Journal of Environmental Biology
p-ISSN: 0254-8704 • e-ISSN: 2394-0379 • CODEN: JEBIDP

JEB®

Original Research Paper
Volume 47 Issue 6 November 2026 pp. 1199-1206
DOI: http://doi.org/10.22438/jeb/47/6/MRN-5529

J. Environ. Biol., 2026
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Journal website : www.jeb.co.in ★ E-mail : editor@jeb.co.in

Role of Aloe-emodin in inhibition of FtsA of *Staphylococcus aureus* using *in-silico* studies

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Received: 29 August 2024 **Revised:** 11 June 2026 **Accepted:** 21 August 2026
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Abstract

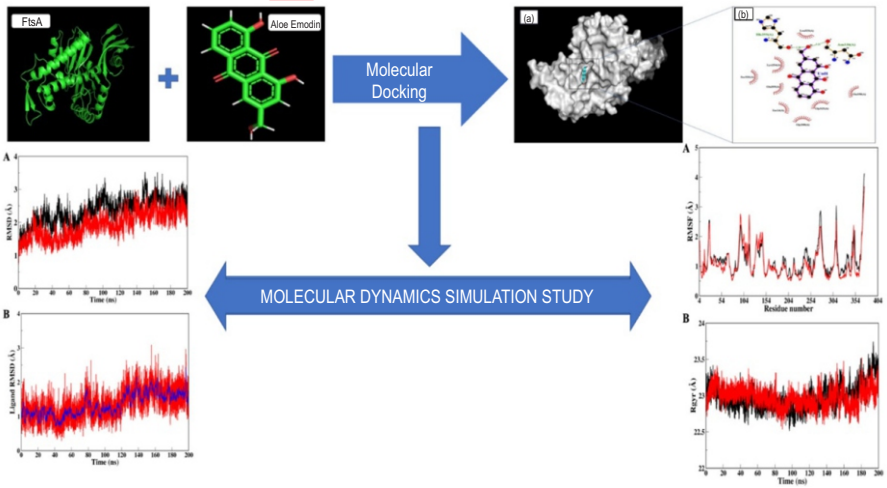
Aim: The study aimed to evaluate the antibacterial potential of *Aloe vera* phytochemicals against bovine bacterial endometritis caused by *Staphylococcus aureus* using *in-silico* approaches.

Methodology: The essential bacterial protein FtsA of *Staphylococcus aureus* was selected as target for molecular docking with major antibacterial phytocompounds of *Aloe vera.* Standard antibiotics, including Gentamicin and Enrofloxacin, were also docked for comparison. The best protein–ligand complex was further validated through molecular dynamics simulation and thermodynamic analysis.

Results: Among all compounds, Aloe emodin showed the highest binding affinity with FtsA (−8.5 kcal mol^{-1}), followed by Lupeol (−8.2 kcal mol^{-1}), Sitosterol-β (−7.9 kcal mol^{-1}), Campesterol (−7.7 kcal mol^{-1}) and Anthracene (−7.6 kcal mol^{-1}). In comparison, Gentamicin and Enrofloxacin exhibited lower binding energies.

Interpretation: The findings indicate that Aloe emodin possesses strong inhibitory potential against FtsA and may serve as a promising plant-derived therapeutic candidate for bovine bacterial endometritis.

Key words: *Aloe vera*, Cattle, Endometritis, Molecular docking, *Staphylococcus aureus*



How to cite: Arya, D., M. Srivastava, R. Tyagi, S. Sharma, S. Asthana, P. Chaudhary1 and M. Sharma: Role of Aloe-emodin in inhibition of FtsA of *Staphylococcus aureus* using *in-silico* studies. *J. Environ. Biol.*, **47,** 1199-1206 (2026).

Introduction

The primary aim of dairy industry is to achieve one calf per year (Dillon *et al.,* 2006) and improve pregnancy rates (Borakhatariya *et al.,* 2018), however, challenges like poor heat detection, lack of skilled personnel for artificial insemination, and reproductive diseases such as endometritis and repeat breeding affect fertility. These issues lead to economic losses, including reduced milk production and income from calf sales, and higher maintenance costs for non-pregnant cows (Bisla *et al.,* 2018). Reproductive diseases, including endometritis (Sharma, 2017), metritis, and retained fetal membranes, significantly impact dairy animals' fertility (Deori and Arundhati, 2015). Endometritis, in particular, is a leading cause of infertility, with incidence rates ranging from 5% to 32% in cows and 6% to 30% in buffaloes (Gupta and Deopurkar, 2005). Also, dairy cattle reported with endometritis associated with poorer reproductive performance, including a lower chance of conception following the first insemination, an increased risk of pregnancy loss and a reduced overall pregnancy rate during lactation (Bogado Pascottini *et al*., 2017).

Staphylococcus aureus is commonly found in humans and is a part of our natural microbial population (Weber, 2005). Though typically harmless, it can cause various skin and soft tissue infections as an opportunistic pathogen (Stryjewski and Chambers, 2008; Tong *et al.,* 2015). Resistance to penicillin emerged in the 1940s (Rammelkamp and Maxon, 1942), followed by resistance to methicillin in the 1960s (Jevons, 1961) and vancomycin resistance in the 1990s (Hiramatsu *et al.,* 1997). The present study focused on the *S. aureus* FtsA protein as a potential drug target. FtsA is crucial for bacterial cell division, as it anchors the FtsZ protein to the cytoplasmic membrane (Fujita *et al.,* 2014). Besides *S. aureus,* FtsA protein has been identified in other Gram-positive organisms (Mura *et al.,* 2017) and Gram- negative pathogens (Paradis-Bleau *et al.,* 2005). Consequently, molecules that inhibit FtsA protein could prove beneficial in combating a wide array of pathogens. During bacterial cell division, a multi-protein complex known as divisome, comprising over 20 proteins, forms at the midcell (Aarsman *et al.,* 2005). FtsZ, one of these proteins, organizes into the Z-ring structure, facilitating physical separation of daughter cells (Lutkenhaus and Addinall, 1997).

Polymerized FtsZ is linked to the cytoplasmic membrane by FtsA via its C- terminal membrane-targeting sequence (MTS) (Pichoff and Lutkenhaus, 2005). Optical microscopy studies have shown that the fusion of yellow fluorescent protein (YFP) with MTS- bound FtsZ (FtsZ-YFP-MTS) creates an indentation in a liposome membrane but does not induce liposome division (Osawa *et al.,* 2008). Conversely, when FtsZ-YFP is combined with FtsA (an FtsA gain-of-function mutant), it prompts the formation of a continuous septum in a GTP/ATP- dependent manner (Osawa and Erickson, 2013). This suggests that FtsA plays a role in tethering FtsZ to the membrane and essential for subsequent cell division. Traditional antibiotic therapy for various infections, including bovine endometritis, face challenges due to residual effects and concerns about antibiotic resistance (Shukla and Sharma, 2005; Singh *et al.,* 2008). To address these issues, efforts are being made to explore herbal alternatives, as they are cost-effective and lack harmful residual effects. Phytotherapy offers advantages such as enhanced disease resistance and improved natural healing (Kumar *et al.,* 2018). The use of herbal medicine has gained renewed attention due to concerns about the cost, side effects, and symptomatic nature of many conventional therapeutic approaches (Kumar and Rai, 2011). Additionally, a number of experimental researches have been carried out to uncover useful drugs to treat a variety of medical conditions.

Conducting experiments with various drugs, whether allopathic or herbal, presents challenges such as high cost, time constraints, the need for skilled personnel, laboratory setup, and procurement of experimental animals. As an alternative, bioinformatics approaches, particularly molecular docking, are employed by researchers to predict the efficiency of drugs. Bioinformatics is a multidisciplinary field that combines biology, computer science, and information technology to analyze biological data. It has become an essential tool in biomedical research, supporting advancements in genomics, protein engineering, drug discovery, veterinary sciences, and related fields through the use of computational tools and online resources (Arya *et al.,* 2024). *In-silico* technology, especially molecular docking, has been found to reduce overall drug development cost by 50% (White, 2007) and further validation of docking results were carried out by molecular dynamics studies. Arya *et al.* (2023) conducted an *in-silico* study comparing the antibacterial activity of Tulsi and Garlic against *S. aureus* and *E. coli* using molecular docking. Tyagi *et al.* (2018) demonstrated the activity of MMV019838 on Mtb using MDS (Molecular Dynamic Simulation) and Sharma *et al.* (2023) exhibited potential of MMV675968 as inhibitor of ec-DHFR (*Escherichia coli* dihydrofolate reductase). In a recent *in-silico* investigation, Mamatha *et al.* (2025) screened phytochemicals against the ClfA protein of *Staphylococcus aureus* using virtual screening, molecular docking, ADMET analysis, and molecular dynamics simulations. Based on their computational assessment, Oridonin and Salvianolic Acid A were identified as potential drug candidates for further preclinical evaluation in the treatment of bovine mastitis caused by *S. aureus.*

In the present study, molecular docking results were validated using the MDS to find an efficient herbal medication for treating bacterial endometritis. Molecular dynamics simulations have emerged as a robust computational approach for the discovery and optimization of novel antimicrobial agents and therapeutic strategies aimed at combating bacterial infections (Sharma *et al.,* 2024). The ultimate objective was to explore the therapeutic potential of *Aloe vera*-derived natural compounds as alternative antimicrobial agents for the management of bovine endometritis. The novelty of this study lies in the identification of Aloe-emodin as a potential inhibitor of the *Staphylococcus aureus* cell division protein FtsA through an integrated molecular docking and molecular dynamics simulation approach. To the best of our knowledge, this is the first study to explore the interaction of *Aloe vera* phytochemicals with FtsA in the context of bovine endometritis. The findings reveal a strong and stable binding of Aloe-emodin to FtsA, suggesting its potential as a natural

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antibacterial lead compound for the development of alternative therapeutic strategies against bovine uterine infections. The findings offer valuable insights into the development of plant-based therapeutic candidates and contribute to the search for sustainable alternatives to conventional antibiotics in veterinary medicine, particularly in the context of increasing antimicrobial resistance.

Materials and Methods

Selection of bacteria and target proteins: *S. aureus* was selected for the current investigation due to its prevalence and pathogenicity in causing endometritis in the dairy herd of Instructional Dairy Farm, Govind Ballabh Pant University of Agriculture and Technology, Pant Nagar and Bakht *et al.* (2024) reported that *Staphylococcus aureus* was detected in 17.96% of bovine endometritis cases. Among the *S. aureus* isolates, methicillin-resistant *S. aureus* (MRSA) accounted for 50.72% and 37.68% based on phenotypic and genotypic assessment, respectively. Similarly, bovine-resistant *S. aureus* (BRSA) was identified in 36.23% of isolates using phenotypic methods and 18.84% using genotypic methods. The crystal structures of the target protein identified by their PDB (Protein Data Bank) ID, were obtained from the Protein Data Bank (PDB) at www.rcsb.org. The targeted protein was FtsA (3WQU), of *S. aureus*. The 3-D structures, along with their respective IDs, were retrieved from the PubChem database. *Aloe vera* phytochemicals involved in the study were Aloe-emodin (9792), Anthracene (8111), Campesterol (151215), Lupeol (50645939) and Sitosterol-β (192962). The 3-D structure of Aloe emodin and FtsA is shown in Fig. 1.

Interaction study with autodock tool: Autodock vina was employed for molecular docking subsequent to the preparation of both protein and ligand. The selected phytochemicals were docked with specific bacterial target protein, with each docking procedure generating nine poses in Autodock. Blind docking was performed to assess and compare binding affinity and interactions. Following docking, the resulting structures were analysed using LIGPLOT (Sidhu *et al.*, 2020). The 2-D representation of the 3-D docked structure of protein and ligand was utilized to estimate the quantity of hydrogen bonds, the distance between these bonds, and the involved amino acid residues.

Preparation of system: The protein structure of FtsA (3WQU - a complex) was obtained from the RCSB Protein Data Bank. Since there was no available apo structure, the bound ligands were removed from the co-crystal structure, and treated as the apo

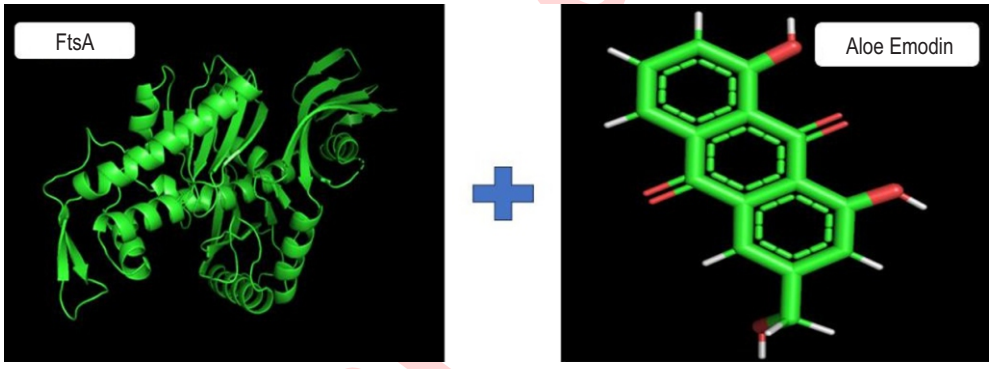


Fig. 1: 3-D structure of protein (FtsA) and ligand (Aloe-emodin).

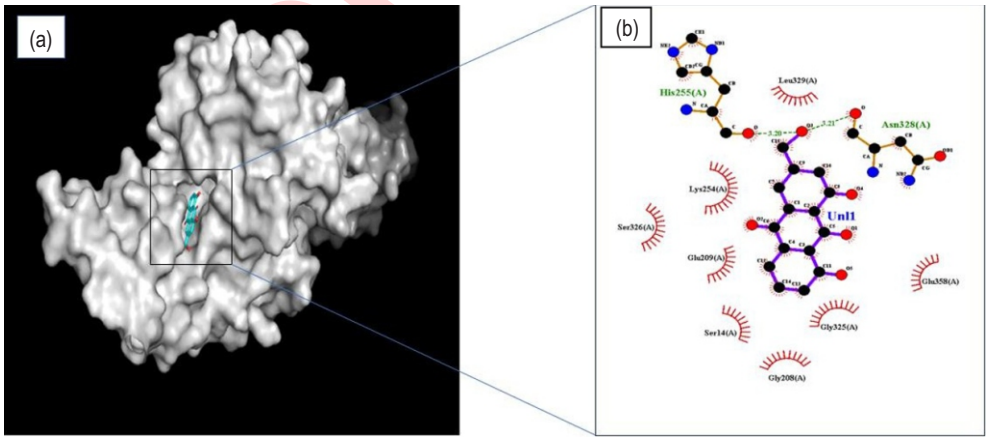


Fig. 2: (a) Docked 3D structure of FtsA with Aloe-emodin (space filling model). (b) Interaction of protein-ligand docked complex predicted by LIGPLOT+: 2D representation of 3D structure showing H-bonds and interacting amino acids.

form. Both the apo structure and the docked complex with our lead molecule were prepared using the Protein Preparation Wizard in Maestro (Schrödinger Release 2020-1: Maestro, Schrödinger, LLC, New York, NY, 2020). The preparation utilized the OPLS3 force field model (Jorgensen *et al.,* 1996; Jorgensen, 2002). Ligands were prepared using LigPrep, version 4.2 (Schrödinger, LLC, New York, NY, 2020-1).

Atomistic molecular dynamic simulations: All-atom molecular dynamics (MD) simulations for each system were conducted using the AMBER22 software suite (Case *et al.,* 2023). AMBER has been widely utilized to analyze protein- ligand interactions. Both the apo-structure and the complex (apo-acomplex + ligand) were subjected to a 200 ns simulation. Details of the simulation are provided in Table 2. All systems were solvated in an orthorhombic box filled with TIP3P water, with a 12 Å padding in all directions. The AMBERff14SB force field (Maier *et al.,* 2015) was applied to the proteins, hydrogen atoms were added, and counter ions were included to neutralize the system. The systems underwent minimization in three stages to relax and remove bad contacts. In the first stage, 2000 steps of minimization were performed, including 1000 steps of steepest descent followed by 1000 steps of conjugate gradient. The first two stages involved position restraints of 10 and 2 Kcal mol^{-1} Å-2 on the entire protein to relax the solvent molecules. The third stage of minimization was carried out without restraints. The SHAKE algorithm was used to constrain bonds involving hydrogen atoms. The systems were then heated for 20 ps from 0K to 300K and equilibrated for 500 ps at 300K and 1 atm pressure. Simulations were conducted in the NPT ensemble with a 2.0 fs timestep. The coordinates were saved every 20 ps, referred to as "frames" in this study. For post-MD analysis, the CPPTRAJ module was used to calculate the RMSD (root mean square deviation) of backbone atoms, RMSF (root mean square fluctuation) of Cα atoms, and the radius of gyration (Rgyr).

Free energy analysis through MM-GBSA/PBSA (Molecular Mechanics-Generalized Born Surface Area/ Poisson–Boltzmann Surface Area) methods.

The average binding energy for the equilibrated MD trajectories of the COM system was calculated using MM-GBSA/PBSA methods in Amber22 (Case *et al.,* 2023). To perform this calculation, 500 frames were extracted at equal intervals from the stable trajectory. The binding free energy (ΔGbind) for each system was determined as follows:

$$\Delta Gbind = Gcom - (Grec + Glig) \quad (1)$$

Where, Gcom, Grec, and Glig are the absolute free energies of the complex, receptor, and ligand, respectively, averaged over the equilibrium trajectory. The free energy (G) for each species is calculated using the MM-GBSA and MM-PBSA methods as follows:

$$G = Egas + Gsol - TS \quad (2)$$
$$Egas = Eint + Eele + Evdw \quad (3)$$
$$Gpolar, PB(GB) = Eele + Gsol\text{-}polar, PB(GB) \quad (4)$$
$$Gnon\text{-}polar, PB(GB) = Evdw + Gsol\text{-}np, PB(GB) \quad (5)$$
$$Gsol = GPB(GB) + Gsol\text{-}np \quad (6)$$
$$Gsol\text{-}np = \gamma SAS \quad (7)$$

Where, T is the temperature and S is the total solute entropy. Egas represents the gas-phase energy, which is the sum of the internal energy (Eint), van der Waals energy (Evdw), and electrostatic energy (Eele). These values are computed using parameters from the Amberff14SB force field (Maier *et al.,* 2015). Gsol is the solvation free energy, which is divided into polar and non-polar contributions. The polar solvation contribution (Gsol-polar, PB(GB)) is calculated by solving the Poisson-Boltzmann (PB) and Generalized-Boltzmann (GB) equations (Genheden and Ryde, 2015). The total polar interaction (Gpolar, PB(GB)) is the sum of Eele and Gsol-polar, PB (GB). The non-polar solvation contribution (Gsol-np) was estimated using the constant γ = 0.0072 kcal/mol/$Å^2$ and the solvent-accessible surface area (SAS), determined using a water probe radius of 1.4 Å (Sitkoff *et al.,* 1994). The dielectric constants for the solute and solvent were set to 1 and 80, respectively. The total non-polar interaction contribution (Gnon-polar, PB (GB)) was calculated as the sum of Evdw and Gsol-np, PB (GB). The binding free energy contribution of each residue in the protein-ligand complex was computed using the GB model with the same number of frames. All the images were created using the VMD (Humphrey *et al.,* 1996) and graphs were prepared using the XMGRACE (Turner, 2005).

Results and Discussion

For docking analysis AutoDock Vina, a software tool recognized for providing faster processing and more reliable docking predictions than AutoDock4 was used in this study. (Pandya *et al.,* 2014). The docking results for Aloe emodin, one of the phytoconstituent of *Aloe vera* against FtsA of *S. aureus* is presented in Table 1. The binding energy of FtsA against Aloe emodin was -8.5 Kcal mol^{-1} followed by Lupeol (-8.2 Kcal mol^{-1}), Sitosterol- β (-7.9 Kcal mol^{-1}), Campesterol (-7.7 Kcal mol^{-1}) and Anthracene (-7.6 Kcal mol^{-1}). Among all the phytochemicals of *Aloe vera* under study, Aloe emodin showed the maximum binding energy with FtsA. The observed inhibitory interaction of Aloe-emodin (AE) with the FtsA protein of *Staphylococcus aureus* is consistent with the diverse pharmacological activities previously reported for this anthraquinone derivative. AE, chemically identified as 1,8-dihydroxy-3-(hydroxymethyl) anthraquinone, is a naturally occurring bioactive compound isolated from medicinal plants such as *Rheum palmatum* and *Aloe vera*. Previous studies have demonstrated that AE exhibits potent antibacterial, antioxidant, anti-inflammatory, and antitumor activities, highlighting its therapeutic potential (Luo *et al.,* 2024).

In the present study, the favorable binding affinity and stable protein–ligand interactions observed during molecular docking and molecular dynamics analyses suggest that AE may interfere with the functional activity of FtsA, an essential protein involved in bacterial cell division. This observation supports previous reports describing the antimicrobial efficacy of AE against a variety of pathogenic microorganisms (Luo *et al.,* 2024).

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Aloe emodin shows significant efficacy against *Staphylococcus aureus* and multidrug-resistant *S. aureus* (MRSA), as well as several Gram-negative bacteria including *Escherichia coli, Proteus mirabilis* and *Klebsiella* species (Zhao *et al.,* 2025). This further supports the antimicrobial potential of anthraquinone derivatives and strengthens the rationale for exploring structurally related compounds such as Aloe-emodin as potential antibacterial agents targeting essential bacterial proteins like FtsA.

Furthermore, the natural abundance, cost-effectiveness, and favorable safety profile of Aloe-emodin make it an attractive candidate for antimicrobial drug development. Recent advances in nanotechnology-based delivery systems have further demonstrated that nano-formulated Aloe-emodin can improve bioavailability, biocompatibility and therapeutic efficacy, thereby enhancing its potential as a promising antibacterial agent targeting key proteins involved in bacterial proliferation (Luo *et al.,* 2024). Additionally, a study by Jasso *et al.* (2005) supported the antibacterial and analgesic properties of Aloe emodin. Moreover, the use of emodin from *Aloe vera* against bacteria was reported to lead to the disruption of bacterial cell walls and a decrease in fluidity (Liu *et al.,* 2015). When docked with Aloe-emodin, FtsA demonstrates a binding energy of -8.5 Kcal mol^{-1}, establishing it as the most favourable interaction compared to other phytochemicals present in *Aloe vera*. Targeting FtsA offers a dual advantage, addressing antibiotic resistance concerns and facilitating the development of medications with minimal or low side effects. Given its presence in both Gram-positive and Gram-negative organisms and its crucial role as a cell division protein, FtsA presents a promising avenue for treating a broad spectrum of bacterial infections (Raghunathan *et al.,* 2018). James *et al.* (2015) suggested that FtsA is indispensable for *S. aureus* but not essential for higher organisms. Targeting such proteins offers advantages in addressing antibiotic resistance issues and minimizing potential side effects.

Aloe-emodin has been reported to substantially inhibit the production of key virulence determinants, including violacein in *Chromobacterium violaceum,* pyocyanin, pyoverdin, elastase, exoprotease, alginate, and rhamnolipids in *Pseudomonas aeruginosa,* as well as prodigiosin, exoprotease, and surface hydrophobicity in *Serratia marcescens* (Bano, 2025). These observations suggest that emodin can attenuate bacterial pathogenicity by interfering with quorum sensing-regulated virulence pathways, thereby reducing biofilm formation and virulence expression. Atun *et al.* (2025) also confirmed the antibacterial efficacy of *Aloe vera* against *Staphylococcus aureus* through *in-vitro* assays (nano-emulsion can enhance its antibacterial activity), while *in-silico* docking analyses revealed favorable binding of its phytoconstituents to the PBP-3 receptor. These findings support the antimicrobial potential of *Aloe vera* and corroborate with the present results. On LIGPLOT analysis, it was observed that the ligand was bonded with protein by two hydrogen bonds, one at His225 and the other at Asn328. Amino acids participating in this interaction included Leu329, Lys254, Ser326, Glu209, Ser14, Gly208, Gly325 and Glu358, as illustrated in Fig. 2 and detailed in Table1. For the comparative study, FtsA was also docked with standard antibiotics used against bovine endometritis *i.e.,* gentamicin and enrofloxacin, and the observed binding energy was-7.9 Kcal mol^{-1} and -6.7 Kcal mol^{-1}, respectively, which was less than Aloe-emodin. For further validation of docked complex (FtsA + Aloe emodin), molecular dynamic simulation studies were carried out.

Molecular dynamics simulations were performed to evaluate the activity of predicted hits. Post-MD analysis, including RMSD and RMSF, was conducted to understand the behavior of the lead molecules. The RMSD analysis of the apo vs. COM systems showed that all systems reached global equilibrium after 20 ns (Fig. 3A). Compared to the apo system, the COM system demonstrated greater stability, with the COM system being notably more stable overall (Fig. 3A). The dynamic stability of hit was also assessed, revealing that the ligand-acomplex remained exceptionally stable at around 2 Å (Fig. 3B), indicating that the acomplex is tightly bound in the binding pocket. The RMSF analysis further showed that the ligand reduced the protein's flexibility in certain regions of the COM system (Fig. 4A). The binding of acomplex restricted the protein's internal dynamics, confirming its strong binding within the pocket. Additionally, the radius of gyration (Rgyr) indicated that the COM system was more compact than the apo system (Fig. 4B). MMPBSA analysis was performed to support the MD simulation results, with binding

Table 1: 2-D representation of FtsA-Aloe-emodin complex

Protein	Ligand	Binding energy (Kcal mol^{-1})	No. of hydrogen bond	Amino acid involved in H-Bond	Amino acid residues
FtsA	Aloe- emodin	-8.5	2	His225, Asn328	Leu329, Lys254, Ser326, Glu209, Ser14, Gly208, Gly325, Glu358

Table 2: Comprehensive table of systems considered for the study with simulations details

ID	Systems	Time (ns)	Total no. of atoms	Water molecules	Ions
1	Apo-acomplex	200	62078	18784	37 Na^+
2	Apo-acomplex+ ligand= COM	200	62094	18782	37 Na^+

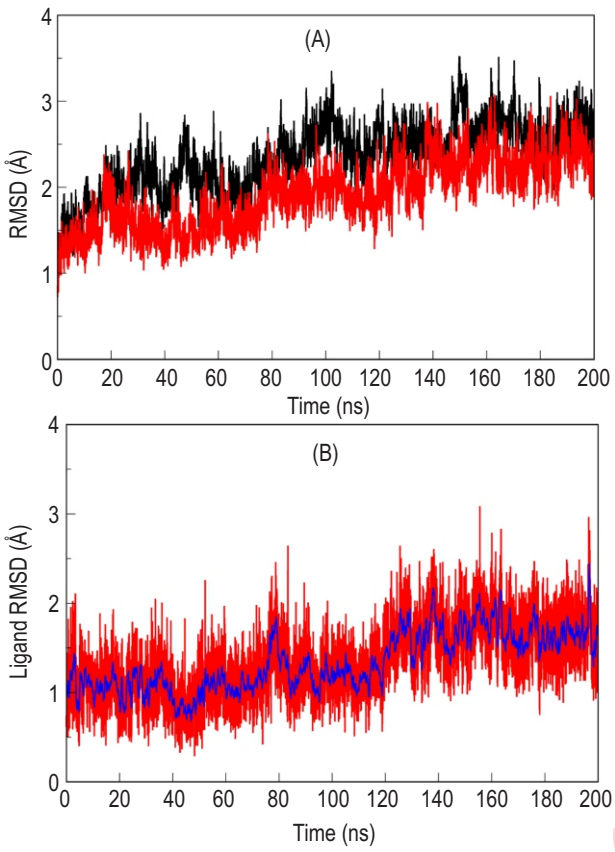


Fig. 3: The analysis of MD simulation studies. (A) Root-mean square deviation (RMSD) of protein apo and COM over the time of 200 ns Black and Red color represents apo and COM system respectively; (B) The ligand RMSD of acomplex (COM). The blue line represents the average of ligand RMSD obtained through the course of simulation.

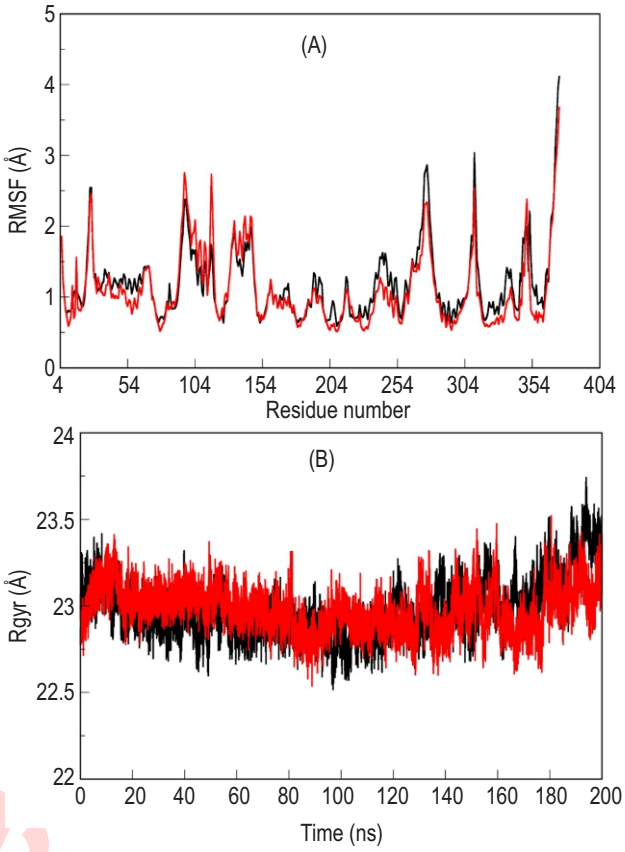


Fig. 4: (A) The root mean square fluctuation (RMSF) Cα atomic fluctuation of apo and COM and (B) Radius of Gyration (Rgyr) of apo-vs.-COM. Black and red color represent apo and COM system respectively.

Table 3: Displaying binding free energy of COM

Complex	Binding free energy ΔG (kcal mol^{-1})
COM	-34.44

free energy calculated for each trajectory using 500 frames extracted from the converged simulation. The results revealed that the COM system exhibited a significantly high binding affinity of -34.44 kcal mol^{-1} (Table 3). The thermodynamic analysis provided quantitative values indicating that the ligand demonstrates strong binding energy, suggesting its potential for further experimental validation. Alqahtani *et al.* (2026) performed MD simulations and confirmed the stable protein–ligand interactions and identified that tschimganin from *Aloe vera* as a promising bioactive compound with strong binding affinity, supporting the pharmaceutical potential of *Aloe vera* constituents. Another study also performed molecular docking and molecular dynamics simulations, and showed that *Aloe vera* constituents such as quercetin and aloe-emodin can stably interact with CASP3 and MMP-9, indicating strong binding at the active sites. In addition, experimental assays together with RT-qPCR analysis revealed that aloe-emodin exhibits antibacterial activity against Gram-positive bacteria and can downregulate MMP-9 gene expression (Tang *et al.,* 2025).

Roney *et al.* (2024) reported that Aloe emodin showed favorable pharmacokinetic properties, complying with Lipinski's rule of five. Molecular dynamics simulations revealed stable but conformationally dynamic interactions within the aloe emodin–TGF-β1 complex over time, supported by MM-PBSA/GBSA binding free energy analysis (similar to those applied in the present study). Overall, aloe emodin, a bioactive compound of *Aloe vera,* has been identified as a potential therapeutic candidate with relevant biological activity. Overall, molecular dynamics analysis confirmed the stability of the docked complexes under physiological conditions, offering deeper understanding of their interaction patterns. This supports the robustness of the *in-silico* predictions presented in this study.

The present study is relevant to the ongoing scenario of research towards finding the novel plant-based antibacterial agents, due to increasing antimicrobial resistance in veterinary

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field. By evaluating the antibacterial property of *Aloe vera* phytochemicals against FtsA, an essential cell-division-associated protein of *Staphylococcus aureus*, the study provides computational insights into their potential molecular interactions with an important bacterial target. Among the screened compounds, aloe-emodin showed favorable binding affinity and was further investigated through molecular dynamics simulation, which supported the stability of aloe-emodin–FtsA interaction under simulated conditions. These findings suggest that aloe-emodin may serve as a promising phytochemical for further investigation against *S. aureus* and demonstrate the utility of computational approaches for prioritizing bioactive phytochemicals before experimental validation. This may save laboratory cost, labor cost and other *in-vitro* experimental expenses. However, the predicted interactions require confirmation through *in-vitro* antibacterial assays, biochemical studies, and subsequent pharmacological investigations to establish the actual antibacterial efficacy and therapeutic potential of aloe-emodin to advance effective drug discovery for bovine bacterial endometritis.

Acknowledgment

The authors sincerely acknowledge the technical support received from Translational Health Science and Technology Institute (THSTI), NCR Biotech Science.

Authors' contribution: D. Arya: Manuscript preparation and Molecular docking; **M. Srivastava:** MD simulation analysis; **R. Tyagi:** Molecular docking methodology; **S. Sharma:** Supervision on MD simulation analysis; **S. Asthana:** MD simulation interpretation; **P. Chaudhary:** Manuscript edition; **M. Sharma:** Complete study design and supervision.

Funding: Author is not supported by any funding source.

Research content: The research content of manuscript is original and has not been published elsewhere.

Ethical approval: No ethical approval is required for the study as the study is completely computational. Consent was obtained from all the authors.

Conflict of interest: The authors declare that there is no conflict of interest.

Data availability: Data and material is enclosed with manuscript.

Consent to publish: All authors agree to publish the paper in *Journal of Environmental Biology.*

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