptors, enzymes required for bacterial survival,

Reviewer

Describe the results obtained from the research. The author compiles,
analyzes, evaluates and integrets and compares the latest findings with findings

Mainy F Amin

Thank you for the valuable comment. The Discussion section has now been thoroughly revised. We have expanded the paragraphs, added deeper analysis and interpretation of the findings

and factors that contribute to host tissue damage. The results offer new insights into the ability of *M. oleifera* compounds to disrupt multiple virulence mechanisms relevant to dental infection progression, highlighting their potential as supplementary agents in comprehensive conservative dental therapy[18, 19].

Interaction potential of four compounds derived from *Moringa oleifera* extract against key virulence-associated proteins of cariogenic and endodontic pathogens. Scoring functions are used by docking programs to estimate this binding energy[20]. A binding energy, a numerical depiction of the interaction between a ligand and a protein, can be estimated by molecular docking software. The sensitivity of various scoring functions to various kinds of interactions (such as hydrophobic and hydrogen bonding interactions) may vary. Higher binding affinities are generally indicated by lower (more negative) binding energies, which also imply a more stable and favorable interactions[21, 22]. According to the docking data, almost all test ligands form 2–4 hydrogen bonds, mainly with key residues such as Lys238, Tyr123, His206, Ala39, and Val99. These residues are part of the same binding pocket as the native ligand, so the interaction of the test ligand can be said to overlap with the physiological binding site. This overlap indicates that the ligand is able to inhibit the proteolytic activity of Cystalysin through direct competition with the natural ligand. The greater the number of H-bonds, the more stable the interaction, and this is consistent with the relatively low ΔG and Ki values[18].

In SrpA, the test ligands generally form 1–3 H-bonds, with important residues such as Lys340, Lys373, Asp434, Thr372, which are known to be located in the sialic-acid–binding groove of SrpA. When a ligand interacts with these residues, it indicates that the ligand is in the same location as native sialic acid, so the interaction can be said to be overlapping[23]. Ligands with lower ΔG (Compound **3** or **4**) also typically show stronger overlap, indicating potential as SrpA–sialoglycan adhesion inhibitors.

Ligands to FimA show the formation of 2–3 H-bonds with residues such as Lys59, Ser75, Glu70, Val105, which are residues corresponding to the native ligand interaction site (generally in the adhesin groove). When the test ligands bind to these residues, their interactions overlap with the native binding pocket[24], indicating that the ligands can block FimA adhesion. Some ligands also interact through hydrophobic contacts (Leu104, Ile73), enhancing the stability of the complex.

Meanwhile, RadD shows a very similar interaction pattern: ligands form 1–3 H-bonds mainly with Gly36, Arg45, Tyr195, Lys73, residues that are part of the RadD interaction domain. Most ligands show overlap with the native ligand binding site, especially if they interact with Arg and Lys, which are the main electrostatic residues in RadD. More negative ΔG values for some ligands indicate the potential of ligands to competitively disrupt the RadD adhesion mechanism[25].

In Ddl, ligands form 2–4 hydrogen bonds, mainly with active residues such as Glu223, Asp293, Lys251, Phe295. These residues are located in the catalytic pocket, so the interactions of the test ligands can be categorized as overlapping with the native active site of the ligand (*D*-alanine substrate). Ligands that interact with Glu223 or Lys251 usually have the greatest potential to inhibit the formation of D-Ala-D-Ala, which is critical for cell wall biosynthesis[26].

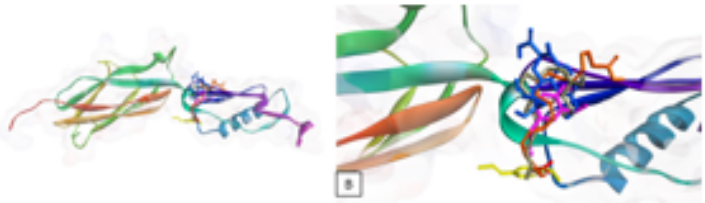


Figure 3. Conformations of the native ligand, *M. oleifera* compounds, and positive controls at SrpA (A), ligand conformational positioning receptor, and (B) Close-up view.

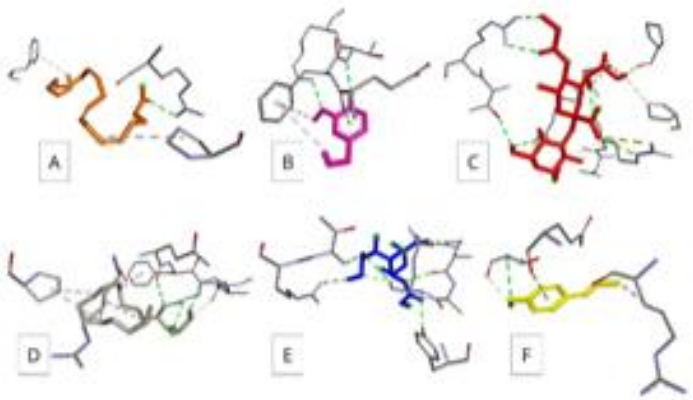


Figure 4. Molecular interactions of SrpA receptor with (A) Arachidonic acid, (B) eugenol, (C) native ligand, (D) phytosphingosine, (E) positive control, and (F) *trans*-anethole.

Figure 5. Conformations of the native ligand, *M. oleifera* compounds, and positive controls at Cystalysin (A), ligand conformational positioning receptor, and (B) Close-up view.

Figure 6. Molecular interactions of Cystalysin receptor with (A) Arachidonic acid, (B) eugenol, (C) native ligand, (D) phytosphingosine, (E) positive control, and (F) *trans*-Anethole.

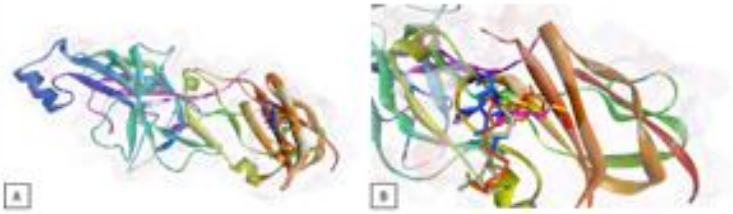


Figure 7. Conformations of the native ligand, *M. oleifera* compounds, and positive controls at FimA (A), ligand conformational positioning receptor, and (B) Close-up view.

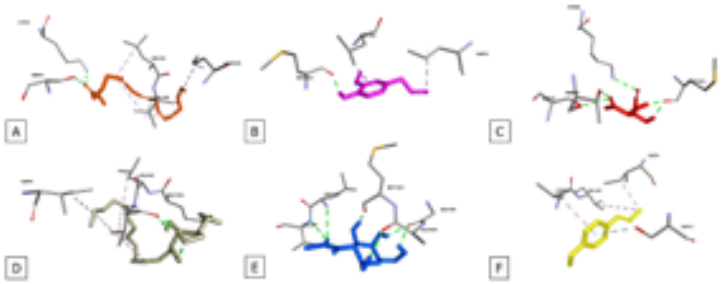


Figure 8. Molecular interactions of FimA receptor with (A) Arachidonic acid, (B) eugenol, (C) native ligand, (D) phytosphingosine, (E) positive control, and (F) *trans*-anetholes

The complexes of ligand-receptor stabilized their binding in active or binding sites by forming numerous hydrogen bonds across several targets with important catalytic or binding-site residues[27]. Lower (larger) binding energies and maybe stronger inhibitory effects are the outcome of compounds that can form hydrogen bonds. These compounds are thus more likely to stay anchored inside the active site. For instance, eugenol formed hydrogen bonds with Lys238 and Tyr123 in Cystalysin, important catalytic residues essential for PLP-dependent activity. This deep connection raises the possibility of significant enzyme function disruption. Phytosphingosine presented the most hydrogen bonds compared to the other compounds, which generated an extensive hydrogen bond complex. Hydrogen bond networks are hydrogen bonds that connect the side chains of numerous residues throughout the protein. Hydrogen bond networks stabilize the overall protein structure and have been shown to play a role in activation and allostery[28]. Eugenol also forms a fairly strong hydrogen bond with the receptor, which is characterized by the number of hydrogen bonds formed. These polar interactions imply that these substances can successfully stabilize their binding to vital virulence proteins, which may interfere with the mechanisms of bacterial colonization or survival[29]. The conformations of all the ligands were illustrated in **Figures 3**, **5**, **7**, **19**, and **11** followed by the molecular interactions of hydrogen bonds and hydrophobic interactions for each ligand in a specific receptor were demonstrated in **Figures 4**, **6**, **9**, **10**, and **12**. Each ligand was presented in different color for easier identification of the interactions in those figures, red for native ligand, blue for positive control, orange for arachidonic acid, purple for eugenol, grey for phytosphingosine, and yellow for trans-anethole.

By encouraging van der Waals interactions with nonpolar residues in protein binding sites, hydrophobic interactions play an equally substantial role in ligand affinity in molecular docking. These interactions can be maximized by compounds with long hydrophobic chains or aromatic sections, which improve binding stability and hydrogen bond complementarity[30, 31]. Phytosphingosine and arachidonic acid showed the most frequent hydrophobic interactions among a number of targets in this analysis, interacting with a wide variety of hydrophobic residues across targets, such as Phe295 and Leu145 in Ddl, Ile73 and Leu105 in FimA, and Ala39 and Ile205 in Cystalysin. For lipophilic compounds, which depend on embedding into hydrophobic pockets to establish effective binding, these interactions are especially significant. The moderate-to-strong binding energies seen for these compounds are explained by the presence of extensive hydrophobic interactions, which in some cases are coupled with hydrogen bonding. This supports the compounds' potential as multi-target inhibitors of oral bacterial virulence factors[32].

Figure 10. Conformations of the native ligand, *M. oleifera* compounds, and positive controls at RadD (A), ligand conformational positioning receptor, and (B) Close-up view.

Figure 11. Molecular interactions of FimA receptor with (A) Arachidonic acid, (B) eugenol, (C) native ligand, (D) phytosphingosine, (E) positive control, and (F) *trans*-anethole.

Figure 22. Conformations of the native ligand, *M. oleifera* compounds, and positive controls at Ddl (A), ligand conformational positioning receptor, and (B) Close-up view.

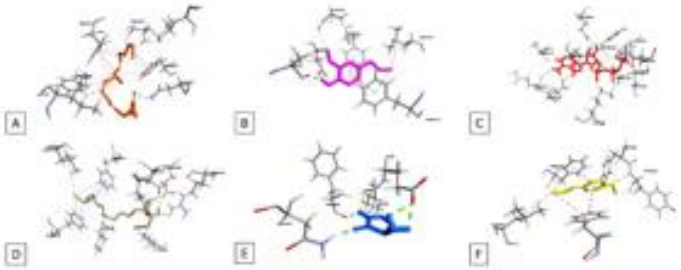


Figure 13. Molecular interactions of Ddl receptor with (A) Arachidonic acid, (B) eugenol, (C) native ligand, (D) phytosphingosine, (E) positive control, and (F) *trans*-anethole.

CONCLUSION

This study found that Moringa oleifera-derived compounds—eugenol, trans-anethole, arachidonic acid, and phytosphingosine—exhibit promising multi-target binding affinities against major virulence proteins associated with cariogenic and endodontic infections. Molecular docking demonstrated that phytosphingosine had the most consistent and comprehensive anticipated interactions across various sites, indicating more potential to interfere with multiple bacterial virulence processes at the same time. All ligands tested are capable of interacting directly with the natural binding pockets of Cystalysin, SrpA, FimA, RadD, and DdI. These interactions consistently involve important catalytic or adhesion-related residues and are supported by the formation of stable hydrogen bonds and multiple hydrophobic contacts. Based on the overall docking profile, these ligands show potential for inhibiting essential enzyme pathways and virulence adhesins. These findings address the research objective by confirming that the compounds studied have multi-target binding capabilities with antibacterial activity through the simultaneous inhibition of pathogen adhesion and metabolic function. The tested compounds could serve as promising lead compounds for the development of multi-target antibacterial agents. Their ability to bind competitively in the native ligand pocket indicates an effective mechanism for inhibiting bacterial virulence factors and essential enzymes, making them relevant candidates for further enzyme evaluation. These results support the concept that molecules derived from natural products can act on multiple bacterial targets, and methodologically demonstrate the usefulness of integrated docking analysis for the initial screening of multi-target inhibitors.

Based on these computational findings, phytosphingosine could be used as a supplementary agent in conservative dental therapy by targeting multiple mechanisms involved in bacterial adhesion, survival, and tissue damage associated with cariogenic and endodontic infections.

Acknowledgement
The authors would like to express their sincere gratitude to Universitas Trisakti for providing the facilities and support that enabled the completion of this research.

Author Contributions:
Conceptualization, MFA, DK,TA, DH; methodology, MFA, DK, TA, DH; software, DK, DH ; validation, MFA, DK, TA, DH ; formal analysis, MFA, DK, TA, DH ; investigation, MFA, DK, TA, DH ; resources, MFA, DK, TA, DH ; data curation, DK, DH; writing original draft preparation, MFA, DK, TA, DH; writing review and editing, MFA, DK, TA, DH; visualization, DK, DH; supervision, MFA, DK, TA, DH; All authors have read and agreed to the published version of the manuscript

Funding: No funding was received for this study

Institutional Review Board Statement: Ethical approval was waived because the study does not involve human subjects or animal experiments.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data used to support the findings of this study are included within the article. Raw data that support the findings of this study are available from the author, upon reasonable request.

Conflicts of Interest: The authors declare no conflict of interest.

REFERENCES

1. Könönen E, Gursoy M, Gursoy UK. Periodontitis: a multifaceted disease of tooth-supporting tissues. Journal of clinical medicine. 2019;8(8):1135.
2. Giambartolomei GH, Delpino MV. Immunopathogenesis of hepatic brucellosis. Frontiers in Cellular and Infection Microbiology. 2019;9:423.

Reviewer
The conclusion contains the answers to the research problem formulation,
not by including the statistical results, but in the form of conclusions derived

Mainy F Amin
We appreciate the reviewer's comment. The conclusion section has now been thoroughly revised. The revised conclusion provides a clear synthesis of the findings in direct relation to the stated research objectives.

Reply

Reviewer
Please complete it, for an example you can see the previous PJD publication

Mainy F Amin
Thank you, we have added it

Reply

Reviewer
Please complete it, for an example you can see the previous PJD publication

Mainy F Amin
Thank you, we have added it

Reply

Reviewer
Please complete it, for an example you can see the previous PJD publication

Mainy F Amin
Thank you, we have added it

Reply

Reviewer
Please complete it, for an example you can see the previous PJD publication

3. Kwon T, Lamster IB, Levin L. Current concepts in the management of periodontitis. International dental journal. 2021;71(6):462-76.

4. Miller DP. Microbial Biofilms and Pathobiology of Gingivitis and Periodontitis. Oral Biofilms in Health and Disease: Springer; 2025. p. 275-309.

5. Simanian EJ. Determination of RadD-Dependent Gene Regulation in Fusobacterium nucleatum in Response to Streptococcus sanguinis: UCLA; 2013.

6. Zhu F, Zhang H, Yang T, Haslam SM, Dell A, Wu H. Engineering and dissecting the glycosylation pathway of a streptococcal serine-rich repeat adhesion. Journal of Biological Chemistry. 2018;293(13):4952.

7. Hasegawa Y, Nagano K. Porphyromonas gingivalis FimA and Mfa1 fimbriae: Current insights on localization, function, biogenesis, and genotype. Japanese Dental Science Review. 2021;57:190-200.

8. Batson S, de Chiara C, Majce V, Lloyd AJ, Gobec S, Rea D, et al. Inhibition of D-Ala: D-Ala ligase through a phosphorylated form of the antibiotic D-cycloserine. Nature communications. 2017;8(1):1939.

9. Şenel S. An overview of physical, microbiological and immune barriers of oral mucosa. International journal of molecular sciences. 2021;22(15):7821.

10. Elbestawy MK, El-Sherbiny GM, Moghannem SA. Antibacterial, antibiofilm and anti-inflammatory activities of eugenol clove essential oil against resistant Helicobacter pylori. Molecules. 2023;28(6):2448.

11. Chamlagain M, Hu J, Sionov RV, Steinberg D. Anti-bacterial and anti-biofilm activities of arachidonic acid against the cariogenic bacterium Streptococcus mutans. Frontiers in microbiology. 2024;15:1333274.

12. Glenz R, Kaiping A, Göpfert D, Weber H, Lambour B, Sylvester M, et al. The major plant sphingolipid long chain base phytosphingosine inhibits growth of bacterial and fungal plant pathogens. Scientific reports. 2022;12(1):1081.

13. Medeiros M, Alves M, Santos B, Silva E, Araújo F, Bezerra M, et al. Evaluation of the antibacterial activity of trans-anethole against Enterococcus cloacae and Enterococcus faecalis strains of food origin. Brazilian Journal of Biology. 2023;83:e269245.

14. Dixit K, Chauhan B, Jain R. Anti-Inflammatory Potential of Medicinal Plants in the Management of Inflammatory Diseases: A Review of Mechanisms and Bioactive Compounds. Journal of Drug Delivery & Therapeutics. 2025;15(6).

15. Ojewumi ME, Obanla OR, Atauba DM. A review on the efficacy of Ocimum gratissimum, Mentha spicata, and Moringa oleifera leaf extracts in repelling mosquito. Beni-Suef University Journal of Basic and Applied Sciences. 2021;10(1):87.

16. Jaya FB, Syamsunarno MRAA, Sahiratmadja E. Moringa oleifera Lam. to accelerate wound healing: a review. Journal of the Medical Sciences (Berkala Ilmu Kedokteran). 2023;55(3).

17. Baky NAA, Fouad LM, Ahmed KA, Alzokaky AA. Mechanistic insight into the hepatoprotective effect of Moringa oleifera Lam leaf extract and telmisartan against carbon tetrachloride-induced liver fibrosis: plausible roles of TGF-β1/SMAD3/SMAD7 and HDAC2/NF-κB/PPARγ pathways. Drug and Chemical Toxicology. 2025;48(1):84-97.

18. Yasir M, Park J, Han E-T, Han J-H, Park WS, Choe J, et al. Identification of Marine compounds inhibiting NF-κBInducing kinase through molecular docking and molecular dynamics simulations. Biomolecules. 2024;14(12):1490.

19. Vikhar Danish Ahmad A, Khan SW, Ali SA, Yasar Q. Network pharmacology combined with molecular docking and experimental verification to elucidate the effect of flavan-3-ols and aromatic resin on anxiety. Scientific Reports. 2024;14(1):9799.

20. Fattouche M. Multi-combined Drug-likeness, 3D-QSAR Modeling, Molecular docking and Molecular Dynamics Analysis of several series of pharmaceutical: Université Mohamed Khider (Biskra-Algérie); 2024.

21. Zothantluanga JH, Chetia D. A beginner's guide to molecular docking. Sciences of Phytochemistry. 2022;1(2):90-3.

22. Pantsar T, Poso A. Binding affinity via docking: fact and fiction. Molecules. 2018;23(8):1899.

23. Buchanan CJ, Gaunt B, Harrison PJ, Yang Y, Liu J, Khan A, et al. Pathogen-sugar interactions revealed by universal saturation transfer analysis. Science. 2022;377(6604):eabm3125.

24. Skolnick J, Zhou H. Implications of the essential role of small molecule ligand binding pockets in protein–protein interactions. The Journal of Physical Chemistry B. 2022;126(36):6853-67.

25. Komarov IV, Bugrov VA, Cherednychenko A, Grygorenko OO. Insights into modeling approaches in chemistry: assessing ligand-protein binding thermodynamics based on rigid-flexible model molecules. The Chemical Record. 2024;24(2):e202300276.

26. Nocentini A. d-Alanine-d-alanine ligase. Metalloenzymes. 2024:83-91.

27. Chen D, Oezguen N, Urvil P, Ferguson C, Dann SM, Savidge TC. Regulation of protein-ligand binding affinity by hydrogen bond pairing. Science advances. 2016;2(3):e1501240.

28. Bertalan É, Lešnik S, Bren U, Bondar A-N. Protein-water hydrogen-bond networks of G protein-coupled receptors: Graph-based analyses of static structures and molecular dynamics. Journal of Structural Biology. 2020;212(3):107634.

29. Zhao G, Liu X, Wang S, Bai Z, Zhang S, Wang Y, et al. Hydrogen bonding penalty used for virtual screening to discover potent inhibitors for Papain-Like cysteine proteases of SARS-CoV-2. Chemical Biology & Drug Design. 2022;100(4):502-14.

30. Bitencourt-Ferreira G, Veit-Acosta M, de Azevedo Jr WF. Van der Waals potential in protein complexes. Docking Screens for Drug Discovery: Springer; 2019. p. 79-91.

31. Li J, Ma X, Guo S, Hou C, Shi L, Zhang H, et al. A hydrophobic-interaction-based mechanism triggers docking between the SARS-CoV-2 spike and angiotensin-converting enzyme 2. Global Challenges. 2020;4(12):2000067.

32. Du X, Li Y, Xia Y-L, Ai S-M, Liang J, Sang P, et al. Insights into protein–ligand interactions: mechanisms, models, and methods. International journal of molecular sciences. 2016;17(2):144.

5. Bukti surat manuskrip diterima
30 Maret 2026

Date: 30 March, 2026

Padjadjaran Journal of Dentistry (PJD)

Manuscript Acceptance Letter

Dears,
Meiny Faudah Amin, Dikdik Kurnia, Taufiq Ariwibowo, Dicky Hardi

We are pleased to inform you that our reviewers have accepted and recommended your manuscript entitled **"Multi-target potential of moringa oleifera-derived compounds against cariogenic and endodontic virulence proteins revealed by molecular docking: An in silico experimental study"** for publication in Vol 38 No 1 of Padjadjaran Journal of Dentistry (PJD).

Thank You for Choosing to Publish in Our Journal

Best Regards

Chief Editor

Prof. Dr. Nina Djustiana, drg, MKes

Co Editor in Chief

Dr Anne Agustina Suwargiani, drg, MKM,

6. Bukti publikasi

31 Maret 2026

https://doi.org/10.24198/pjd.vol38no1.65729

PADJADJARAN JOURNAL OF DENTISTRY
p-ISSN : 1979-0201 e-ISSN : 2549-6212
In affiliation with Indonesia Dental Association
Published by Universitas Padjadjaran

Multi-target potential of moringa oleifera-derived compounds against cariogenic and endodontic virulence proteins revealed by molecular docking: an in silico experimental study

Meiny Faudah Amin, Dikdik Kurnia, Taufiq Ariwibowo, Dicky Hardi

Abstract

Introduction: Dental infections are multifactorial diseases involving bacterial biofilms and host immune responses. Natural compounds with antibacterial activity, such as *Moringa oleifera*, have been explored as alternatives to conventional antibiotics. This study aimed to evaluate the interaction profiles of four Moringa oleifera–derived compounds against multiple virulence-associated proteins of cariogenic and endodontic pathogens using in silico molecular docking. **Methods**: This study was an in silico experimental study using molecular docking simulations to evaluate the binding energy of four *M. oleifera*-derived compounds (eugenol, trans-anethole, arachidonic acid, and phytosphingosine) with five key virulence-associated proteins of cariogenic and endodontic pathogens (Cystalysin, SrpA, FimA, RadD, and DdI). AutoDock 4.0 was used for the docking simulations. Docking results were analyzed based on binding energy (ΔG) and inhibition constant (Ki) values. The best binding conformations were selected according to the lowest binding energy and visualized to identify key ligand–protein interactions using Discovery Studio Visualizer. **Results**: The phytosphingosine-DdI exhibited the lowest binding energy of -7.42 kcal/mol, followed by eugenol with three different receptors (Cystalysin, SrpA, and FimA) and arachidonic acid-RadD. The lowest inhibition constant was shown by the phytosphingosine-DdI complex at 3.61 μM. Each compound interacted with various targets, but phytosphingosine exhibited the most consistent and widespread predicted binding via hydrogen bonds with Glu222, Arg291, Glu306, Asp293, Lys251, and hydrophobic interactions of Phe295, Phe245, Phe175, and Leu145. **Conclusion:** This in silico molecular docking study demonstrated that *Moringa oleifera*–derived compounds, particularly phytosphingosine, exhibit strong binding affinity toward key virulence-associated proteins of cariogenic and endodontic pathogens. These findings highlight the potential of *M. oleifera* as a natural source of antibacterial agents and support further experimental validation of its therapeutic applications in oral infections.

Keywords

Molecular docking, moringa oleifera, dental caries, cariogenic bacteria, virulence factors

ABOUT THE AUTHORS

Meiny Faudah Amin
https://orcid.org/0000-0002-2572-0931
Universitas Trisakti
Indonesia
Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti Jakarta Barat, Indonesia

Dikdik Kurnia
https://orcid.org/0000-0001-9789-9785
Universitas Padjadjaran
Indonesia
Department of Chemistry, Faculty of Mathematics, and Natural Sciences, Universitas Padjadjaran Sumedang, Indonesia

Taufiq Ariwibowo
https://orcid.org/0000-0003-3230-3623
Universitas Trisakti
Indonesia
Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti Jakarta Barat, Indonesia

Dicky Hardi
https://orcid.org/0009-0004-2320-9891
Universitas Trisakti
Indonesia
Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti Jakarta Barat, Indonesia

PADJADJARAN JOURNAL OF DENTISTRY
p-ISSN : 1979-0201 e-ISSN : 2549-6212
In affiliation with Indonesia Dental Association
Published by Universitas Padjadjaran

HOME ABOUT LOGIN REGISTER CATEGORIES SEARCH CURRENT ARCHIVES

Home > Vol 38, No 1 (2026) > Amin

Download this PDF file

PADJADJARAN JOURNAL OF DENTISTRY

ORIGINAL ARTICLE

Multi-target potential of *moringa oleifera*-derived compounds against cariogenic and endodontic virulence proteins revealed by molecular docking: an in *silico* experimental study

Meiny Faudah Amin[1*]
Dikdik Kurnia[2]
Taufiq Ariwibowo[1]
Dicky Hardi[1]

[1]Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti Jakarta Barat, Indonesia
[2] Department of Chemistry, Faculty of Mathematics, and Natural Sciences, Universitas Padjadjaran Sumedang, Indonesia

* Correspondence:
meiny.faudah@trisakti.ac.id

Received: 27 January 2026
Revised: 26 Februari 2026
Accepted: 20 March 2026
Published: 31 March 2026
DOI:10.24198/pjd.vol38no1.68102

ABSTRACT

Introduction: Dental infections are multifactorial diseases involving bacterial biofilms and host immune responses. Natural compounds with antibacterial activity, such as *Moringa oleifera*, have been explored as alternatives to conventional antibiotics. This study aimed to evaluate the interaction profiles of four Moringa oleifera–derived compounds against multiple virulence-associated proteins of cariogenic and endodontic pathogens using in silico molecular docking. **Methods:** This study was an in silico experimental study using molecular docking simulations to evaluate the binding energy of four *M. oleifera*-derived compounds (eugenol, trans-anethole, arachidonic acid, and phytosphingosine) with five key virulence-associated proteins of cariogenic and endodontic pathogens (Cystalysin, SrpA, FimA, RadD, and DdI). AutoDock 4.0 was used for the docking simulations. Docking results were analyzed based on binding energy (ΔG) and inhibition

ABOUT THE AUTHORS

Meiny Faudah Amin
https://orcid.org/0000-0002-2572-0931
Universitas Trisakti
Indonesia
Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti Jakarta Barat, Indonesia

Dikdik Kurnia
https://orcid.org/0000-0001-9789-9785
Universitas Padjadjaran
Indonesia
Department of Chemistry, Faculty of Mathematics, and Natural Sciences, Universitas Padjadjaran Sumedang, Indonesia

Taufiq Ariwibowo
https://orcid.org/0000-0003-3230-3623
Universitas Trisakti
Indonesia
Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti Jakarta Barat, Indonesia

Dicky Hardi
https://orcid.org/0009-0004-2320-9891
Universitas Trisakti
Indonesia
Department Conservative Dentistry, Faculty of Dentistry, Universitas Trisakti Jakarta Barat, Indonesia

Refbacks

There are currently no refbacks.