Molecular docking study and MM/GBSA analysis of novel phytochemicals from *Eclipta alba* (L.) against hepatitis c virus`

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Article History: Received: 02/05/2023 Revised: 25/06/2023 Accepted: 12/07/2023

Abstract

About 180 million individuals have acquired the hepatitis C virus (HCV). Damage to the liver, including cirrhosis, hepatic decompensation, and hepatocellular cancer, may worsen over time if not properly treated. Pegylated interferon-α and ribavirin are used in the conventional treatment nowadays. Moreover, this treatment is associated with substantial side effects in individuals. To overcome this problem, we chose the plant source of *Eclipta alba (L.)*, which treats antiviral activity. This study aims to determine the binding mode and hydrogen bond interaction of *E. alba* phytochemicals with the HCV NS5B polymerase enzyme. We describe Molecular docking analysis using Maestro12.7 software. Qikprop tool was used for assessing "drug-likeness" of the ligand. The binding between the NS5B polymerase protein (PDB ID: 3CJ5) and the ligand data demonstrated that most ligands formed H-bonds with residues (SER 476, TYR 477 and LEU 474) and pi-cation contacts with ARG 501. The docking score of phytoconstituents ranges from -7.561 to -5.029 kcal/mol, and reference sofosbuvir -7.541 kcal/mol. All phytoconstituents showed an excellent binding affinity against NS5B polymerase, but the best crucial score is Quercetin -7.561 kcal/mol. Quercetin stands out as a prospective drug candidate for further developing anti-HCV drugs.

Keywords: Anti-HCV, *Eclipta alba*, Glide and NS5B polymerase.

INTRODUCTION

Humans have used conventional medicinal plants for several years due to their potential therapeutic activity without side effects. In 2008, the World Health Organization (WHO) stated that over eighty percent of the global population uses conventional therapies derived from plants (G.V. Pierangeli and L.R Windell, 2009). The quest for herbal medicines has resulted in the finding of new drug molecules for various disorders, including liver diseases. (Kuruvilla 2002; Hosseinzadeh *et al.*, 2015) Here, we focus on the anti-HCV activity of *E.alba* (L.), a herb arranged in small clusters belonging to the Asteraceae family and native to Asia. It is commonly grown in waterlogged lands, hedges, and highways. The stiffened nodal points appear in the root. The hairy, brownish-red, and 40cm-tall branches are variable in size. Combining two carpels to form dry fruits with a single seed. (Guenné *et al.*, 2020; Timalsina and H.P. Devkota, 2021) *E.alba* contains more active constituents such as Alkaloids, Cardiac

glycoside, Carbohydrates, Steroids, Terpenoids, Phenol, Triterpenes, Protein, Resins, Saponins, Phlobatanins, Tannin, Phenolic compounds, and Flavonoids. (Hoque, 2019) Coumestans are included in herbal formulations intended to treat liver cirrhosis and viral hepatitis. (Wagner *et al.*, 1986) Secondary metabolites known as phytochemicals have therapeutic activity, such as anti-inflammatory, anti-mutagenic, anti-thrombogenic, antioxidant, anti-allergic, anticancer, antiviral, anti-bacterial, neuroprotective, antidiabetic, and hepatoprotective (Jahan, 2014). It is broadly utilized in India for enlarged liver as a cholagogue and deobstruent. Fever may be treated using an aqueous infusion of the entire plant. Mainly People use it for blackening, strengthening and promoting hair growth. This plant treats Scorpio sting and snakebite in China and Brazil (Wyson *et al.*, 2016).

One single strand of RNA makes up the Hepatitis C virus's genome. The length of the viral genome is around 9,400 nucleotides, and it encodes a single polyprotein with roughly 3,010 amino acids belonging to the Flaviviridae family, genus hepacivirus (Naika *et al.*, 2015). It comprises four structural and six non-structural proteins. NS5B was vital in viral replication (Venkatesan and J.F Dass 2017). In this study, we target NS5B polymerase. Until now, efficient drugs are unavailable for treating HCV, and potent natural plant compounds to inhibit the protein NS5B polymerase has become essential. Natural bioactive chemicals have a wider range of pharmacological activity, are less expensive to produce, and pose less health risks than their synthetic counterparts. An alternate and potentially curative path for curing HCV infection may be found in naturally occurring substances. The synthetic medications now used to treat HCV are expensive, have adverse reactions, and may cause drug resistance (Rehman *et al.*, 2016). HCV infection treatment may benefit from the use of a specific and potent medication such an inhibitor of NS5B. Molecular docking studies can achieve it. The field of molecular docking has come out in the last three decades, managed by the demand for structural molecular biology and structure-based drug discovery. Here, we will focus on molecular docking, a crucial method for investigating protein-ligand interactions that ultimately aids in the development of effective pharmaceuticals. The present study aims to conduct molecular docking studies to identify the potent HCV phytoconstituent of *E. alba* to inhibit the NS5B polymerase. The interest of molecular docking studies is to know the binding mode of the ligands on NS5B polymerase and the structural requirements essential for NS5B polymerase. The GLIDE molecular docking tool was used to analyze a dataset including 42 phytoconstituents.

METHODS

Preparation of Phytochemical Library

The phytochemical library was prepared by searching literature survey on PubMed, Science Direct, Google Scholar, Research Gate and other databases. Based on this, we have chosen forty-two phytoconstituents from the *E. alba* medicinal plant. We downloaded the SDF format of the 2D structure of all phytochemicals from the NCBI PubChem database. Further, a Computational investigation was performed on the Maestro 12.7 software (Schrodinger LLC, NY, USA, 2021-1) (Teli *et al.*, 2021)

Protein Preparation

The HCV protein of NS5B Polymerase enzyme complex with small fragments (SX6) X-ray crystal structure was obtained from Protein Data Bank [PDB Code: 3CJ5; Resolution: 1.92 Å]. The crystal structure was deleting the ligand and the cofactors. The Prep Wizard tool (Maestro software) was used for protein preparation pre-processing, deleting H_2O molecules exceeding 5Å from the hetero atom states— reorienting side-chain OH groups and relieving possible steric clashes by optimization and minimization using the OPLS-3e force field. A Root Mean Square Deviation (RMSD) limit of 0.3Å is used to restrict the minimizing to the supplied protein coordinates (Pattar et al., 2020).

Receptor Grid Generation

We can grid box typically by employing the receptor grid generation. Docking of ligand was not carried out prior to this step. The active site represents an enclosing box at the centroid of the workspace. Receptor grid generation with a suitable bond order as well as formal charges required a prepared protein structure. It consists of 4 tabs (Receptor, Site, Constraints and Rotatable), which make a grid. To make the grid, we used the advanced Glide settings X-axis 13 Å, Y-axis 10 Å, and Z-axis 10 Å centred. All ligands will be docked into this grid structure.

Ligand Preparation

We used the LigPrep tool (Schrodinger, LLC, NY, USA, 2009) for Ligand preparation. The ligands selected for the present study consist of *E.alba* phytochemicals and reference ligands. The structures of 42 phytochemicals and reference ligands retrieved two-dimensional (2D) structures in SDF format. The last step of LigPrep was minimizing the size of the molecules employing the OPLS-3e force field at a P^H of 7.2 in the Schrodinger Impact program until minimal RMSD of 0.12 Å was attained. After that, docking analysis was performed using the optimized ligands (Sahayarayan *et al.,* 2021).

Molecular Docking Analysis

Molecular docking on the prepared receptor against all ligands with the help of the ligand docking tool was used in Maestro. Extra precision (XP) docking was used to place each ligand into the active regions of NS5B polymerase with as few intermediate configurations as possible. The ligand interaction tool provides a visual illustration of the interaction between 2D ligands and amino acid residues in the NS5B polymerase. Then view the resulting docking studies output from the pose viewer (Choudhary *et al.,* 2020).

ADME/T Prediction

We used the Maestro (QikProp module) for the ADME/T evaluation (QikProp, 2020). Drug-likeness properties of the organic compounds show excellent binding affinities toward NS5B Polymerase. So, pharmacokinetic parameters were determined.

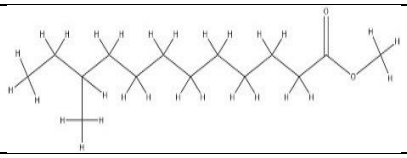
Prime MM/GBSA Analysis

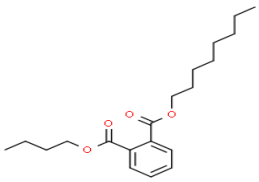
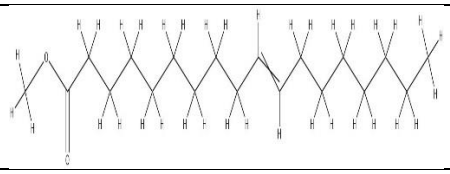
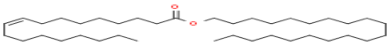
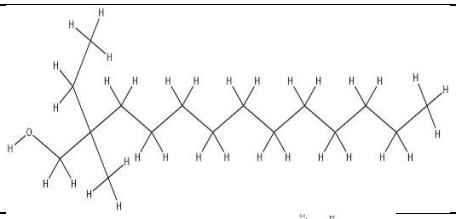
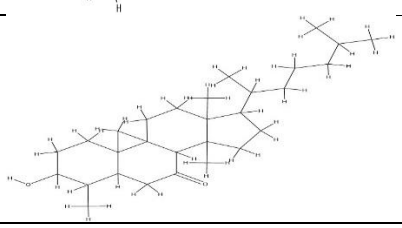
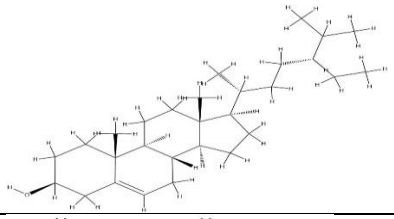
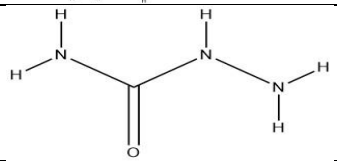
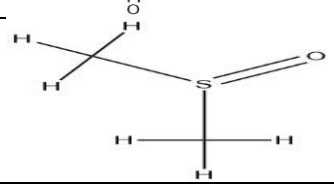
We calculate the binding free energy of each ligand. The post-docked ligands used as an input in the MMGBSA tool (Prime Version 4.8). Schrodinger displayed the free-energy difference between different ligand molecules, as measured by the relative score (ΔG bind) (Pattar *et al.,* 2020).

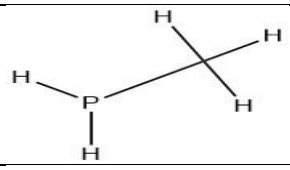
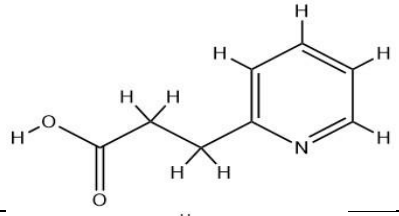
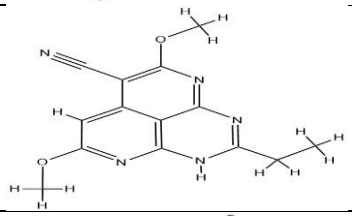
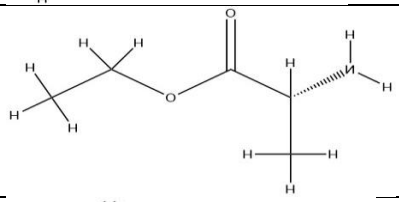
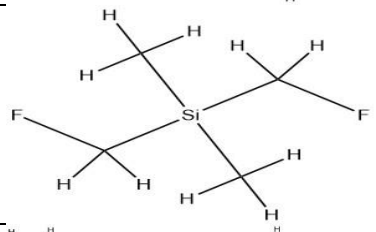
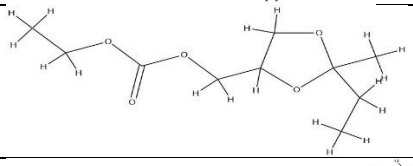
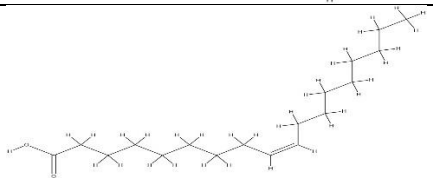
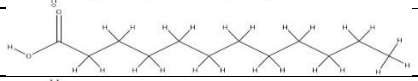
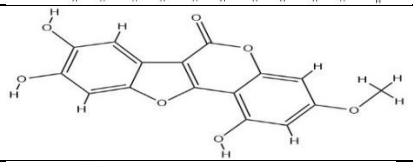
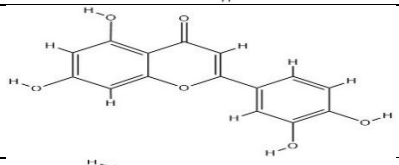
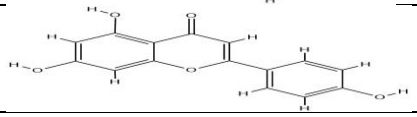
RESULTS

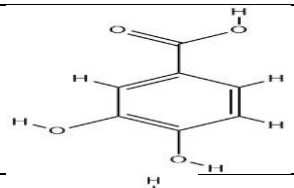
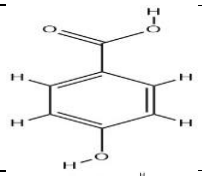
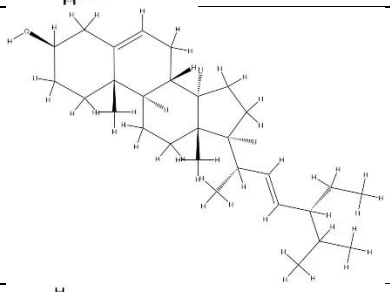
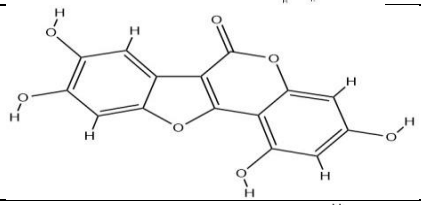
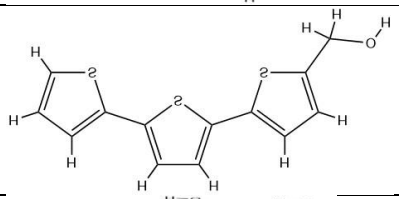
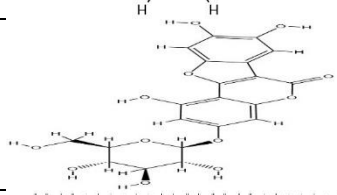
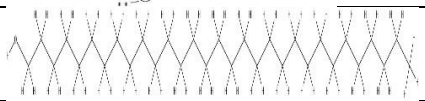
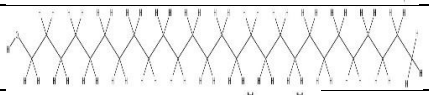
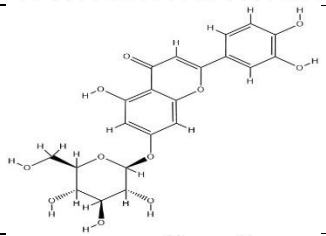
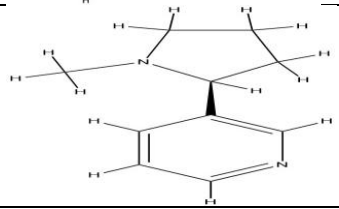
Modern drug design frequently uses computational techniques to comprehend the interactions between drug and its receptor. Based on the results of this review, it is clear that molecular docking is a useful tool for understanding the workings of drug-receptor interaction and designing new, more effective inhibitors. This molecular docking study tested forty-two ligands against the target protein of the NS5B Polymerase enzyme (PDB-3CJ5). Based on the literature survey, we selected phytochemicals from *E. alba*, listed in **Table 1**.

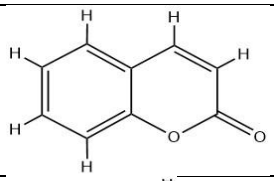
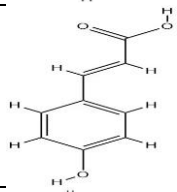
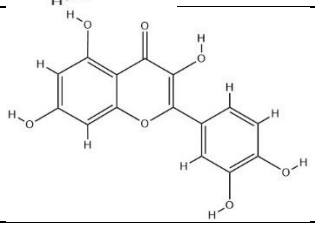
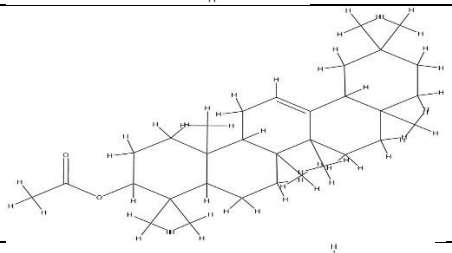
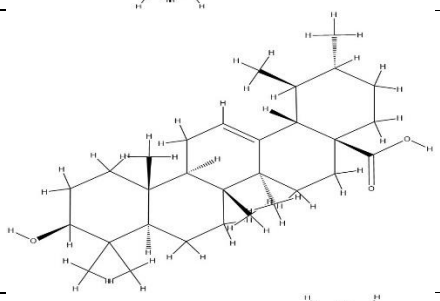
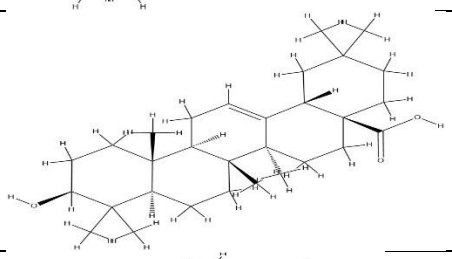
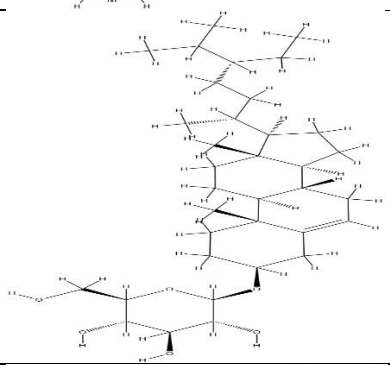
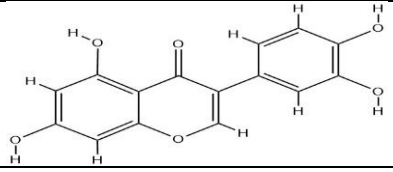
Table: 1 List of Phytochemical Library of *E. alba*

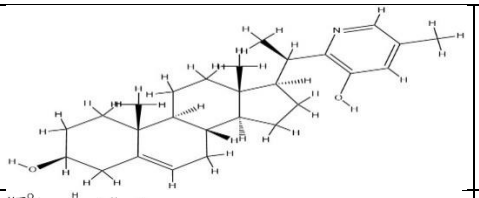
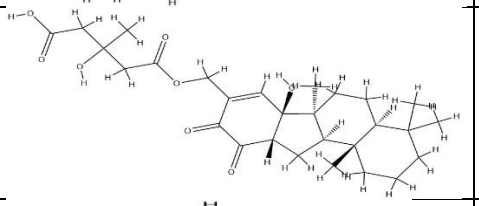
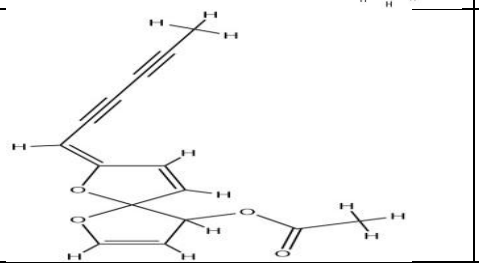
s.no	Phytochemicals name	PubChem Id	Structure	Reference
1	Dodecanoic acid, 10 methyl, methyl ester	521323		(Wyson *et al.,* 2016)

2	Butyl octyl phthalate	66540		
3	10-Octadecenoic acid methyl ester	25642		
4	Oleic acid, eicosyl ester	6436542		
5	1-Heptatriacotanol	537071		
6	Tridecanol, 2-ethyl-2- methyl	545928		
7	9,19-Cyclocholestan-3-ol-7-one,4a dimethyl-[20R]	621450		
8	Beta-Sitosterol	222284		
9	Hydrazinecarboxyamide	5196		(Chauhan *et al.*, 2012)
10	Sclerosol	679		

11	Phoshine	68973		
12	2-Pyridinepropanoic acid	564292		
13	1H-Pyrimido[4,5,6-IJ][2,7] Naphthyridine-6-Carbonitrile,2-Ethyl -5,8-Dimethoxy	90473389		
14	L-Alanine, Ethyl ester-	76507		
15	Bis(fluoromethyl) (Dimethyl)Silane	548461		
16	2-ethyl-2-methyl	45095315		(Udayashankar *et al.*, 2019)
17	Oleic acid	445639		
18	Dodecanoic acid	3893		
19	Wedelolactone	5281813		(Manvar *et al.*, 2012)
20	Luteolin	5280445		
21	Apigenin	5280443		

22	3,4-Dihydroxybenzoic Acid	72		
23	4-Hydroxybenzoic Acid	135		
24	Stigmasterol	5280794		(Sharma *et al.*, 2012)
25	Demethylwedelolactone	5489605		
26	A-Terthienylmethanol	454740		
27	Demethylwedelolactone-7-Glucoside	6325048		
28	Hentriacontanol	68345		
29	Heptacosanol	74822		
30	Luteolin-7-Glucoside	5280637		
31	Nicotine	89594		(Le *et al.*, 2018)

32	Coumarin	323		
33	P-Coumaric Acid	637542		
34	Quercetin	5280343		
35	ß-Amyrin	345510		(Jadhav *et al.*, 2009)
36	Ursolic Acid	64945		
37	Oleanolic Acid	10494		
38	Daucosterol	5742590		(Jahan *et al.*, 2014)
39	Orobol	5281801		

40	Ecliptalbine	10692897		
41	Dasyscyphin C	11562458		
42	Polyacetylene	5458646		

ADME/T study report of *E. alba* phytochemicals

The drug-likeness properties of **Table 2** show all the phytochemical library ligands were analysed using the Qikprop 6.7 (Schrodinger model). "Lipinski's rule" and "Rule of three" were determined (Lipinski *et al.*, 1997; Mishra and Dahima, 2019; Jorgensen and E.M Duffy, 2000) Our ADME/T parameter study report revealed that almost sixteen compounds' properties are within the recommended ranges.

Table: 2 ADME/T study result of *E. alba* selected phytochemicals

S.no	Phyto Compound name	#rotor	HOA	% HOA	QPlogBB	CNS	QPlogKp	QPlogHERG	QPlogKhsa	RO5	RO3	PSA
1	Quercetin	5	2	51.649	-2.419	-2	-5.544	-5.109	-0.343	0	1	143.331
2	p-coumaric acid	4	3	67.337	-1.079	-2	-3.611	-2.254	-0.671	0	0	34.543
3	Orobol	5	3	64.39	-1.845	-2	-4.468	-4.977	-0.249	0	0	121.873
4	Luteolin-7-glucoside	10	1	66.61	-3.672	-2	-6.368	-5.657	-0.791	2	2	201.34
5	Luteolin	4	3	61.205	-1.955	-2	-4.888	-5.023	-0.198	0	0	121.442
6	Demethylwedelolactone	4	2	53.854	-1.97	-2	-5.23	-4.578	-0.448	0	0	135.564
7	Daucosterol	13	1	74.308	-2.119	-2	-3.278	-5.403	0.969	2	1	102.728
8	Dasyscyphin	8	2	53.151	-2.457	-2	-5.465	-2.642	0.51	1	2	168.944
9	Coumarin	0	3	94.38	0.014	1	-1.931	-3.829	-0.56	0	0	40.678

10	Butyl octyl phthalate	12	1	100	-1.128	-2	-1.391	-6.098	0.822	1	1	64.512
11	Apigenin	3	3	73.192	-1.446	-2	-3.989	-5.114	-0.039	0	0	99.755
12	4-hydroxybenzoic acid	2	3	63.757	-0.803	-1	-3.744	-1.618	-0.8	0	0	72.976
13	3,4-dihydroxybenzoic acid	3	2	52.448	-1.243	-2	-4.648	-1.515	-0.899	0	0	94.684
14	2-Pyridine propanoic acid	3	3	76.293	-0.644	-1	-2.917	-2.17	-0.638	0	0	64.193
15	2-ethyl-2-methyl	4	3	100	-0.387	0	-2.534	-4.047	-0.14	0	0	61.658
16	1H-Pyrimido[4,5,6-IJ][2,7]Naphthyridine-6-Carbonitrile,2-Ethyl-5,8-Dimethoxy-	4	3	93.102	-0.72	-1	-2.81	-4.624	-0.036	0	0	85.703
	Recommended values	0 – 15		>80 great <25 poor	–3.0 – 1.2		–8.0 to – 1.0	below –5	–1.5 – 1.5	Max 4	Max 3	7.0 – 200

Molecular docking result of *E. alba* phytochemicals

The molecular docking analysis of *E. alba* phytochemicals docked with NS5B polymerase HCV protein (PDB ID - 3CJ5). **Table 3** displayed that glide ligand efficiency spanned between -0.546 and -0.156. The *E. alba* phytochemicals $Glide_{evdw}$ have detected values -31.424 to -11.724. Glide energy from -50.318 to -21.43kcal/mol.

Table: 3 Molecular Docking study result of *E. alba* selected phytochemicals

S.no	Phytocompound name	Docking score kcal/mol	Glide ligand efficiency	Glide e_{evdw}	Glide energy kcal/mol	Interaction residues	H-bond distance Å	Pi-pi stacking	Pi-cation
1	Quercetin	-7.561	-0.344	-29.722	-36.932	LEU 474 ARG 498	2.11 2.02	TYR 477	ARG 501 ARG 501
2	Dasyscyphin C	-7.409	-0.206	-27.589	-50.318	ARG 501 ARG 501 LYS 531 SER 476 TYR 477	2.02 2.41 1.96 1.91 1.75	---	---
3	Orobol	-7.084	-0.337	-29.108	-38.025	ARG 501 LEU 474 ARG 498	1.93 1.84 1.92	---	ARG 501
4	luteolin-7 glucoside	-6.557	-0.205	-31.392	-41.347	LEU 474 ARG 498	2.15 1.94	TYR 477	ARG 501 ARG 501
5	3,4dihydro benzoic acid	-6.006	-0.546	-11.724	-21.43	SER 476 TYR477	1.98 1.76	TYR 477	ARG 501
6	2 Pyridinepropanoic acid	-5.621	-0.511	-14.6	-24.114	SER 476 TYR477	1.91 1.90	---	---
7	Coumarin	-5.455	-0.496	-16.631	-22.293	SER 476 TYR477	2.21 2.10	---	ARG 501

8	1H-Pyrimido[4,5,6-IJ][2,7]Naphthyridine-6-Carbonitrile,2-Ethyl-5,8-Dimethoxy	-5.236	-0.249	-29.042	-37.194	SER 476	2.15	---	ARG 501
9	4-hydroxybenzoic acid	-5.18	-0.518	-19.149	-27.912	SER 476 TYR477	2.20 2.11	TYR 477	ARG 501
10	Demethylwedelolactone-7-glucoside	-5.134	-0.156	-31.424	-36.61	ARG501 LEU474	2.42 2.24	---	---
11	Butyl octyl phthalate	-5.029	-0.21	-30.314	-38.348	ARG501 TYR477 SER 476	2.21 1.98 2.22	---	---
R	Sofosbuvir	-7.541	-0.209	-31.764	-45.485	ARG 501 SER 476 ARG 498 TYR 477	2.53 2.69 2.00 2.02	---	---

The drug-likeness properties had ligands complex with NS5B protein 2D and 3D structures top five complexes illustrated separately in **Figure 1** with the NS5B. Quercetin docked to NS5B with a score of -7.561 kcal/mol and established two H-bonds with the residues LEU 474 and ARG 498 at distances of 2.11 and 2.02Å, respectively. Pi-pi stacking was created with TYR 477, and two pi-cations interacted at ARG 501. **Figure 2** shows Dasyscyphin C and NS5B have a binding energy of -7.409 kcal/mol. It forms five H-bonds with ARG 501, ARG 501, LYS 531, SER 476, and TYR 477; the distances were 2.02, 2.41, 1.96, 1.91 and 1.75 Å, respectively. **Figure 3** represents the docked Orobol created with the NS5B protein complex by three hydrogens bonding amino residues ARG 501, LEU 474, and 498 of the NS5B. With H-bond distances 1.93, 1.84, and 1.92 Å, separately, a binding energy of -7.084 kcal/mol and forms pi-cation with the residue of ARG 501. **Figure 4** illustrates the binding energy of

luteolin-7-glucoside to NS5B was calculated to be -6.557 kcal/mol. It forms two H-bonds with the amino acid residues: LEU 474 and ARG 498 of the NS5B at distances of 2.15 and 1.94 Å. It forms pi stacking at TYR 477 and two pi-cation formed at ARG 501. **figure 5** demonstrates the docking complex of the 3,4-dihydroxybenzoic acid and the NS5B polymerase protein. It began with 2 H-bonds with NS5B residues: SER 476 and TYR477, at 1.98 and 1.76 Å with the binding energy of -6.006 kcal/mol. It contains pi stacking with TYR 477 and Pi-cation at ARG 501. **Figure 6** depicted the standard drug sofosbuvir displaying a docking score was -7.541kcal/mol and attaches to ARG 501; SER 476; ARG 498, and TYR 477 at the NS5B binding site via four H-bonds with a distance of 2.53, 2.69, 2.00, and 2.02 Å, respectively. We compared the binding energies of all the ligands to the reference sofosbuvir. The drug-likeness had phytochemicals that expressed good binding interactions with protein NS5B polymerase. From the result, Quercetin had the best crucial score (-7.561kcal/mol) compared to other docked phytochemicals. So, we suggested that this good docking score of Quercetin may possess against Hepatitis C Virus infection. Our findings Quercetin had potent action on the HCV.

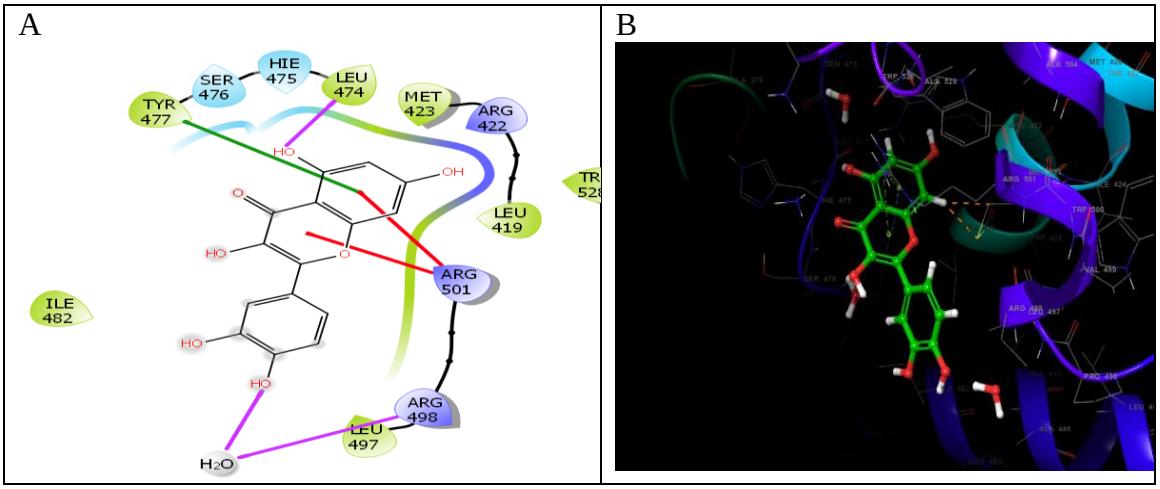


Figure 1: Molecular docking complex of Quercetin - 3CJ5 protein: 2D & 3D structures.

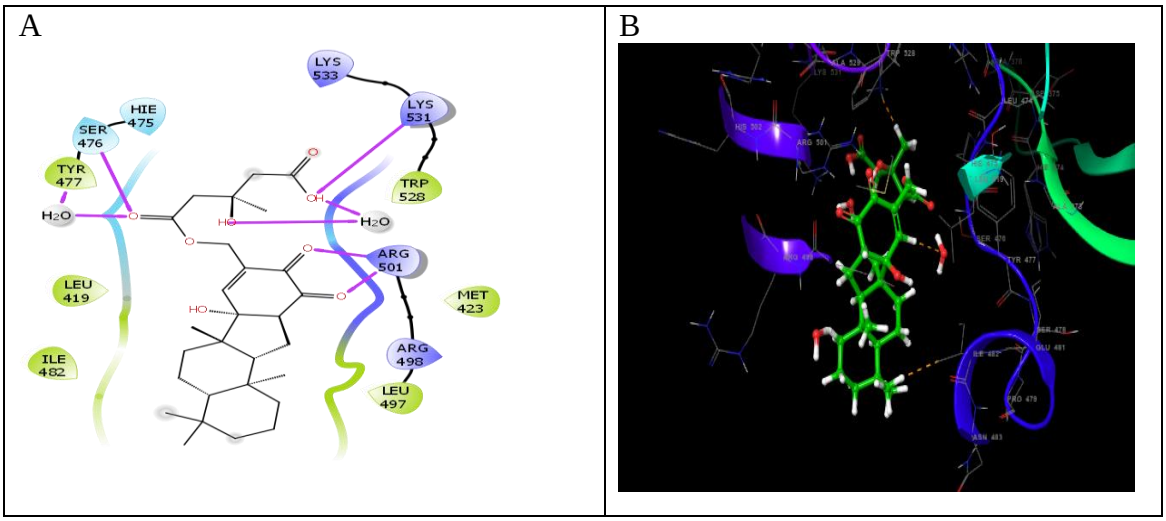


Figure 2: Molecular docking complex of Dasyscyphin C - 3CJ5 protein: 2D & 3D structures.

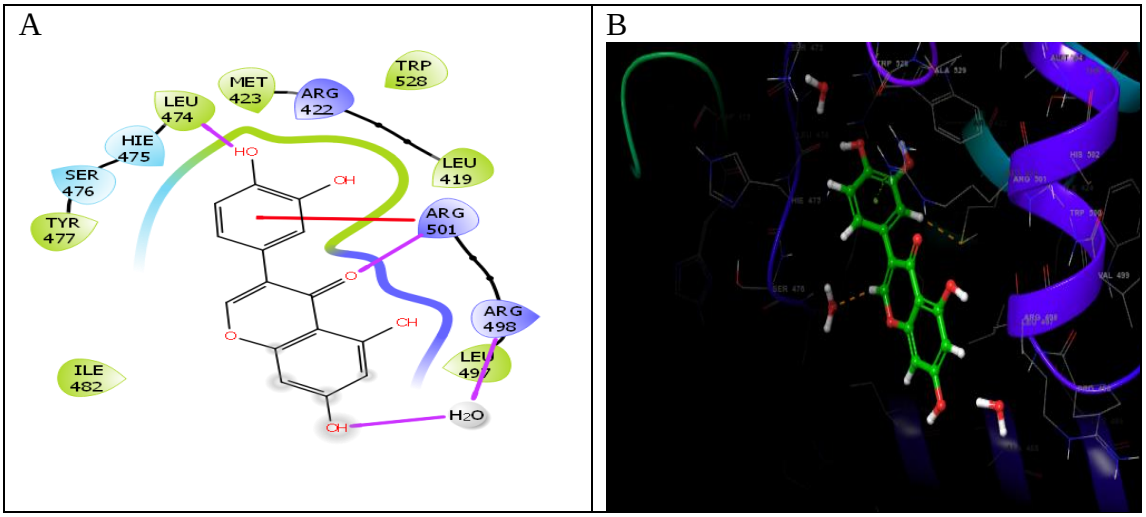


Figure 3: Molecular docking complex of Orobol - 3CJ5 protein: 2D & 3D structures.

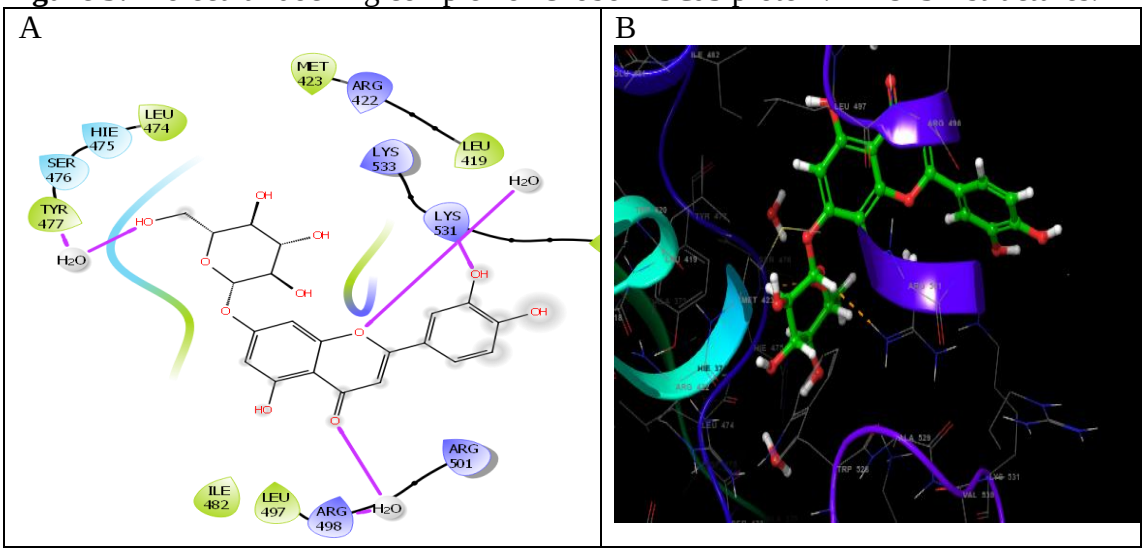


Figure 4: Molecular docking complex of Luteolin-7 glucoside - 3CJ5 protein: 2D & 3D structures.

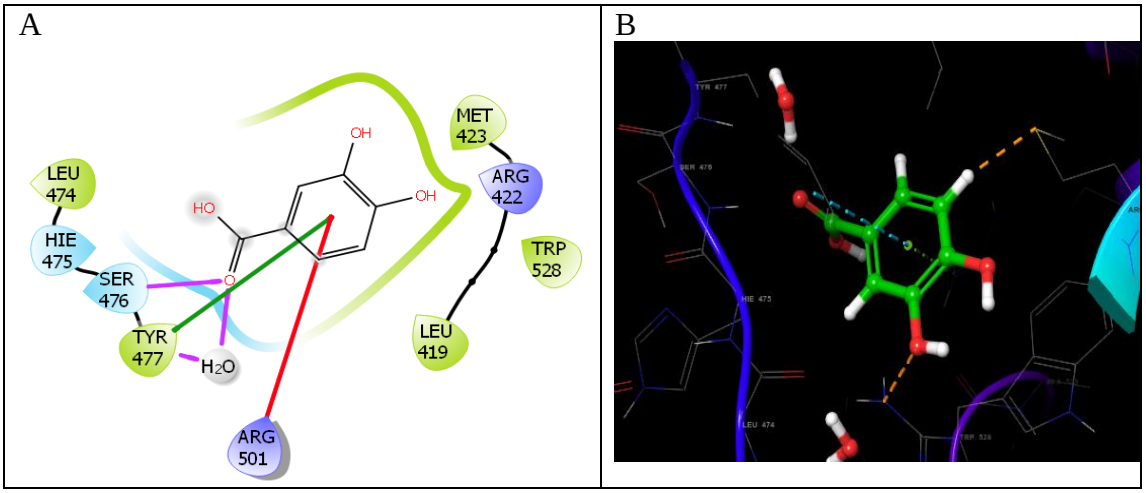


Figure 5: Molecular docking complex of 3,4-dihydroxybenzoic acid against 3CJ5 protein: 2D & 3D structures.

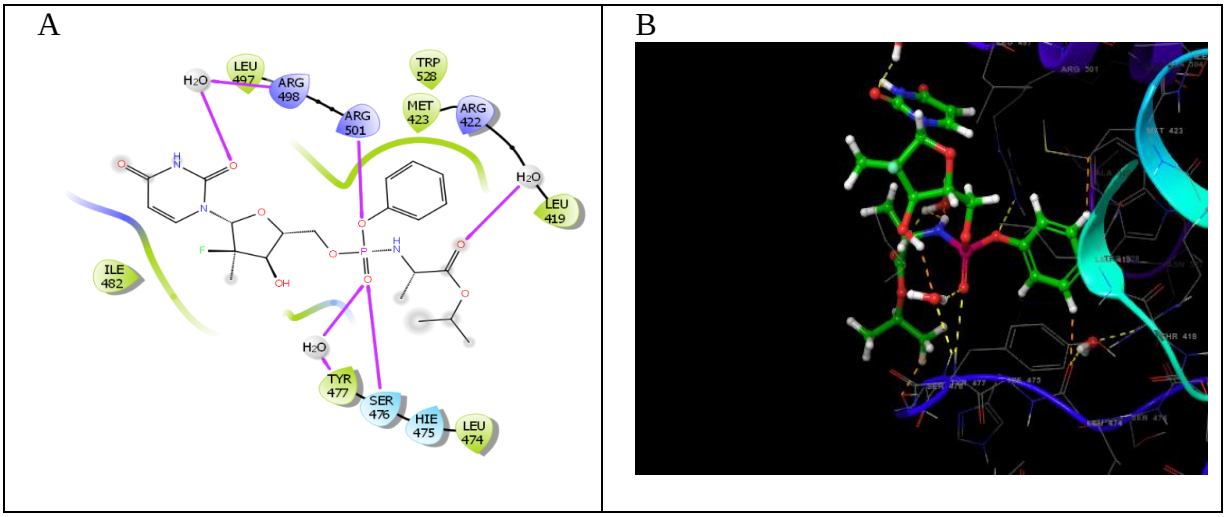


Figure 6: Molecular docking complex of sofosbuvir-NS5B polymerase protein: 2D & 3D structures.

The prime MM/GBSA binding free energy calculation

We calculated the binding free energy according to the pose docking complex with the help of the excellent/MM–GBSA method. Molecular docking and evaluation with MM-GBSA free-regulating energy point out with the postscoring approach for HCV (PDB ID: 3CJ5) target, and the values are listed in **(Table 4).** From the MM-GB/SA calculation reports, the dG bind values were noticed in the range of -22.4 (4-hydroxybenzoic acid) to -50.39 (Butyl octyl phthalate) kcal/mol. And also, dG Bind (NS), dG Bind Lipo, dG Bind Coulomb, and dG vdw value energies contribute to total binding energy. The scoring task sets the validity of docking by evaluating the lowest energy pose forecast. The docking of ligands acquires the MM-GBSA free energy and Glide score into the incorporate pocket is more fixed.

Table 4: Binding free energy determined by prime MM/GBSA

s.no	Phytocompound name	MMGBSA dG Bind	dGBind (NS)	dGBind Colomb	dGBind Lipo	dGBind vdW
1	Quercetin	-27.5	-42.2	-11.83	-7.25	-31.13
2	Dasyscyphin C	-44.53	-53.19	-27.89	-8.95	-33.09
3	Orobol	-34.52	-38.26	-33.25	-9.46	-28.51
4	luteolin-7 glucoside	-37.2	-41.09	-20.62	-8.67	-38.51
5	3,4dihydroxy benzoic acid	-23.75	-24.95	-9.98	-7.56	-18.75
6	2-Pyridinepropanoic acid	-36.3	-38.78	-9.29	-12.56	-14.31
7	Coumarin	-37.03	-38.2	-4.33	-14.01	-15.99
8	1H-Pyrimido[4,5,6-IJ][2,7]Naphthyridine-6-Carbonitrile,2-Ethyl-5,8-Dimethoxy	-38.37	-46.32	-11.04	-7.75	-36.01

9	4-hydroxybenzoic acid	-22.4	-28.94	-1.66	-9.63	-20.44
10	Demethyl wedel lactone-7-glucoside	-31.99	-39.49	-12.14	-13.16	-37.63
11	Butyl octyl phthalate	-50.39	-54.55	-14.48	-18.24	-39.63

NS-No Strain

DISCUSSION

According to the latest updates, there are no anti-HCV vaccinations available to memorialize this potentially lethal virus. Other chances of dual therapy (INF α and RBV) and triple therapy Direct-Acting Antiviral (DAA) all these synthetic drugs to treat the hepatitis c virus were primarily unsuccessful because of their severe side effect. But conventional herbal remedies show significant potential as novel antiviral drug candidates against NS5B polymerase, which is also our target enzyme because it's vital in replicating the hepatitis C virus (HCV). This study first screened the phytochemicals from the medicinal plant *E. alba*, and then Drug-likeness properties were evaluated by the QikProp tool for selected 42 ligands. Unfit phytochemicals filtered by the ADME/T parameters such as "Lipinski's rule" or "Rule of Five" (RO5) and "Rule of three" parameters forecast oral bioavailability from this only sixteen ligands passed within the limit. This molecular docking score report reveals all the ligands had anti-hepatitis activity, but we suggest that Quercetin -7.561 Kcal/mol (2H-bond) binding affinity is similar to the standard drug sofosbuvir. Our in-silico study approaches the potent ligands proven to target protein NS5B polymerase inhibitor from the *E. alba* phytochemicals. So, it could be more concentrated on NS5B polymerase inhibitors and has excellent drug-likeness properties. In the quest to develop effective antiviral drugs, quercetin stands out as a prospective drug candidate. Hence it is predicted to be fit for human consumption without side effects.

CONCLUSION

In this work, molecular docking studies were carried out in *E. alba* phytochemicals using Glide Maestro software to outline how ligands interact with the target NS5B polymerase enzyme. The docking data represents that novel phytoconstituents have good hydrogen bond interactions with SER 476, TYR 477 and pi cation with ARG 501 residue at the allosteric site, particularly the thumb II Site of the NS5B polymerase enzyme. Quercetin clearly expressed the blocking of the enzyme activity. The initiated molecular docking model has displayed scope for developing novel phytoconstituent establishment with potent NS5B inhibitory activity.

ACKNOWLEDGEMENTS:

We thank Schrodinger Evolutionary Maestro Software, LLC, NY, USA, 2021-1.

AUTHOR CONTRIBUTIONS

Concept and design, collection of data and interpretation of data were carried out by Geetha J. Drafting the article and revising the content were carried out by Jayaprakash Shanmugam.

FINANCIAL SUPPORT

There is no external funding for this work.

CONFLICTS OF INTEREST

The authors report no conflicts of interest in this work.

ETHICAL APPROVALS

This work does not elaborate on animals or human trials.

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