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RESEARCH ARTICLE

In silico studies of phytochemicals from *Eruca sativa* Mill. targeting Gram-positive bacterial resistance

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Abstract

This study shows an *in silico* analysis of phytochemicals from *Eruca sativa* Mill. targeting Gram-positive bacterial resistance. *Eruca sativa* is a desert medicinal plant which belongs to the Brassicaceae family and contains bioactive phytochemicals that shows potential against Gram-positive bacterial resistance. Peptidoglycan hexamuropeptide is a major bacterial cell-wall constituent that serves as a specific target for antibacterial proteins. It plays an essential role in the antibacterial defense mechanism in Gram-positive bacteria, such as *Staphylococcus aureus, Listeria monocytogenes, Staphylococcus epidermidis and Streptococcus pneumoniae,* by conserving cell-wall integrity and resistance against antibacterial stress. A total of 47 phytochemicals from *E. sativa* were investigated for binding affinity, molecular docking studies and favourable absorption, distribution, metabolism, excretion and toxicity (ADMET) profiles with target peptidoglycan hexamuropeptide in Gram -positive bacteria. Molecular docking studies were used to analyze their binding molecular docking interactions with the target protein which ranged from -3.90 to -5.20 kcal/mol, in comparison to the reference target protein (Azalomycin F). Most of the phytochemicals showed favourable ADMET profiles with low toxicity. These results suggest that *in silico* studies of phytochemicals from *E. sativa* may demonstrate promising antibacterial activity against peptidoglycan hexamuropeptide in Gram-positive bacteria.

Keywords: *Eruca sativa*; peptidoglycan molecular docking; peptidoglycan hexamuropeptide

Introduction

Antibacterial resistance is one of the most serious global health issues of recent times. The indiscriminate and unjustified usage of antibiotics has led to the growth of resistant bacterial strains, resulting in many therapies that were previously effective becoming progressively less effective (1). The World Health Organization (WHO) warns that drug-resistant infections could result in up to 10 million deaths per year by 2050 without prompt intervention (2). Particularly, multidrug-resistant (MDR) Gram-positive bacteria, such as *Staphylococcus aureus, Listeria monocytogenes, Staphylococcus epidermidis and Streptococcus pneumoniae,* are responsible for numerous severe and deadly infections (3). With the help of horizontal gene transfer and self-generated genetic mutations, these pathogens have formed multiple resistance mechanisms that significantly decrease the potency of commonly prescribed antibiotics such as ampicillin and cefoxitin (4). Acknowledging this intense AMR situation, there is an urgent demand to discover novel antibacterial agents that continue to remain efficacious (5). Plant-derived phytochemical compounds stand as an alternative resource in this study, offering various phytochemical compound structures and identifiable mechanisms of biological activity (6). *Eruca sativa* Mill., usually called rocket, is an essential member of the Brassicaceae family and widely valued for its medicinal properties. It is rich in various phytochemical compounds such as glucosinolates, flavonoids, phenolic acids, terpenoids and alkaloids, which play an essential role in its therapeutic potential (7). *Eruca sativa* is a promising source of natural antimicrobial agents, due to the hydrolysis products of phytochemical compounds, glucosinolates into isothiocyanates, which show strong antibacterial and antioxidant activities (8). These phytochemicals from the medicinal desert plant *E. sativa* are valuable candidates in novel drug discovery as antibacterial agents (9). In this *in silico* studies a total of 47 phytochemical compounds from *E. sativa* were investigated for their binding affinity, molecular docking studies and favourable absorption, distribution, metabolism, excretion and toxicity (ADMET) profiles against the Gram-positive bacterial target peptidoglycan hexamuropeptide (PDB ID: 2MTZ), to measure their potential effectiveness against Gram-positive bacteria (10). This target protein shows an essential role in cell wall biosynthesis and its suppression can severely disturb cell wall integrity, finally leading to bacterial death (11). The selection of these 47 phytochemical compounds was based on published literature data from PubChem, IMPAT, Dr. Duke's Phytochemical and Ethnobotanical Database and accessible structural databases (12). *In silico* methods such as ADMET evaluation, protein target prediction and molecular docking are progressively used in drug discovery by predicting promising therapeutic candidates (13). This integrated approach points to the significance of *E. sativa* phytochemical compounds against drug-resistant Gram-positive bacteria (14).

Materials and Methods

Prediction of bioactive phytochemicals of *Eruca sativa*

The selection of bioactive phytochemicals of *E. sativa* was performed through an organized study of phytochemical and natural product databases. At first, an extensive search was conducted in PubChem, IMPAT, Dr. Duke's Phytochemical and Ethnobotanical Database and peer-reviewed literature indexed in Scopus and Google Scholar to accumulate all reported phytochemicals from *E. sativa* (15).

Pharmacokinetic categorization (Absorption, distribution, metabolism, excretion and toxicity (ADMET) studies)

To measure the toxicity and pharmacokinetic activity of selected phytochemicals, ADMETlab 2.0 (version 2020; accessed on 12 March 2024) was engaged (https://admetmesh.scbdd.com). ADMETlab 2.0 gives extensive factors such as absorption, distribution, metabolism, excretion and low toxicity (16). For absorption, human intestinal absorption (HIA) was considered, where compounds with predicted HIA ≥ 70 % were categorized as well absorbed. Metabolic stability was assessed by evaluating potential suppression of major cytochrome P450 isoforms, considering CYP2D6 (17). Distribution included blood–brain barrier permeability (log BB), where values between -1.0 and +0.3 were taken as acceptable for non-CNS targeted compounds, pointing to moderate but controlled penetration. Toxicological evaluation comprised hepatotoxicity (categorized as 0 = non-toxic and 1 = toxic). Absorption, distribution, metabolism, excretion and toxicity profiling assisted in identifying phytochemicals with favorable safety and pharmacokinetic properties (18).

Prediction of target proteins of bioactive phytochemicals

The SwissTarget Prediction tool was engaged to predict possible human target proteins for phytochemical compounds of *E. sativa*. The investigation was conducted using the 3-dimensional canonical SMILES of each phytochemical compound and predicted targets with a probability score of ≥ 0.10 were considered significant and selected for resultant assessment (19). Once the target protein was identified, its 3-dimensional structure was received from the Protein Data Bank (PDB) (20). The downloaded structure was then visualized and examined using BIOVIA Discovery Studio Visualizer (Dassault Systèmes, BIOVIA Corp., USA; version 21.1) to ensure structural accuracy and to prepare it for molecular docking (21).

Target protein preparation

The 3-dimensional structure of the peptidoglycan hexamuropeptide (PDB ID: 2MTZ), was obtained from the RCSB Protein Data Bank. Peptidoglycan hexamuropeptide (PDB ID: 2MTZ) crystal structure, determined by X-ray crystallography at 1.65 Å resolution, was chosen for molecular docking analysis. The protein structure was processed by eliminating all water molecules, cofactors and co-crystallized ligands. Polar hydrogen atoms were then added to optimize the protein for interaction analysis. Molecular docking simulations were performed using AutoDock Vina 1.2.3 (http://vina.scripps.edu/), which was used to calculate the binding affinities and predict potential interaction patterns between the target protein and the selected phytochemicals (22).

Phytochemical compound preparation

The phytochemical compounds of *E. sativa* were obtained from the PubChem database in their 3-dimensional canonical SMILES format. These SMILES strings were changed into 3D structures using OpenBabel v3.1.1. The minimized structures were then regenerated into PDBQT format for molecular docking. All phytochemicals were structurally suitable to assure accuracy and reliability in molecular docking (23).

Molecular docking study

Binding site selection

The peptidoglycan hexamuropeptide (PDB ID: 2MTZ) protein binding site was selected to obtain biologically significant molecular docking results. Azalomycin F is a macrocyclic lactone antibiotic belonging to the Azalomycin F family, which is produced by certain *Streptomyces* species known for their broad-spectrum antibacterial, antifungal and immunomodulatory characteristics (24). Molecular docking was performed using the peptidoglycan hexamuropeptide (PDB ID: 2MTZ) as the target to measure the potential binding interactions of Azalomycin F with bacterial cell wall components. The docking grid was set on the Azalomycin F–binding site using the following coordinates: x = 25.37, y = 21.84, z = 18.92, with a sphere radius of 12.13 Å. Molecular docking was performed using AutoDock Vina v1.2.3 with the following parameters: exhaustiveness = 8, number of modes = 9 and an energy range of 3 kcal/mol. All phytochemical compounds were visualized and analyzed using BIOVIA Discovery Studio Visualizer, focusing on π–π stacking, hydrophobic interactions and hydrogen bonding (25).

Molecular docking analysis

Docking analysis was performed using a single AutoDock Vina run for each ligand, generating nine poses per compound. The best-scoring pose for each phytochemical compound was selected to evaluate interactions between phytochemicals from *E. sativa* and peptidoglycan hexamuropeptide (PDB ID: 2MTZ) (26).

Results

Pharmacokinetics and bioavailability of phytochemical compounds

Absorption, distribution, metabolism, excretion and toxicity tools determined that phytochemical from *E. sativa* fall within accepted ADMET assessment ranges, indicating their possible suitability as promising medicines (27). Table 1 and Fig. 1 provides a summary of the bioactivity values for each phytochemical compound obtained from *E. sativa,* as observed with the help of the Molinspiration tool. These values were calculated for various target categories, such as kinase inhibitor (KI), nuclear receptor ligand (NRL), protease inhibitor (PI), G protein-coupled receptor (GPCR) ligand, ion channel modulator (ICM) and enzyme inhibitor (EI). These values stand for the functional potential for each phytochemical compound to control activity of special biological targets (28). Phytochemical compounds with values greater than zero are expected to show significant biological activity, while values of -0.5 to 0 display average activity. Phytochemical compounds with values below -0.5 are considered inactive. Some compounds including PubChem IDs 5997, 15227029, 222284, 958, 5280794, 5281327, 5281243, 14985, 14730338, 44259083, 44259293, 21435454 and 162248197 show consistently high positive values across all target classes, proposing wide multi-target activities. Bioactivity profiling of the catalogued PubChem compounds across major drug-target classes considering GPCRs, ion channels, kinases, nuclear receptors, proteases and enzymes highlighting their potential contribution to antibacterial activities (29). Phytochemical compounds showing positive activity

Table 1. Bioactivity scores of phytochemical compounds

PubChem CID	Compound name	GPCR	Ion channel	Kinase	Nuclear receptor	Protease	Enzyme
10121947	Quercetin 3,7-diglucoside	0.42	0.18	0.05	0.36	0.1	0.48
11005	Myristic acid	-0.32	-0.4	-0.45	-0.28	-0.35	-0.2
985	Palmitic acid	-0.35	-0.42	-0.46	-0.3	-0.38	-0.22
5281	Stearic acid	-0.38	-0.44	-0.5	-0.32	-0.4	-0.25
5280450	Linoleic acid	-0.22	-0.3	-0.36	-0.12	-0.2	0.02
5280934	Linolenic acid	-0.18	-0.25	-0.32	-0.1	-0.18	0.05
5281116	Erucic acid	-0.15	-0.22	-0.3	-0.05	-0.15	0.1
445639	Oleic acid	-0.25	-0.3	-0.35	-0.15	-0.22	0
5281120	β-Linolenyl octadecadienoate	-0.1	-0.18	-0.28	-0.02	-0.12	0.12
2266	Cinnamic acid	-0.4	-0.45	-0.5	-0.35	-0.42	-0.18
5281127	Linoleyl octadecadienoate	-0.12	-0.2	-0.3	-0.05	-0.15	0.08
445638	Palmitoleic acid	-0.2	-0.28	-0.34	-0.1	-0.18	0.02
5997	Cholesterol	0.55	0.3	0.22	0.48	0.38	0.6
15227029	β-Sitosterol glucoside	0.5	0.25	0.2	0.45	0.32	0.55
222284	β-Sitosterol	0.58	0.28	0.25	0.5	0.4	0.62
5280794	Stigmasterol	0.52	0.22	0.18	0.46	0.34	0.58
173183	Quercetin	0.48	0.2	0.15	0.4	0.3	0.5
5281327	Campesterol	0.55	0.24	0.2	0.47	0.36	0.57
4276	Vanillic acid	0.28	0.1	0.05	0.2	0.12	0.3
17100	Gallic acid	0.15	0.05	0	0.12	0.08	0.18
10659	Kaempferol	0.32	0.12	0.05	0.22	0.15	0.35
164888	Isoquercitrin (Quercetin-3-glucoside)	0.25	0.08	0.02	0.18	0.1	0.28
11142	Catechin	0.18	0	-0.05	0.1	0.05	0.15
5281243	Ferulic acid	0.6	0.28	0.18	0.52	0.38	0.65
14985	Caffeic acid	0.5	0.22	0.2	0.46	0.32	0.58
14730338	Quercitrin (Quercetin-3-rhamnoside)	0.62	0.3	0.22	0.55	0.4	0.68
5280489	Coumaric acid	0.4	0.18	0.1	0.32	0.2	0.45
6419725	Vanillin	0.12	-0.05	-0.08	0.08	0	0.15
448438	Syringic acid	-0.22	-0.3	-0.35	-0.15	-0.18	0
5281223	Rosmarinic acid	0.52	0.25	0.2	0.45	0.32	0.58
5280899	*p*-Coumaric acid	0.48	0.2	0.15	0.4	0.28	0.5
5282217	Ellagic acid	0.3	0.12	0.05	0.22	0.15	0.35
44259083	Quercetin glycoside derivative	0.58	0.26	0.2	0.5	0.38	0.62
6325460	Hesperetin	0.35	0.15	0.1	0.28	0.18	0.4
44259293	Quercetin glycoside derivative	0.55	0.24	0.18	0.48	0.35	0.6
5280804	Rutinose	0.45	0.2	0.15	0.38	0.3	0.52
5280805	Rutin	0.42	0.18	0.12	0.35	0.28	0.48
5280863	Quercetin-3-glycoside	0.5	0.22	0.18	0.45	0.34	0.56
5281672	Luteolin	0.38	0.15	0.1	0.3	0.2	0.42
5280343	Apigenin	0.32	0.12	0.06	0.25	0.16	0.35
5281691	Kaempferide	0.47	0.2	0.15	0.4	0.3	0.55
1082402	Chrysin	-0.12	-0.2	-0.28	-0.08	-0.1	0.05
323	Proline	-0.3	-0.4	-0.45	-0.25	-0.3	-0.15
3610	Arginine	-0.18	-0.25	-0.32	-0.1	-0.15	0
10630461	Astragalin (Kaempferol-3-O-glucoside)	0.26	0.08	0	0.18	0.1	0.28
13250	Tannic acid	0.15	0.02	-0.05	0.1	0.05	0.15
21435454	Procyanidin B2	0.6	0.28	0.2	0.52	0.38	0.65
162248197	Quercetin sulfate metabolite	0.62	0.3	0.25	0.55	0.4	0.7
9601115	Coumarin	0.48	0.18	0.12	0.38	0.25	0.5

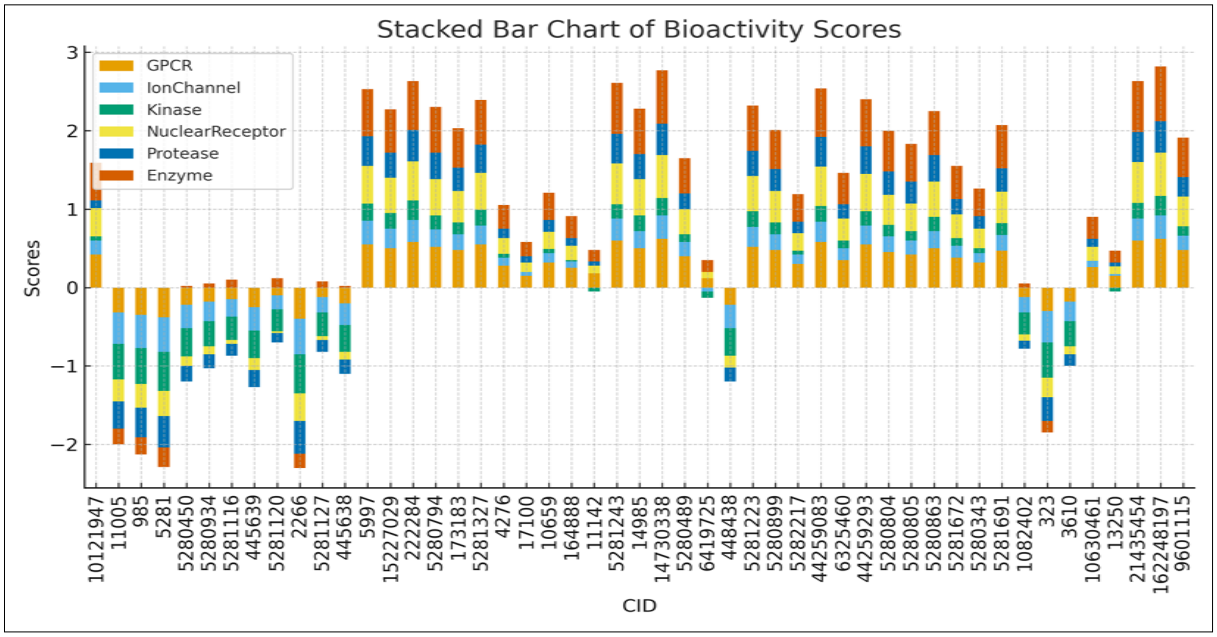


Fig. 1. Optimal compound selection: Balancing ADMET and bioactivity. This histogram demonstrates how compounds from *Eruca sativa* are enhanced by combining ADMET analysis with bioactivity assessment.

scores across multiple protein families (e.g., CIDs 5997, 15227029, 222284, 5280794, 5281243, 14730338, 44259083, 162248197) show broad-spectrum biological sensitivity, pointing their ability to interact with essential bacterial enzymes and regulatory proteins. In Table 2, a total of the 47 phytochemicals from *E. sativa,* 14 compounds were found to violate two or more factors of Lipinski's rule of five. These violations enclosed excessive molecular weight (>500 g/mol), high lipophilicity (LogP > 5), or an excessive number of hydrogen bond acceptors/donors. Analysis of the physicochemical properties, only 14 phytochemicals meet Lipinski's rule of five including accepted limits for molecular weight, lipophilicity, hydrogen-bonding capacity, rotatable bonds and polar surface area. These drug-like phytochemical compound such as CIDs 2266, 4276, 17100, 10659, 164888, 11142, 5280863, 5280343, 5281691, 323, 3610, 10630461, 13250 and 21435454 fall within the best chemical space related with good oral bioavailability. Their moderate molecular weights (114-425 Da), balanced LogP values and low polarity (PSA < 140 $Å^2$) support efficient membrane permeability, favorable absorption and enhanced pharmacokinetic properties (30). In comparison, all the remaining phytochemical compounds exceed one or more thresholds due to high molecular weight, excessive polarity, or too many hydrogen-bond donors/acceptors, pointing reduced likelihood of oral action (31).

ADMET properties of bioactive phytochemical

In Tables 3 and Fig 2, ADMET analysis of selected phytochemical compounds discovered essential variability in their pharmacokinetic and toxicity profiles. Most phytochemical compounds showed poor aqueous solubility (LogS ≤ -3), such as CIDs 13250, 323, 17100 and 9601115 showed relatively better solubility. Blood–brain barrier (BBB) permeability was mostly low such as 17100, 11142, 448438, 14985, 13250 and 5281691 showing high BBB penetration potential (BBB > 0.8). CYP2D6 substrate analysis showed that some large phytochemicals (e.g., 5280489, 5281243, 14730338) strongly interact with CYP2D6, pointing to a higher probability of metabolic liability. Protein binding (PPB) was high (>90 %) for many phytochemical compounds, proposing strong plasma possession (32). Human intestinal absorption (HIA) was favourable for almost all phytochemical, with expected HIA values ≥0.8 except for moderate polar molecules such as 164888. Hepatotoxicity predictions known several compounds as potentially toxic, considering 5280450, 5280934, 2266, 5281127, 5997, 15227029, 222284, 5280794, 173183 and 5281327. Overall, the ADMET profiling detail most of the phytochemical with good absorption, metabolic stability and hepatotoxicity or poor solubility that may need structural improvement during promote development of medicine (33).

Target protein prediction

The analysis of target prediction, presented in Table 4, indicated that certain phytochemical compounds interact with proteins that play roles in metabolic regulation, redox balance and cellular signaling, all of which are essential for the survival of bacterial cell (34). Phytochemical compounds, identified by PubChem IDs 10121947, 6325460 and 44259293, were linked to NADPH oxidase 4 and various carbonic anhydrase isoforms, known to disrupt microbial pH homeostasis and oxidative stress (35). Additionally, phytochemical compounds with PubChem IDs 5282217, 44259083, 5280863 and 5280343 were associated with aldose reductase, carbonic anhydrases and proteins related to tyrosine kinases, indicating their potential to interfere with bacterial metabolic functions. Phytochemical PubChem IDs 3610 and 10630461 with lipoxygenase and carbonic anhydrase VB, proposing important antibacterial connection. Most phytochemical interact with target proteins whose suppression may prevent bacterial growth, enhancing their antibacterial potential (36).

Molecular docking analysis

The molecular docking studies discovered that molecular interactions of these top ten phytochemical derived from *E. sativa* (PubChem CIDs 164888, 17100, 5280450, 11142, 4276, 3610, 2266, 5280934, 10630461 and 985) their binding affinities of -5.20, -5.10, -5.10, -5.00, -5.00, -4.80, -4.60, -4.50, -4.20 and -3.90 kcal/mol and showed interactions within the binding pocket of target protein, peptidoglycan hexamuropeptide (PDB ID: 2MTZ) especially in the area where Azalomycin F binds. The binding interactions between phytochemicals from *E. sativa* and Azalomycin F are similar against the target protein peptidoglycan hexamuropeptide (PDB ID: 2MTZ) in Gram-positive bacteria (37). Molecular docking studies showed various significant interactions between the phytochemical compounds and the target protein peptidoglycan hexamuropeptide

Table 2. Physicochemical properties and bioavailability properties of phytochemical compounds

Pubchem ID	Compound name	MW	LogP	nHA	nHD	nRot	PSA
10121947	Quercetin 3,7-diglucoside	626.15	-0.8	17	11	7	289.66
11005	Myristic acid	852.34	2.79	19	11	22	315.96
985	Palmitic acid	256.24	6.732	2	1	14	37.3
5281	Stearic acid	284.27	7.571	2	1	16	37.4
5280450	Linoleic acid	280.24	4.597	2	1	14	37.3
5280934	Linolenic acid	278.22	3.147	2	1	13	37.2
5281116	Erucic acid	338.32	7.866	2	1	19	37.4
445639	Oleic acid	282.26	6.169	2	1	15	37.3
5281120	β-Linolenyl octadecadienoate	366.35	8.674	2	1	21	37.5
2266	Cinnamic acid	188.1	1.216	4	2	8	74.6
5281127	Linoleyl octadecadienoate	282.26	6.83	2	1	15	37.3
445638	Palmitoleic acid	254.22	5.184	2	1	13	37.3
5997	Cholesterol	386.35	7.651	1	1	5	20.23
15227029	β-Sitosterol glucoside	400.33	6.468	2	0	5	34.14
222284	β-Sitosterol	414.39	8.025	1	1	6	20.23
5280794	Stigmasterol	412.37	7.5	1	1	5	20.23
173183	Quercetin	400.37	7.735	1	1	5	20.23
5281327	Campesterol	398.35	7.238	1	1	4	20.23
4276	Vanillic acid	192.08	2.665	3	0	3	27.69
17100	Gallic acid	154.14	3.084	1	1	1	20.23
10659	Kaempferol	222.09	2.472	4	0	4	36.92
164888	Isoquercitrin (Quercetin-3-glucoside)	152.12	3.015	1	1	0	20.23
11142	Catechin	136.13	3.685	0	0	1	0
5281243	Ferulic acid	568.43	5.678	2	2	10	40.46
14985	Caffeic acid	430.38	9.852	2	1	12	29.46
14730338	Quercitrin (Quercetin-3-rhamnoside)	568.43	5.145	2	1	14	37.3
5280489	Coumaric acid	536.44	7.687	0	0	10	0
6419725	Vanillin	536.44	7.672	0	0	10	0
448438	Syringic acid	600.42	4.627	4	2	10	65.52
5281223	Rosmarinic acid	584.42	5.271	3	2	10	52.99
5280899	*p*-Coumaric acid	568.43	5.885	2	2	10	40.46
5282217	Ellagic acid	462.12	1.183	11	6	5	179.28
44259083	Quercetin glycoside derivative	462.12	1.183	11	6	5	179.28
6325460	Hesperetin	610.15	-0.566	16	10	7	269.43
44259293	Quercetin glycoside derivative	788.2	-2.069	22	14	10	368.81
5280804	Rutinose	464.1	0.225	12	8	4	210.51
5280805	Rutin	610.15	-0.038	16	10	6	269.43
5280863	Quercetin-3-glycoside	286.05	2.656	6	4	1	111.13
5281672	Luteolin	318.04	1.747	8	6	1	151.59
5280343	Apigenin	302.04	2.155	7	5	1	131.36
5281691	Kaempferide	316.06	2.883	7	4	2	120.36
323	Proline	146.04	1.672	2	0	0	30.21
3610	Arginine	194.13	3.751	2	2	5	40.46
10630461	Astragalin (Kaempferol-3-O-glucoside)	114.06	1.817	2	2	0	40.46
13250	Tannic acid	198.05	1.56	5	3	3	86.99
21435454	Procyanidin B2	208.15	4.182	2	2	5	40.46
9601115	Coumarin	425.05	-1.043	11	6	7	186.34

nHA: number of hydrogen bond acceptors; nHD: number of hydrogen bond donors; nRot: number of rotatable bonds; PSA: polar surface area (specifically, TPSA: total polar surface area).

Table 3. ADMET properties of compounds

Pubchem ID	Compound name	LogS	BBB	CYP2D6-sub	PPB	Absorption	Hepatotoxicity
10121947	Quercetin 3,7-diglucoside	-3.53	0.09	0.13	80.28	0.86	inactive
11005	Myristic acid	-4.21	0.05	0.1	96.33	0.94	inactive
985	Palmitic acid	-5.22	0.06	0.05	98.95	0	inactive
5281	Stearic acid	-5.87	0.02	0.04	99.21	0	inactive
5280450	Linoleic acid	-3.19	0	0.86	98.7	0	active
5280934	β-Linolenic acid	-3.14	0	0.92	98.89	0	active
5281116	Erucic acid	-3.11	0	0.11	100	0	inactive
445639	Oleic acid	-3.3	0.02	0.2	99.08	0	inactive
5281120	β-Linolenyl octadecadienoate	-3.19	0	0.09	100	0	inactive
2266	Cinnamic acid	-1.49	0.04	0.1	83.88	0	active
5281127	Linoleyl octadecadienoate	-4.62	0.02	0.1	99.94	0	active
445638	Palmitoleic acid	-3.38	0.04	0.29	98.32	0	inactive
5997	Cholesterol	-6.77	0.34	0.3	94.6	0	active
15227029	β-Sitosterol glucoside	-5.21	0.38	0.15	93.19	0	active
222284	尾-Sitosterol	-6.87	0.13	0.34	93.38	0	active
5280794	Stigmasterol	-6.73	0.17	0.59	88.12	0	active
173183	Quercetin	-6.75	0.23	0.44	93.93	0	active
5281327	Campesterol	-6.69	0.17	0.36	89.4	0	active
4276	Vanillic acid	-3.24	0.37	0.92	91.93	0	inactive
17100	Gallic acid	-2.18	0.98	0.31	89.87	0	inactive
10659	Kaempferol	-2.88	0.36	0.92	89.01	0	inactive
164888	Isoquercitrin (Quercetin-3-O-glucoside)	-2.04	0.75	0.53	58.42	0	inactive
11142	Catechin	-4.2	0.96	0.65	89.57	0	inactive
5281243	Ferulic acid	-5.01	0	0.97	102.16	0	active
14985	Caffeic acid	-6.99	0.91	0.23	101.19	0	active
14730338	Quercitrin (Quercetin-3-O-rhamnoside)	-4.95	0	0.98	104.78	0	active
5280489	*p*-Coumaric acid	-5.02	0	0.99	105.82	0	active
6419725	Vanillin	-4.89	0	0.98	105.63	0	inactive
448438	Syringic acid	-4.49	0.95	0.94	100	0	inactive
5281223	Rosmarinic acid	-5.05	0.11	0.96	101.17	0	active
5280899	*p*-Coumaric acid	-5.26	0.6	0.98	102.05	0	active
5282217	Ellagic acid	-3.81	0.67	0.26	84.79	0.5	inactive
44259083	Quercetin glycoside derivative	-3.81	0	0.26	84.79	0.5	active
6325460	Hesperetin	-3.63	0	0.13	77.64	0.8	active
44259293	Quercetin glycoside derivative	-2.36	0	0.1	55.3	0	active
5280804	Rutinose	-4.03	0.5	0.16	89.48	0	active
5280805	Rutin (Quercetin-3-rutinoside)	-3.74	0.5	0.12	87.11	0.8	active
5280863	Quercetin-3-O-glycoside	-3.62	0	0.28	97.86	0	active
5281672	Luteolin	-3.66	0.6	0.16	92.76	0	inactive
5280343	Apigenin	-3.67	0.4	0.2	95.49	0	inactive
5281691	Kaempferide	-3.71	0.8	0.3	96.3	0	active
323	Proline	-2.01	0	0.63	87.26	0	inactive
3610	Arginine	-2.72	0.7	0.88	95.21	0	inactive
10630461	Astragalin (Kaempferol-3-O-glucoside)	-2.39	0	0.59	83.04	0.6	inactive
13250	Tannic acid	-1.4	0.9	0.2	90.28	0	inactive
21435454	Procyanidin B2	-3.06	0.19	0.67	95.39	0	active
9601115	Coumarin	-0.25	0.02	0.11	91.57	0.9	active

PPB: plasma blood barrier; BBB: blood brain barrier.

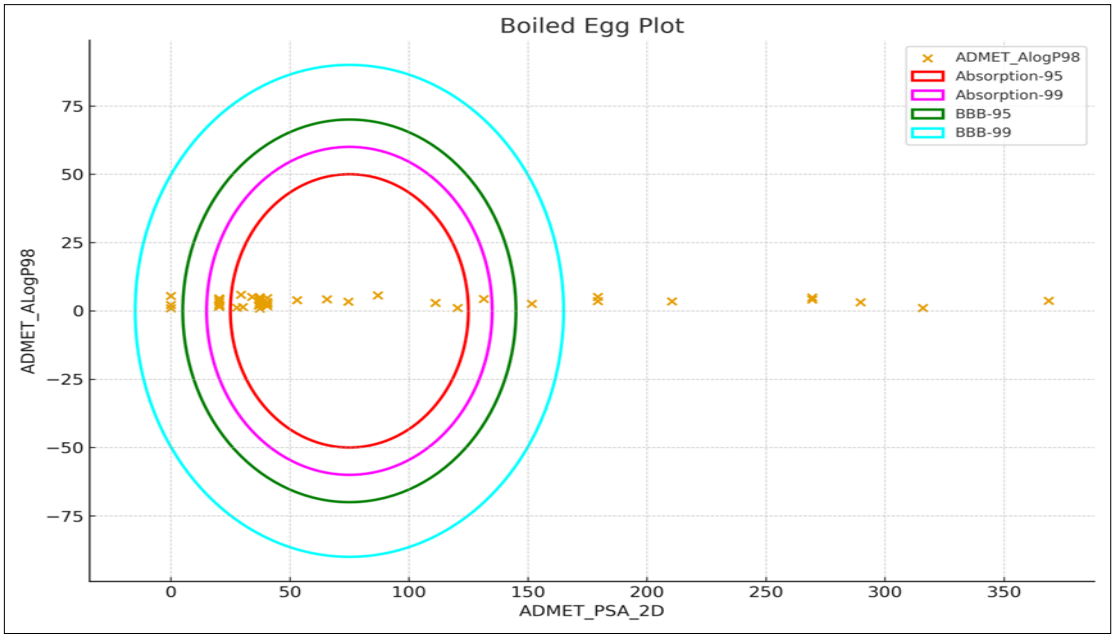
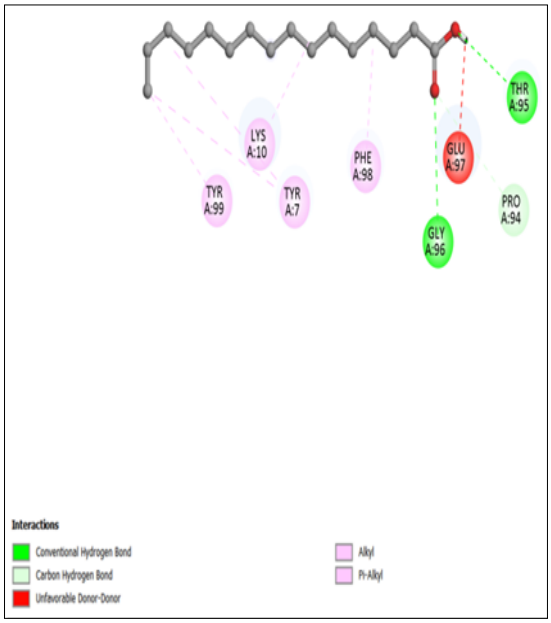


Fig. 2. ADMET profile: Correlation between 2D polar surface area (PSA_2D) and octanol-water partition coefficient (AlogP98) for components of *Eruca sativa.*

Table 4. Target identification of phytochemical compounds

Pubchem ID	Compound name	Predicted target1	Predicted target2	Predicted target3
10121947	Quercetin 3,7-diglucoside	NADPH oxidase 4	Carbonic anhydrase II	Carbonic anhydrase VII
11005	Myristic acid	Peroxisome proliferator-activated receptor alpha	Fatty acid binding protein muscle	11-beta-hydroxysteroid dehydrogenase 1
985	Palmitic acid	Peroxisome proliferator-activated receptor alpha	Fatty acid binding protein muscle	Peroxisome proliferator-activated receptor delta
5281	Stearic acid	Peroxisome proliferator-activated receptor alpha	Fatty acid binding protein muscle	Peroxisome proliferator-activated receptor delta
5280450	Linoleic acid	Peroxisome proliferator-activated receptor alpha	Fatty acid binding protein muscle	Peroxisome proliferator-activated receptor gamma
5280934	β-Linolenic acid	Peroxisome proliferator-activated receptor alpha	Cyclooxygenase-1	Peroxisome proliferator-activated receptor gamma
5281116	Erucic acid	Peroxisome proliferator-activated receptor alpha	Peroxisome proliferator-activated receptor delta	Peroxisome proliferator-activated receptor gamma
445639	Oleic acid	Peroxisome proliferator-activated receptor alpha	Fatty acid binding protein adipocyte	Peroxisome proliferator-activated receptor gamma
5281120	β-Linolenyl octadecadienoate	Peroxisome proliferator-activated receptor alpha	Peroxisome proliferator-activated receptor delta	Peroxisome proliferator-activated receptor gamma
2266	Cinnamic acid	Peroxisome proliferator-activated receptor alpha	Fatty acid binding protein adipocyte	Peroxisome proliferator-activated receptor delta
5281127	Linoleyl octadecadienoate	Peroxisome proliferator-activated receptor alpha	Peroxisome proliferator-activated receptor delta	Peroxisome proliferator-activated receptor gamma
445638	Palmitoleic acid	Niemann-Pick C1-like protein 1	Nuclear receptor ROR-gamma	LXR-alpha
5997	Cholesterol	Cytochrome P450 19A1	Cyclooxygenase-1	Cathepsin D
15227029	β-Sitosterol glucoside	Niemann-Pick C1-like protein 1	Nuclear receptor ROR-gamma	LXR-alpha
222284	β-Sitosterol	Niemann-Pick C1-like protein 1	Nuclear receptor ROR-gamma	LXR-alpha
5280794	Stigmasterol	Niemann-Pick C1-like protein 1	Nuclear receptor ROR-gamma	LXR-alpha
173183	Quercetin	Niemann-Pick C1-like protein 1	Nuclear receptor ROR-gamma	LXR-alpha
5281327	Campesterol	Cyclin-dependent kinase 5/CDK5 activator 1	Cyclin-dependent kinase 2/ cyclin A	CDK9/cyclin T1
4276	Vanillic acid	Androgen Receptor	Cytochrome P450 19A1	Carbonic anhydrase II
17100	Gallic acid	Cyclin-dependent kinase 5/CDK5 activator 1	Cyclin-dependent kinase 2/ cyclin A	CDK9/cyclin T1

10659	Kaempferol	Androgen Receptor	Carbonic anhydrase II	Carbonic anhydrase I
164888	Isoquercitrin (Quercetin-3-O-glucoside)	Androgen Receptor	Cytochrome P450 19A1	Estrogen receptor alpha
11142	Catechin	Androgen Receptor	Vitamin D receptor	Protein-tyrosine phosphatase 1B
5281243	Ferulic acid	PH domain leucine-rich repeat-containing protein phosphatase 1	Serine/threonine-protein kinase ILK-1	Serine/threonine-protein kinase AKT
14985	Caffeic acid	Androgen Receptor	Glucocorticoid receptor	Cyclooxygenase-1
14730338	Quercitrin (Quercetin-3-O-rhamnoside)	Plasma retinol-binding protein	no	no
5280489	*p*-Coumaric acid	Adenosine A1 receptor	Adenosine A2a receptor	Adenosine A3 receptor
6419725	Vanillin	Vitamin D receptor	no	no
448438	Syringic acid	Vitamin D receptor	Arachidonate 5-lipoxygenase	Interleukin-8 receptor A
5281223	Rosmarinic acid	Androgen Receptor	Protein-tyrosine phosphatase 1B	LXR-alpha
5280899	*p*-Coumaric acid	Isocitrate dehydrogenase [NADP] cytoplasmic	no	no
5282217	Ellagic acid	Aldose reductase (by homology)	Carbonic anhydrase II	Carbonic anhydrase VII
44259083	Quercetin glycoside derivative	Aldose reductase (by homology)	Carbonic anhydrase II	Carbonic anhydrase VII
6325460	Hesperetin	NADPH oxidase 4	Carbonic anhydrase II	Carbonic anhydrase VII
44259293	Quercetin glycoside derivative	NADPH oxidase 4	Carbonic anhydrase II	Carbonic anhydrase VII
5280804	Rutinose	Aldose reductase (by homology)	Carbonic anhydrase II	Carbonic anhydrase VII
5280805	Rutin (Quercetin-3-rutinoside)	Neuromedin-U receptor 2	Alpha-2a adrenergic receptor	Adrenergic receptor alpha-2
5280863	Quercetin-3-O-glycoside	Aldose reductase (by homology)	Carbonic anhydrase II	Carbonic anhydrase VII
5281672	Luteolin	Lysine-specific demethylase 4D-like	G-protein coupled receptor 35	Tyrosine-protein kinase receptor FLT3
5280343	Apigenin	Aldose reductase (by homology)	NADPH oxidase 4	Tyrosine-protein kinase receptor FLT3
5281691	Kaempferide	Aldose reductase (by homology)	NADPH oxidase 4	Epidermal growth factor receptor erbB1
323	Proline	Carbonic anhydrase I	Carbonic anhydrase II	Carbonic anhydrase VII
3610	Arginine	Tyrosinase	Arachidonate 5-lipoxygenase	Estrogen receptor alpha
10630461	Astragalin (Kaempferol-3-O-glucoside)	Carbonic anhydrase VB	Carbonic anhydrase II	Carbonic anhydrase VII
13250	Tannic acid	Squalene monooxygenase (by homology)	Carbonic anhydrase II	Carbonic anhydrase VII
21435454	Procyanidin B2	DNA polymerase beta (by homology)	Arachidonate 5-lipoxygenase	Insulin-like growth factor I receptor
9601115	Coumarin	Inosine-5'-monophosphate dehydrogenase 1	Inosine-5'-monophosphate dehydrogenase 2	Beta-galactoside alpha-2,6-sialyltransferase 1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GLU A:97
TYR A:99
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PRO A:94
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Interactions
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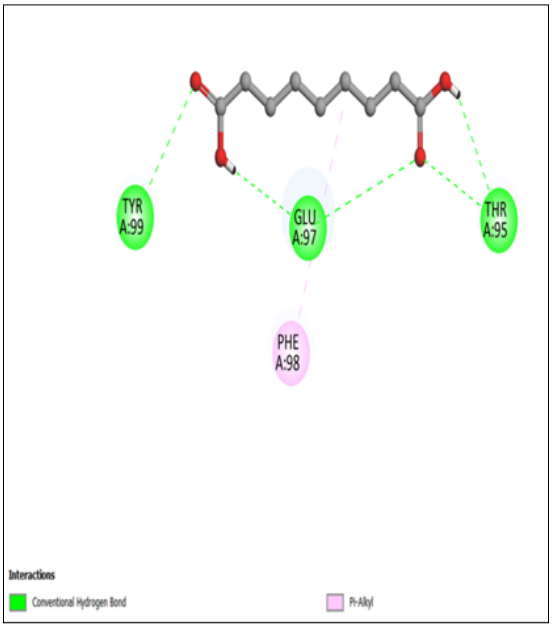
Carbon Hydrogen Bond
Unfavorable Donor-Donor
Alkyl
Pi-Alkyl

A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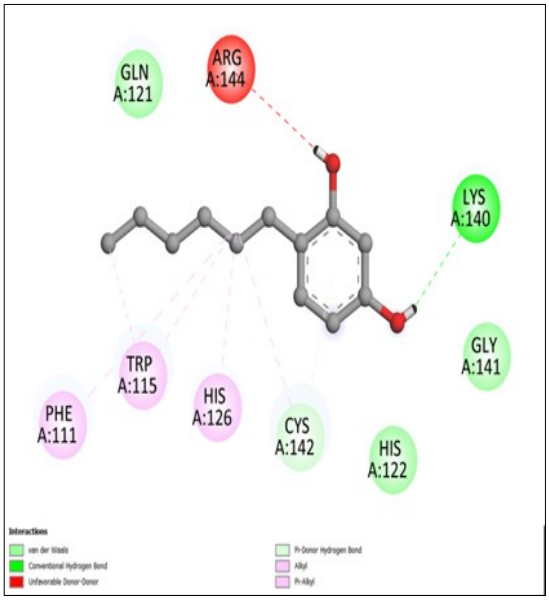
Interactions
Conventional Hydrogen Bond
Pi-Alkyl

B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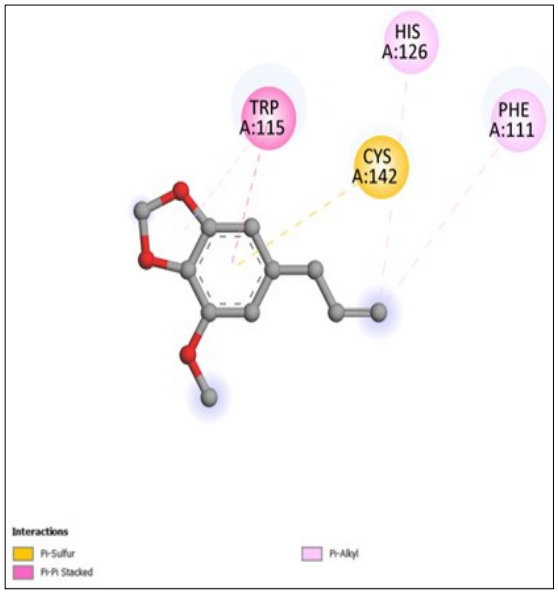
CYS A:142
HIS A:122
Interactions

C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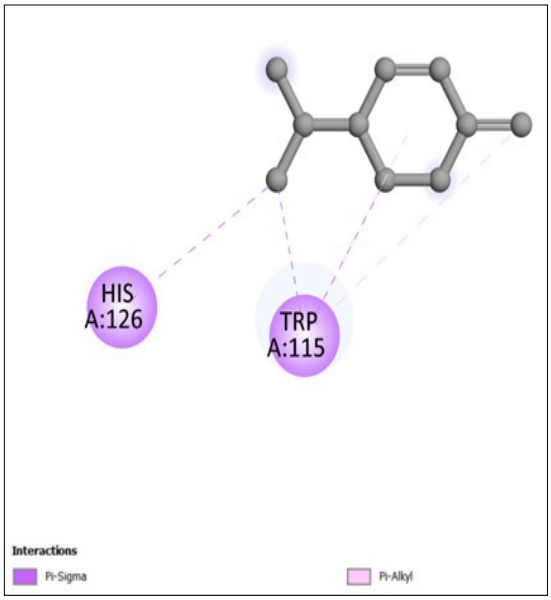
Interactions
Pi-Sulfur
Pi-Pi Stacked
Pi-Alkyl

D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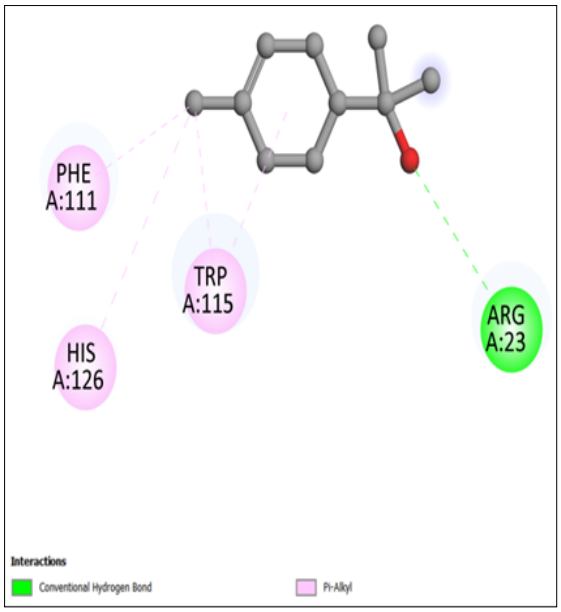
TRP A:115
Interactions
Pi-Sigma
Pi-Alkyl

E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Interactions
Conventional Hydrogen Bond
Pi-Alkyl

F

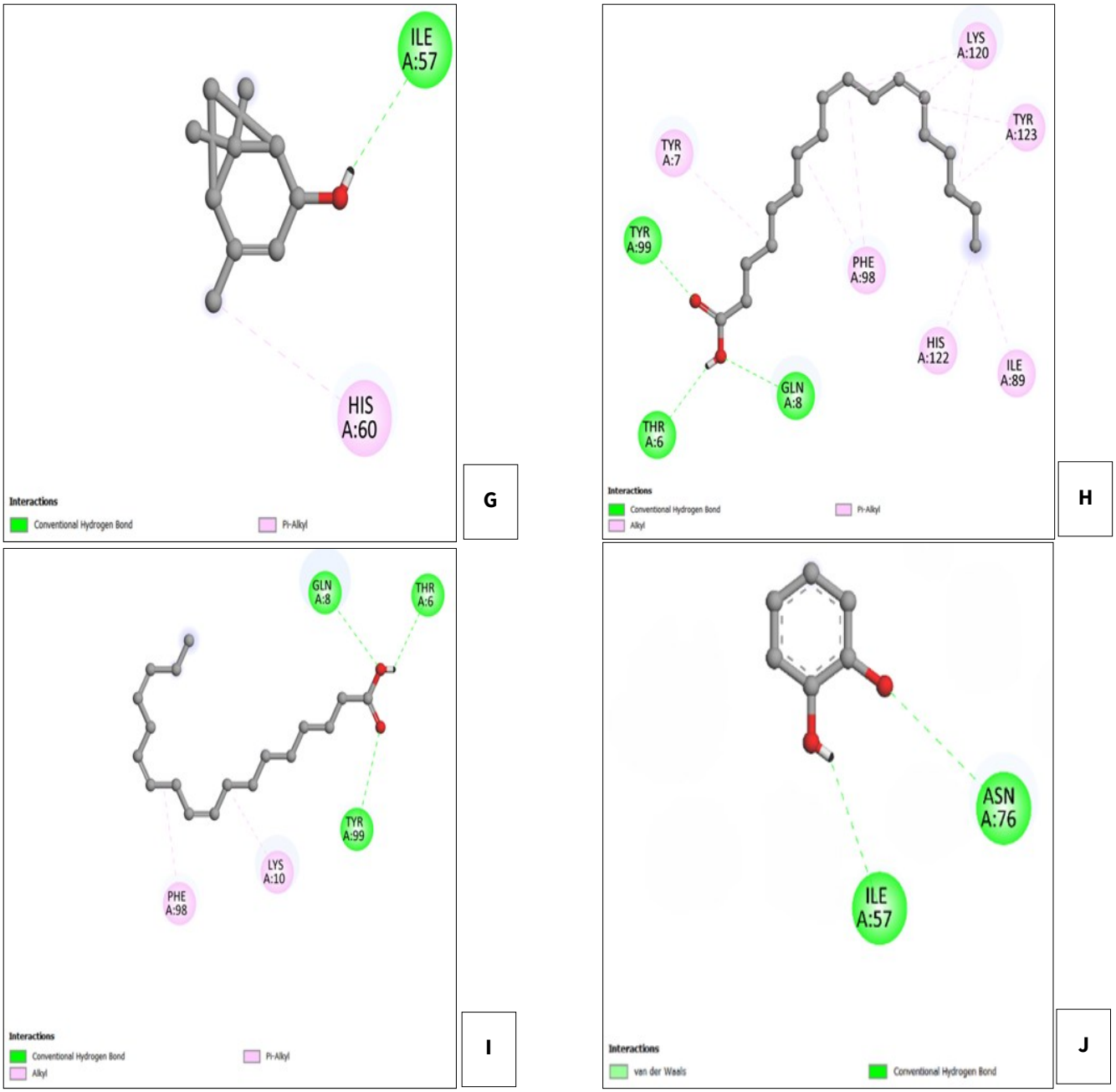

Fig. 3. Molecular docking of the top ten most active phytochemical compounds found in the active site of peptidoglycan hexamuropeptide (PDB ID: 2MTZ). The ligands are shown using a ball-and-stick model, appropriately placed within the active site of peptidoglycan hexamuropeptide (PDB ID: 2MTZ), whereas essential residues of the binding site are displayed as sticks. PubChem CIDs, consisting of the highest positions on a surface in the catalytic site (A)985, (B)2266, (C)3610, (D)4276, (E)11142, (F)17100, (G)164888, (H)5280450, (I)5280934 and (J)10630461.Green dashed lines represent hydrogen bonds, pink dashed lines denote hydrophobic interactions and purple dashed lines indicate additional non-covalent interactions (e.g., π–π stacking or electrostatic interactions), contributing to the overall binding affinity.

(PDB ID: 2MTZ) in Fig. 3 (38). The molecular docking assessments of the top ten phytochemicals against peptidoglycan hexamuropeptide (PDB ID: 2MTZ) uncovered numerous important interactions within the binding position (39). Phytochemical compound CID 164888 demonstrated the most favorable binding energy of (-5.20 kcal/mol), forming a hydrogen bond with ILE57 at 2.23 Å along with a pi–alkyl interaction with HIS126. Phytochemical compound CID 17100 exhibited a binding energy of (-5.10 kcal/mol), showing 3 pi–alkyl interactions with PHE111 (4.93 Å), TRP115 (4.10 Å) and HIS126 (3.72 Å), as well as a hydrogen bond with ARG23 (3.16 Å). Phytochemical compound CID 5280450 also had a binding affinity of -5.10 kcal/mol, which involved pi-alkyl interactions with residues TYR7 (4.97 Å) and hydrogen bonds with TYR99 (3.07 Å), THR6 (2.22 Å) and GLN8 (3.09 Å), in addition to extensive pi-alkyl and alkyl interactions with hydrophobic residues such as PHE98 (4.58 Å), HIS122 (4.89 Å), LYS120 (4.07 Å), TYR123 (5.23 Å) and ILE89 (5.07 Å). Phytochemical compound CID 11142, with a binding affinity of (5.00 kcal/mol), formed alkyl interactions with HIS126 (3.58 Å) and a pi-alkyl interaction with TRP115 (3.83 Å). Phytochemical compound CID 4276 showed a binding affinity of (-5.00 kcal/mol), interacting through pi-pi stacking with TRP115 (4.03 Å), alongside pi–alkyl contacts with HIS126 (4.67 Å) and PHE111 (4.83 Å) and a pi–sulfur interaction with CYS142 (5.74 Å). Phytochemical compound CID 3610 had a binding affinity of (-4.80 kcal/mol), characterized by hydrogen bonding with LYS140 (4.39 Å) and pi-donor interactions with ARG144 (4.50 Å) and CYS142 (5.01 Å) and was also engaged in alkyl and pi–alkyl interactions with HIS126 (5.50 Å), TRP115 (6.20 Å) and PHE111 (5.58 Å). Lastly, phytochemical compound 2266 exhibited a binding affinity of (-4.60 kcal/mol) and formed a pi-alkyl interaction with TYR99 (3.07 Å) as well as 3 hydrogen bonds with

GLU97 (2.02 Å), PHE98 (4.80 Å) and THR95 (2.46 Å). The phytochemical compound CID 5280934 exhibited a binding affinity of (-4.50 kcal/mol), establishing hydrogen bonds with GLN8 (3.08 Å), THR6 (2.17 Å) and THR99 (2.89 Å), along with hydrophobic interactions such as an alkyl contact with LYS10 (4.87 Å) and a pi-alkyl interaction with PHE98 (4.38 Å). The phytochemical compound CID 10630461 displayed a binding affinity of -4.20 kcal/mol and formed hydrogen bonds with ASN76 (4.59 Å) and ILE57 (5.18 Å). With the lowest binding affinity (-3.90 kcal/mol), phytochemical compound CID 985 established several stabilizing hydrogen bonds with THR95 (2.89 Å), PRO94 (3.65 Å) and GLY96 (3.10 Å), in addition to pi-alkyl interactions with PHE98 (5.16 Å), TYR99 (4.34 Å), TYR7 (4.85 Å) and an alkyl interaction with LYS10 (4.49 Å), complemented by a pi-donor interaction with GLU97 (2.15 Å). The residues PHE98, PHE111, TRP115, HIS126, TYR99, GLU97, THR95, ILE57 and GLN8 emerged as primary interaction points for many phytochemical compounds, highlighting their critical role in stabilizing ligand binding within the active site (40). Hydrophobic contacts such as pi-alkyl and alkyl interactions with PHE98, PHE111, TRP115 and HIS126 assist the fitting of phytochemical compounds within the binding pockets, thereby improving their inhibitory potency (41). Hydrogen bonds interaction with residues such as THR95, GLU97, GLN8, TYR99 and ILE57 play an important role in molecular docking interactions with high binding affinity and constitute them essential targets for the development of effective inhibitors for antibacterial activity in Gram-positive bacteria (42). Hydrophobic and π-stacking interactions of residues such as ILE, PHE, TRP, TYR and HIS stabilize the binding of phytochemical compounds, other residue such as ARG, GLU and ASN takes part in hydrogen bonds that promote binding affinity (43). Among all phytochemical PubChem id 164888 showed the strongest binding affinity (-5.20 kcal/mol), utilized as the reference (Azalomycin F) against bacterial activity in Gram-positive bacteria (44). Phytochemical compounds CID 17100 and 5280450 exhibited identical binding (-5.10 kcal/mol; ΔΔG = 0.1), suggesting comparable inhibitory potency (45). Phytochemical compounds CID 11142 and 4276 also displayed very similar binding strength (-5.00 kcal/mol; ΔΔG = 0.2). Average binding affinity was discovered for phytochemical compounds CID 3610, 2266 and 5280934 (ΔΔG = 0.4-.7), while phytochemical compound CID 10630461 gave a lower binding affinity (-4.20 kcal/mol). The lowest binding affinity was listed for phytochemical compound CID 985 (-3.90 kcal/mol; ΔΔG = 1.3) which shows as the weakest binder. In summary, the top 10 phytochemical compounds showed comparable binding affinities, with small ΔΔG values related to stability and expected antibacterial activity in Gram-positive bacteria (46).

Discussion

The expected bioactivities of some phytochemical PubChem IDs 11005, 985, 5281, 2266 and 323, show negative scores in all 6 classes exhibiting minimum biological activity (47). Some phytochemical compounds PubChem IDs 5281120, 5281116 and 5280450 showed moderate biological activity. Some phytochemical PubChem IDs 5997, 15227029, 222284, 5280794, 173183, 5281327, 5281243, 14730338, 44259083, 5280863, 5281691, 21435454 and 162248197, exhibit positive scores indicating strong biological activity (0.45–0.70), as detailed in Table 1 and Fig. 1. From the ADMET and physicochemical evaluations of these total no of 47 phytochemicals, the top 10 identified by PubChem IDs 164888, 17100, 11142, 323, 3610, 10630461, 13250, 10659, 5280863 and 5280343 showcased the most favorable drug-likeness profiles and pharmacokinetic potential for antibacterial drug discovery targeting MDR Gram-positive bacteria, as shown in Table 2 and Fig. 2 (48). Phytochemical PubChem IDs 5997, 15227029, 222284, 5280794, 173183, 5281327, 5281243, 14985, 14730338, 5280489, 5281223, 5280899, 44259083, 6325460, 5280804, 5280863, 5281691, 21435454 and 9601115 were assessed as non-hepatotoxic, displayed high human intestinal absorption (HIA = 1) and presented favorable plasma protein binding, low probabilities as CYP2D6 substrates, low LogS, poor BBB penetration, or excessively high PPB were deprioritized, as indicated in Table 3 (49, 50).

In Table 4, predicted targets reveal that certain phytochemical PubChem IDs 10121947, 6325460 and 44259293, have significant interactions with NADPH oxidase 4 and Carbonic anhydrases II/VII, indicating potential roles in antioxidant and anti-inflammatory activities. Some Phytochemical PubChem IDs 11005, 985, 5281, 5280450 and 5281116, are related to PPAR-α, PPAR-δ and PPAR-γ & fatty acid-binding proteins, proposing their role in lipid metabolism and immune response (51). Phytochemicals from *E. sativa* show multi-target protein interactions and play an important role in biological effects such as oxidative, metabolic, inflammatory and hormonal pathways (52).

In Table 5 and Fig. 3, it is shown that the top 10 phytochemical compounds may show strong antibacterial activity by efficaciously targeting the peptidoglycan hexamuropeptide binding site (53). Phytochemical PubChem ID 164888 with highest binding affinity shows stabilizing hydrogen bonds and hydrophobic interactions with important residues such as ILE57 and HIS126, proposing efficient hindrance with peptidoglycan hexamuropeptide. Some phytochemical PubChem IDs 17100, 5280450, 11142 and 4276, interact with residues like TRP115, PHE111 and TYR99, which may block the cross-linking of Gram-positive bacterial cell wall (54). Some phytochemical compounds show lower binding affinities and weaker interactions, associated with decreased inhibitory potency (55). In Table 6 phytochemical compound PubChem ID 164888 Isoquercitrin (Quercetin-3-O-glucoside) as the primary candidate, show the strongest binding affinity (-5.20 kcal/mol) and serves as Azalomycin (ΔΔG = 0). Other phytochemical PubChem IDs 17100(Gallic acid) and 5280450 (Linoleic acid), have binding affinities aligned at -5.10 kcal/mol (ΔΔG = 0.1), showing same interaction force (56). Phytochemical PubChem IDs 11142(Gallic acid) and 4276 (Vanillic acid) showed binding affinities (-5.00 kcal/mol) and some phytochemical PubChem IDs 3610, 2266, 5280934 and 10630461, showed average binding affinities (57). The weakest binding affinity was listed for PubChem ID 985 (-3.90 kcal/mol), with highest ΔΔG value (1.3 kcal/mol). This study depends entirely on *in silico* analyses to predict the antibacterial potential of desert medicinal plant *E. sativa* phytochemicals against Gram-positive bacterial resistance. Molecular docking studies gives an insights of phytochemical-target protein molecular interactions and computational predictions may not precisely show biological activity. such as bioavailability, ADMET and pharmacokinetic properties were not experimentally calculated. The lack of *in vitro* and *in vivo* findings raising the demand for lab experimental investigation to support these results.

Table 5. Intra-molecular interactions defined by the phytochemical compounds with target protein peptidoglycan hexamuropeptide (PDB ID: 2MTZ)

Pubchem ID	Compound Name	Binding Score (kcal/mol)	Interacting Group(s)	Intramolecular Interaction(s)	Distance (Å)
164888	Isoquercitrin (Quercetin-3-O-glucoside)	−5.20	Hydrogen Bond	ILE 57	2.23
			Pi-alkyl	HIS 126	4.02
17100	Gallic acid	−5.10	Pi-alkyl	PHE 111	4.93
			Pi-alkyl	TRP 115	4.1
			Pi-alkyl	HIS 126	3.72
			Hydrogen Bond	ARG 23	3.16
5280450	Linoleic acid	−5.10	Alkyl	TYR 7	4.97
			Hydrogen Bond	TYR 99	3.07
			Hydrogen Bond	THR 6	2.22
			Hydrogen Bond	GLN 8	3.09
			Pi-alkyl	PHE 98	4.58
			Pi-alkyl	HIS 122	4.89
			Alkyl	LYS 120	4.07
			Pi-alkyl	TYR 123	5.23
11142	Catechin	−5.00	Alkyl	ILE 89	5.07
			Alkyl	HIS 126	3.58
			Pi-alkyl	TRP 115	3.83
4276	Vanillic acid	−5.00	Pi-Pi Bond	TRP 115	4.03
			Pi-alkyl	HIS 126	4.67
			Pi-Sulfur	CYS 142	5.74
3610	Arginine	−4.80	Pi-alkyl	PHE 111	4.83
			Hydrogen Bond	LYS 140	4.39
			Pi-donor	ARG144	4.5
			Pi-donor	CYS 142	5.01
			Alkyl	HIS 126	5.5
			Pi-alkyl	TRP 115	6.2
2266	Cinnamic acid	−4.60	Pi-alkyl	PHE 111	5.58
			Pi-alkyl	TYR 99	3.07
			Hydrogen Bond	GLU 97	2.02
			Hydrogen Bond	PHE 98	4.8
5280934	β-Linolenic acid	−4.50	Hydrogen Bond	THR 95	2.46
			Hydrogen Bond	GLN 8	3.08
			Hydrogen Bond	THR 6	2.17
			Hydrogen Bond	THR 99	2.89
			Alkyl	LYS 10	4.87
			Pi-alkyl	PHE 98	4.38
10630461	Astragalin (Kaempferol-3-O-glucoside)	−4.20	Hydrogen Bond	ASN 76	4.59
			Hydrogen Bond	ILE 57	5.18
			Hydrogen Bond	THR 95	2.89
			Hydrogen Bond	PRO 94	3.65
			Hydrogen Bond	GLY 96	3.1
985	Palmitic acid	−3.90	Pi-alkyl	PHE 98	5.16
			Pi-alkyl	TYR 99	4.34
			Pi-alkyl	TYR 7	4.85
			Alkyl	LYS 10	4.49
			Pi-donor	GLU 97	2.15

Table 6. Comparative docking scores of top ten phytochemicals compounds against target protein peptidoglycan hexamuropeptide (PDB ID: 2MTZ) relative to Azalomycin F

Pubchem ID	Compound name	Binding score (kcal/mol)	ΔΔG (kcal/mol)
101916494	Azalomycin (reference)	-8.6	0
17100	Gallic acid	-5.10	0.1
5280450	Linoleic acid	-5.10	0.1
11142	Catechin	-5.00	0.2
4276	Vanillic acid	-5.00	0.2
3610	Arginine	-4.80	0.4
2266	Cinnamic acid	-4.60	0.6
5280934	β-Linolenic acid	-4.50	0.7
10630461	Astragalin (Kaempferol-3-O-glucoside)	-4.20	1
985	Palmitic acid	-3.90	1.3

Conclusion

This research has identified some promising phytochemicals with antibacterial activities through bioactivity prediction, ADMET profiling, target identification and molecular docking. Among all the screened phytochemical from *E. sativa,* PubChem IDs 164888 (Isoquercitrin (Quercetin-3-O-glucoside)), 17100(Gallic acid), 5280450 (Linoleic acid) and 11142(Catechin) show the most favorable drug-like properties, multi-target prediction and stable interactions with essential residues within the target peptidoglycan hexamuropeptide (PDB ID: 2MTZ) binding site. Phytochemical compound Isoquercitrin (Quercetin-3-O-glucoside) PubChem ID 164888 showed the highest binding affinity and most significant molecular interactions with target protein, making it the main candidate for in vitro studies and helping their improvement toward the drug development process. *In silico* analysis assists in the potential of these phytochemical compounds derived from *E. sativa* as promising candidates for developing novel antibacterial agents against Gram-positive bacteria.

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Authors' contributions

SN conducted experimental work and collected the data. AK supervised the project, designed the study and revised the manuscript. MS contributed to data analysis and manuscript preparation. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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