



**DOCKING SIMULATION AND ADMET PREDICTION BASED INVESTIGATION ON
THE PHYTO CHEMICAL CONSTITUENTS OF SIDA ACUTA LEAVES AS A
POTENTIAL ANTI- TUBERCULOID DRUG**

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ABSTRACT

Using Argus lab and Auto dock, the study's objectives are to perform molecular docking of *Sida acuta* phyto constituents against Anti - tuberculoid proteins (3AF3, 5V3Y), and to use Mol Inspiration software to anticipate the ADMET characteristic. The produced extracts of *Sida acuta* were tested for Anti-tubercular activity based on the results of the preliminary phyto chemical screening of the phytochemicals. The ingredients needed to molecularly dock the certain physiochemical components of *Sida acuta* against 3AF3, 5V3Y, two Anti-tuberculoid proteins. Software called Mol Inspiration was used to forecast Argus lab, Auto dock, and ADMET. The Soxhlet apparatus was used to prepare the different solvent extracts of *Sida acuta* leaves using petroleum ether, chloroform, and methanol. Additionally with the extracted extract's Anti - tuberculoid activity was performed. MABA was used to perform an analysis against the reference strain of H37Rv *Mycobacterium tuberculosis*. Using a molecular docking-based analysis with 3AF3 and 5V3Y, we examined the likelihood of an extraordinary interaction between the Anti- tuberculoid proteins and the phyto components of *Sida acuta*. Five compounds were investigated further using the ADMET characteristics. Rich in bioactive compounds, the methanol extract demonstrated encouraging activity against the prevalent strain of *Mycobacterium tuberculosis* (H37Rv). In vitro and in vivo investigation of *Sida acuta* leaves supports their use in traditional medication and intervention based on the isolation of the particular chemicals responsible for the Anti-tuberculoid activity. Additionally, this opens the door for the creation of novel medications to fight tuberculosis.

KEYWORDS: *Sida acuta*, molecular docking, *Mycobacterium tuberculosis* (H37Rv).

INTRODUCTION

Globally, tuberculosis (TB) has significant death rates and is a recurrent, progressive illness. One of the main challenges to the treatment of allelopathy is the drug-resistant phenomena of *Mycobacterium tuberculosis*. Serious health difficulties can result from allelopathic treatment, which is one of its negative side effects. The World Health Organization (WHO) lists tuberculosis (TB) as the primary infectious agent-related cause of death and one of the top 10 causes of death globally.^[1,19,22] Numerous factors have contributed to the ongoing worldwide health danger posed by tuberculosis. Drug resistance, such as extensively drug-resistant tuberculosis (XDR-TB) and multidrug-resistant tuberculosis (MDR-TB), is one example of this. Despite the fact that the present anti-TB medications are thought to be cytotoxic and have minimal efficacy due to the evolution of resistant bacterial strains, there has been no significant active research in the field for more than 40

years. Thus, the development of novel anti-tuberculosis medications that are inexpensive, effective, and have distinct therapeutic targets as well as multi-domain inhibitory effects and few to no adverse effects is desperately needed. When it comes to creating drugs, screening plant metabolites against the virulence of tuberculosis disease could be greatly aided by computational methods based on various algorithms. Plant-based products have little to no negative effects on humans, making them virtual drug development repositories. The wide range of phytochemicals with different functions needed for plant products to have therapeutic effects on human illnesses, such as tuberculosis. The best mycobacteria-inhibitory compounds were found to be produced from plants, having less (or no) negative effects and facilitating a speedy patient recovery. Recently, computational biology and data science have become more popular in the crucial subject of drug discovery. Computational methods can be

used to create new tiny molecules and filter results from a large database. Thus, certain computer models are legitimate substitutes for experiments. One such computational approach is molecular docking, which is the act of predicting a molecule's preferred orientation to another when linked together to form a stable complex. Fig. 1 depicted the fundamental docking procedure. In practice, there are two primary forms of docking, or molecular docking: protein-protein docking and small molecule-protein docking, also referred to as "ligand-protein docking." Here, ligand-protein docking was done using the AutoDock Vina (1.5.6) program. By employing score functions, one can use knowledge of the preferred orientation to forecast the strength of the contact or binding affinity between two molecules. An empirical scoring function in AutoDock Vina (1.5.6) adds up the contributions of several separate terms to determine the affinity, or fitness, of protein-ligand interaction. The Swiss ADME web tool was utilized in this instance. It offers unrestricted access to a collection of quick and dependable predictive models for ADME analysis and moreover shows bioavailability radar for an expedient evaluation of drug-likeness. Therefore, the current study was carried out to identify possible phytochemicals against tuberculosis (TB). There are about 200 species in the flowering plant genus *Sida*, most of which are found in warm climates worldwide. There are reportedly seventeen species in India. In the Ayurvedic system, the majority of *Sida* species found in India are referred to as *Balachatusaya* and are commonly known by the general name "Bala." *Sida acuta* is a tiny, perennial shrub that grows erect and has several branches growing from it. In

Figure 3, the leaves of *Sida acuta* were displayed. *Sida acuta* comprises (+)Syringaresinol, (E) Suberenol, 1,6 Dihydroxy Xanthone, 4- Ketopinoresinol, 7- α - methoxy- α -tocopherol, H-methoxy quindoline, 20-Hydroxyecdysone, Acanthoside-B, β - Sitosterol glucoside, β -tocopherol, Campesetrol, Chlorogenic acid, Cryptolepine, Cryptolepine, Cyclopentadiene, Ecdysterone, ephedrine,erofolin-A, erofolin-B, ferulic acid, heraclenol, ioliolide, isoranmnetin3-o-(b-D-glucopyraanosyl, kampferol, manghaslin, myricetin-7-rhamnoside, myricetin isorhanetin, myricetin, N-Trans feruloyltyramine, oleanolic acid, peltatoside (Etoposide), quercetin 3-(2G-xylosyl rutinoides), quercimeritrin, quinazoline, quindolinone, rutin, scopoletin, sigmasterol, sinapic acid, stigmasterol, syringic acid, taraxast - 1,20(30)-dien-3-one, taraxastane, taraxasterone, thamnomin, tiliroside, ursolic acid, vanillic acid, vomifoliol, xanthyletin, xylitol dimer. Numerous studies have revealed that indigenous people from tropical countries have utilized various parts of *Sida acuta* to treat a variety of health issues. These include rheumatic affections, azoospermia, oligospermia and spermatorrhoea, leucorrhoea, wounds sciatica, nervous and cardiac diseases, cold, cough, asthma, tuberculosis, and respiratory disorders.^[12,13,14,15] Blood disorders, hepatic and biliary disorders, elephantiasis, etc. Are reported techniques. Therefore, the current study was carried out to identify possible phytochemicals against tuberculosis utilizing the aforementioned instruments. The general medication information was displayed in Table 2.

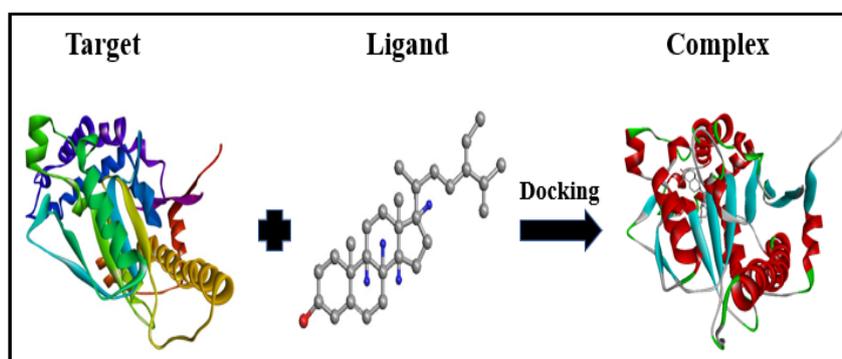


Figure 1: Schematic illustration of docking a small molecule ligand (green) to a protein target (black) producing a stable complex.

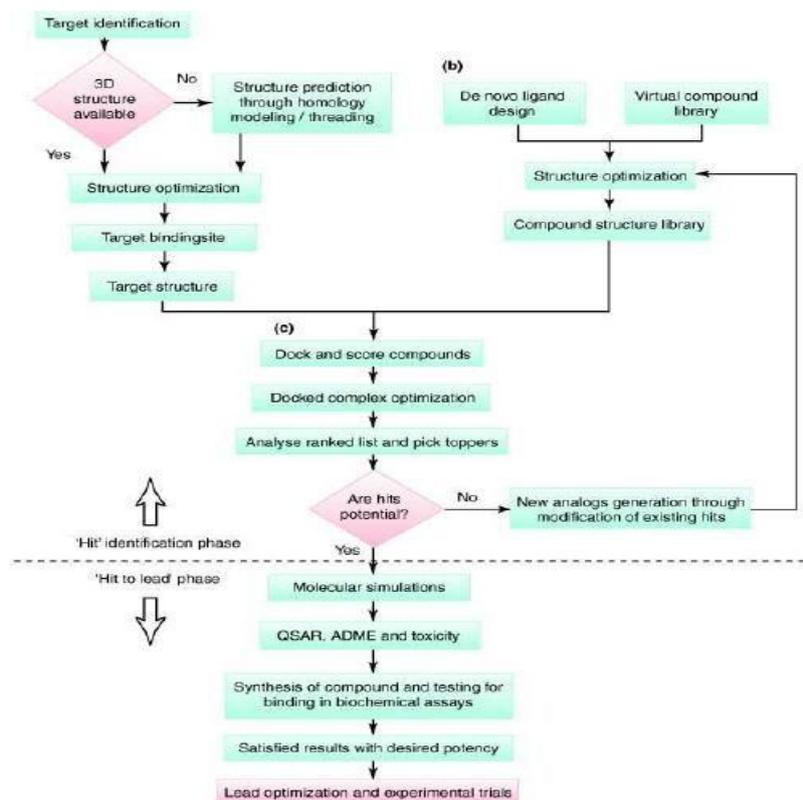


Figure 2: Computer aided drug design procedure.

MATERIALS AND METHTHODS

Molecular docking

The method used to study the intermolecular interactions between two molecules in silico is called molecular docking.^[16,17,18,20,21] The ligand molecule that has the ability to function as an inhibitor is called a micro molecule. Thus, the following phases are involved in the docking process:

Step I: Protein preparation

The protein's three-dimensional structure (3AF3, 5V3Y) 29, 30 should be obtained from the Protein Data Bank (PDB); the structure should then undergo pre-processing. Import the protein files and followed the necessary instructions.

Step II: Ligand preparation

The natural components found in *Sida acuta* leaves were identified and chemsketch was used to sketch a few of the compounds (Beta-sitosterol, Oleanolic acid,

Quindoline, Stigmasterol, and Ursolic acid).^[31,32,33,34]

The LIPINSKY'S RULE OF 5 should be applied while selecting the ligand. Regarding selecting a ligand that complies with LIPINSKY'S RULE.

Step III: Active site prediction

Predicting the prepared protein's active site is the most important step. The receptor may have several active sites; only the one that poses the greatest risk needs to be selected. If heteroatom's or water molecules are present, they are eliminated.

Step IV: Docking

Programs like Argus Lab 4.0.1 and Autodock tools 1.5.6 are used to investigate the interactions between the docked ligand and protein. The scoring function assigns a score based on the selection of the best docked ligand complex. Computer aided drug design procedure was shown in Fig. 2.

Table 2: General information of drugs.

S. No	Structure	Molecular formula	Molecularweight	Molar refractivity	Molar volume	Density
1.	Beta sitosterol	C ₂₉ H ₅₀ O	414.7067	129.21±0.4cm ³	424.3±5.0cm ³	0.97±0.1g/cm ³
2.	Oleanolic acid	C ₂₉ H ₅₀ O ₃	446.7055	131.16±0.3cm ³	442.9±3.0cm ³	1.088±0.06g/cm ³
3.	Quindoline	C ₁₅ H ₁₀ N ₂ O	234.2527	68.43±0.5cm ³	166.7±7.0cm ³	1.40±0.1g/cm ³
4.	Stigmasterol	C ₂₉ H ₄₈ O	412.69082	129.12±0.4cm ³	417.6±5.0cm ³	0.98±0.1g/cm ³
5.	Ursolic acid	C ₃₁ H ₅₂ O ₃	472.74278	138.43±0.3cm ³	455.7±3.0cm ³	1.037±0.06g/cm ³

Acquisition of botanical specimens

The leaves of *Sidaacuta* were gathered in Thirupachanur, in the Villupuram district of Tamilnadu, between June

and July of 2023. V. GANGADEVI, Ph.D., Assistant Professor, PG Head & Research, Department of Botany, Aringar Anna Govt Arts College, Cheyyar, verified the

authenticity of the plant. The gathered plant material was roughly ground into powder after being shade dried.

Collection of *Sida acuta* plant leaves was shown in Fig.3



Figure 3: Leaves of *sida acuta*.



Figure 4: Collection of *sida acuta* plant leaves.

Preparation of extract

The Soxhlet extractor was used on the ground-up plant material. Several solvents, including pet ether, chloroform, and methanol, were used for the extraction over the course of ten to twelve hours, depending on how polar the solvents were. Soxhlet apparatus and packing of

column was shown in Fig 5. The extracted material was sieved and dried using an electric water bath set between 70 and 100 degrees Celsius. The yield % of each extract was then computed. The percentage yield of selected solvent extracts of *Sida acuta* plant were shown in Table: 1.

Table 1: Percentage yield of the selected solvent extracts of *Sida acuta* plant.

S. No	Weight of the leaf powder	Solvent	Temperature	Duration	%yield of the extracts
1.	25g	Petroleum ether	60°C	12hrs	15.6
2.	20.386g	Chloroform	55-60°C	12hrs	17.22
3.	13.22g	Methanol	30°C	12hrs	34.19

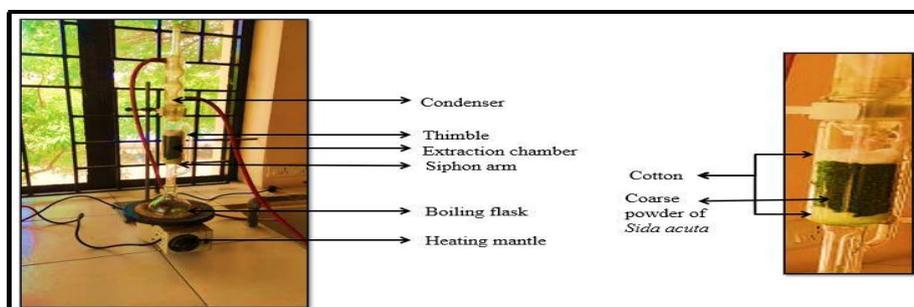


Figure 5: Soxhlet Apparatus & Packing of column.

Qualitative phytochemical analysis of aqueous leaf extract of *Sida acuta*

Phytoconstituents including alkaloids, terpenoids, phenolic compounds, tannins, saponin, and

flavonoids were found in the leaf extract of *Sida acuta*.^[27]

1. Use Dragendorff's Reagent to test for alkaloids
2. Terpenoids Test (Salkowski test)
3. Ferric chloride test, also known as the phenolic

compound test

4. Tannin test (aqueous bromine test, ferric chloride test, and lead acetate test)
5. Saponin evaluation (Froth formation test)

Antimycobacterial activity: (MABA)

To the extract's Antimycobacterial activity was evaluated using the micro plate Alamar Blue Assay (ATCC No. 27294) against the M. Tuberculosis H37RV strain²⁶. This technology exhibits good correlation with BACTEC radiometric methods, is non-toxic, and uses a thermally stable reagent. Alamar Blue is a reagent for cell viability assays that comprises Resazurin (7-Hydroxy-3H-phenoxazin-3-one-10-oxide), a blue dye that is weakly fluorescent, cell permeable, and non-toxic²⁵. Proliferation in human, animal, bacterial, fungal and mycobacterial cells is quantitatively measured using Alamar Blue. When cellular metabolic reduction occurs, resazurin, an oxidation-reduction (REDOX) indicator, changes colorimetric ally. Resaruzin is reduced to Resorufin in live cells (using NADH). In summary, all outer perimeter wells of the sterile 96-well plate received 200 μ L of sterile deionized water to reduce medium evaporation during incubation. A direct serial dilution of compounds in pet ether, chloroform, and methanol ethyl acetate extract of *Sida acuta* was made on a 96-well plate, which was also given 100 μ L of Middle Brook 7H9 broth. 100 to 0.2 μ g/mL were the final medication concentrations examined. For five days, the plates were incubated at 37°C after being covered and sealed with parafilm. Following this, 25 μ L of newly made Alamar Blue reagent combination (1:1) after adding 10% tween 80 to the plate, it was incubated for a full day¹⁹. Isoniazid-1.6 μ g/ml, Ethambutol- 1.6 μ g/ml, Pyrazinamide-3.125 μ g/ml, Rifampicin-0.8 μ g/ml, and streptomycin-0.8 μ g/ml were used as standard drugs²⁵.

RESULT AND DISCUSSION

A molecular docking study was conducted using Argus lab and Autodock tools to investigate the binding affinity and interactions of selected phytoconstituents of *Sida acuta* leaves against chosen anti-tubercular proteins (3AF3, 5V3Y). The leaves of *Sida acuta* were gathered, let to dry in the shade, and then extracted using a Soxhlet equipment and a variety of solvents, including petroleum ether, chloroform, and methanol. The obtained

extracts carried out the initial phytochemical screening for the phytoconstituents of *Sida acuta* leaves. Alkaloids, terpenoids, phenolic compounds, tannins, saponins, and flavonoids are among the chemical tests that are carried out. Lastly, the produced extracts' anti-tubercular efficacy of the *Sida acuta* phytoconstituents was also evaluated. The following are the outcomes for the aforementioned activities

Molecular docking analysis

A variety of useful techniques for drug design and analysis are provided by molecular docking. Using Argus lab 4.0.1 and Autodock tools 1.5.6, molecular docking was used to examine the binding capacity of five bioactive phytoconstituents of *Sida acuta* leaves (Beta-sitosterol, Oleanolic acid, Quindoline, Stigmasterol, and Ursolic acid) against the target Anti-tubercular proteins (3AF3, 5V3Y).^[28,31,32,33,34] The five bioactive substances have been demonstrated to have a high binding energy with the target proteins 3AF3, 5V3Y. In order to prevent tuberculosis, these lead compounds could be employed as an antagonist of the target proteins 3AF3, 5V3Y. The docking results unequivocally demonstrate that the medicines'. Binding energies when employing Argus lab 4.0

The values of beta-sitosterol (-18.7582 Kcal/mol), oleanolic acid (-12.9875 Kcal/mol), quindoline (-10.3612 Kcal/mol), stigmasterol (-17.8312 Kcal/mol) and ursolic acid (-15.6754 Kcal/mol) for the chosen protein 3AF3.

The drug's binding energy using Autodock tools 1.5.6 for the chosen protein 3AF3 are Beta-sitosterol: -9.2, Oleanolic acid: -9.2, Quindoline: -7.5, Stigmasterol: -8.9, Ursolic acid: -7.5.

Beta-sitosterol: -17.0392 Kcal/mol, Oleanolic acid: -17.1925 Kcal/mol, Quindoline: -10.4711 Kcal/mol, Stigmasterol -17.5431 Kcal/mol, and Ursolic acid: -15.8171 Kcal/mol are the drug binding energies for the chosen protein 5V3Y as determined using Argus lab 4.0.1. The binding energy of drugs by using Autodock tools 1.5.6 for the selected protein 5V3Y are Beta-sitosterol: -6.0, Oleanolic acid: -6.1, Quindoline: -6.0, Stigmasterol: -6.3, Ursolic acid: -5.6.

Determination of interaction

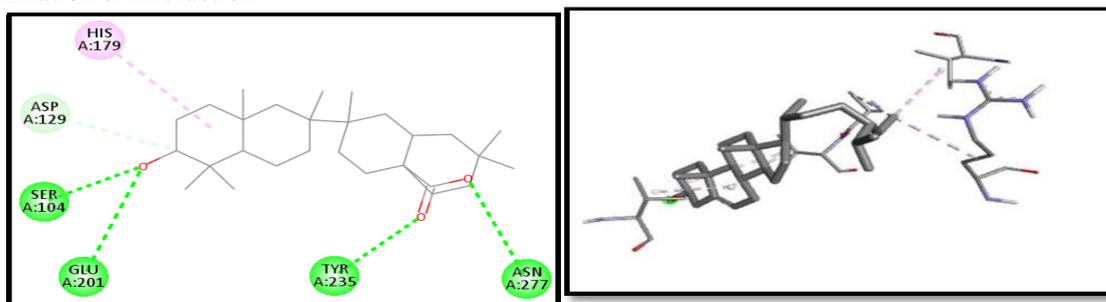


Figure 6: 2D diagram of Beta sitosterol with 3AF3 & 5D diagram of Beta sitosterol.

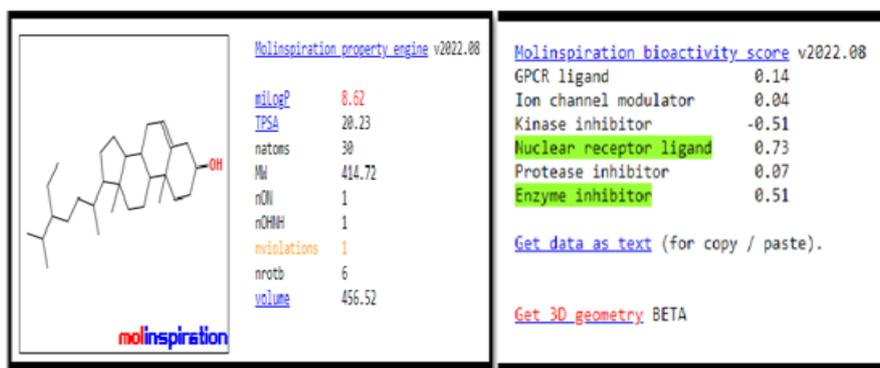
To clarify the interaction, molecular docking studies were conducted. The Discovery Studio visualizer was used to visualization and assesses the best binding affinities. Fig. 6 displays the 2D and 5D interaction diagram of beta sitosterol with 3AF3. Simply click “ligand interactions” in the Discovery Studio file to observe the ligand-protein interaction and identify the amino acids implicated in the hydrogen bonds. The ligand beta-sitosterol formed four hydrogen bonds with SER104, GLY201, TYR235, ASN277 of the target 3AF3. The ligand oleanolic acid formed four hydrogen bonds with SER104, GLY201, TYR235, ASN277 of the target 3AF3. The ligand Quindoline formed two hydrogen bonds with LYS103, ARG238 of the target 3AF3. The ligand Stigmasterol formed two hydrogen bonds with LYS103, GLU201 of the target 3AF3. The ligand Ursolic acid formed two hydrogen bonds with GLU201, TYR201 of the target3A

The ligand beta-sitosterol formed two hydrogen bonds with ARG1677, GLN1678 of the target 5V3Y. The ligand oleanolic acid formed two hydrogen bonds with ARG1677, ARG1662 of the target 5V3Y. The ligand Quindoline formed two hydrogen bonds with ARG A 1677, ARG B 1677 of the target 5V3Y. The ligand Stigmasterol formed one hydrogen bond with ASP 1661 of the target 5V3Y. The ligand Ursolic acid formed one hydrogen bond with GLN 1678 of the target 5V3Y. Amino acids involved in binding between proteins and phytoconstituents were shown in Table:4. Docking scores were determined by comparing the phytoconstituents of *Sida acuta* with Antituberculoid proteins (3AF3, 5V3Y). We can infer the compound’s optimal binding energy from the results. Phytoconstituents have varying binding scores with distinct proteins. Because medications are derived from natural sources and proteins differ (peptide binding protein versus immune system protein).

Certain connections, such as hydrogen bonds, are crucial for the binding of medicines and proteins. Bonds that belong hydrophobic. Better binding effects are estimated by counting the amount of hydrogen bonds in the molecule, which are weak electrostatic interactions between the compound’s proton and electronegative. A hallmark for molecular recognition and biological activity prediction of multitargeted drugs is 3D structural folding at the protein-ligand groove, according to docking studies of phytoconstituents of *Sida acuta* molecules at the bioactive cascade of the 3AF3 and 5V3Y. The provided results show that the ligands are stabilized at the target site by H-binding and improved hydrophobic interaction, which also helps to modify binding affinity and therapeutic efficacy. The results were shown in table 3. In this investigation, the compounds with the highest binding affinities against the 3AF3 protein were beta sitosterol (Argus lab: -18.7582, Autodock: -9.2), oleanolic acid (Argus lab: -12.9875, Autodock: -9.3), and ursolic acid (Argus lab: -15.6754, Autodock: -7.5). Similarly, quindoline (Argus lab: -10.3612, Autodock: -7.5) and stigmasterol (Argus lab: -17.8312, Autodock: -8.9) generated the best binding energy with 3AF3. To illustrate, consider the following: in Fig. 6 green balls and sticks show hydrogen bonds, violet balls and sticks show hydrophobic bonds (Pi-Pi/Pi-sigma/amide-Pi interactions), and pink balls and sticks show hydrophobic interactions (Pi-alkyl/alkyl interaction stacking). The table:5 illustrates the hydrogen bonds formed by docking 3AF3 and 5V3Y with beta sitosterol, oleanolic acid, quindoline, stigmasterol, and ursolic acid in the current investigation. Therefore, this study provides insight into the insilico method, which is a preliminary approach to pre-clinical and clinical trials, for docking unknown medicines using various proteins. Further research, including in vitro and in vivo experiments, are developed after it has been established. Time management, human resource management, and economic balance may all benefit.

Table 4: Amino acids involved in binding between proteins and phytoconstituents.

S. no.	Drugs	Hydrogen bond for 3af3 protein	Hydrogen bond for 5v3y Protin
1.	Beta sitosterol	SER 104 GLY 201 TYR 235 ASN 277	ARG 1677 GLN 1678
2.	Oleanolic acid	SER 104 GLY 201 TYR 235 ASN 277	ARG 1677 ARG 1662
3.	Quindoline	LYS 103 ARG238	ARG A 1677 ARG B 1677
4.	Stigmasterol	LYS 103 GLU 201	ASP 1661
5.	Ursolic acid	GLU 201 TYR 201	GLN 1678

**Table 5: Bioactivity score of the compounds.**

Compound name	Mi Log p	TPSA	ni atom	Mol.wt	nON	nOHNH	N violation	N rot b	Volume
1. Beta-sitosterol	8.62	20.23	30	414.72	1	1	1	6	456.52
2. Oleanolic acid	6.54	57.53	31	432.69	3	2	1	2	454.89
3. Quindoline	2.41	46.01	18	234.26	3	1	0	0	205.13
4. Stigmasterol	7.87	20.23	30	412.70	1	1	1	5	450.33
5. Ursolic acid	7.22	57.53	34	472.75	3	2	1	1	493.94

Table 6: Drug likeness calculations of the compounds (physicochemical properties).

Compound name	Gpcr ligand	Ion channel modulator	Kinase inhibitor	Nuclear receptor ligand	Protease inhibitor	Enzyme inhibitor
1. Beta-sitosterol	0.14	0.04	-0.51	0.73	0.07	0.51
2. Oleanolic acid	0.23	0.08	-0.35	0.63	0.14	0.49
3. Quindoline	0.16	0.22	-0.03	-0.20	-0.40	-0.02
4. Stigmasterol	0.12	-0.08	-0.48	0.74	-0.02	0.53
5. Ursolic acid	0.24	0.04	-0.38	0.72	0.17	0.49

Sida acuta have the following molecular weights: 414.72 for beta-sitosterol, 432.69 for oleanolic acid, 244.26 for quindoline, 412.70 for stigmasterol, and 472.75 for ursolic acid. Only compounds 1 and 5 that were tested were found to be within Lipinski's rule, while compounds 2, 3, 4, 6, and 7 do not follow the rule regarding the number of hydrogen bond donors (NH and OH). Total polar surface area, or TPSA, is a strong indicator of drug transport characteristics such as blood brain barrier permeability, intestinal absorption, and bioavailability. It is strongly correlated with a molecule's hydrogen bonding potential. The phytoconstituents of Sida acuta were found to have a TPSA that falls far below the 160 Å² limit, ranging from 60.48 to 106.30. The TPSA value of Beta-sitosterol is 20.23, Oleanolic acid is 57.53, Quindoline is 46.01, Stigmasterol is 20.23, Ursolic acid is 57.53. A straightforward topological metric called the number of rotatable bonds is used to quantify the flexibility of molecules and is regarded as a reliable indicator of a drug's oral bioavailability. Among all the compounds that were screened, compounds 2, 6, and 7 were rigid because they lacked rotatable bonds, while compounds 1, 3, 5, and 7 were flexible. Furthermore, it

was noted that using synthesized compounds yielded molecules with superior pharmacological action.

The Sida acuta plant's chemical compositions were screened phytochemically, and the results revealed that the leaves of the plant were highly concentrated in alkaloids, phenol, tannins, terpenoids, sterols, saponins, and flavonoids. The results of phytochemical screening of Sida acuta leaves were shown in Table: 7.

The majority of phytochemicals were found in Sida acuta methanolic extract, according to preliminary phytochemical investigations. According to our research, the methanolic extract of Sida acuta leaves included significant concentrations of alkaloids, flavonoids, phenols, tannins, sterols, and terpenoids.^[24]

Thus, this research should offer evidence that the leaves of the Sida acuta plant are useful in treating tuberculosis. However, more sophisticated hyphenated spectroscopic research is required. Additionally, this information might come in useful in the future for investigating this plant's biochemistry.

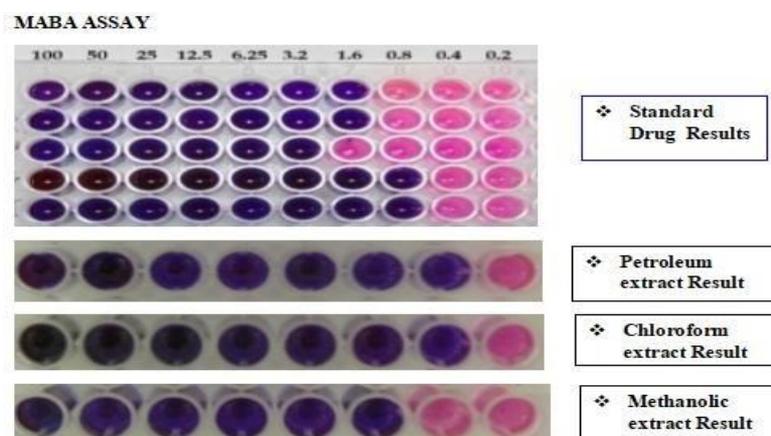
Table 7: Result of phytochemical screening of *Sida acuta* leaves.

S.no	Chemical test	Result
1.	Test for alkaloids (Dragendroff's reagent)	Positive
2.	Test for terpenoids (Salkowski test)	positive
3.	Test for phenolic compounds (Ferric chloride test)	positive
4.	Test for tannins:	
	a) Lead acetate test	positive
	b) Aqueous bromine test	positive
	c) Ferric chloride test	positive
5.	Test for saponins (Froth formation test)	positive
6.	Test for flavonoids	positive

Anti-mycobacterial action of leaf extracts

Globally, tuberculosis is the second biggest cause of death, after HIV/AIDS. Traditional medicines continue to remain the main healthcare system of choice in undeveloped nations, despite the preference of modern people for western techniques of healing. The findings regarding the anti-mycobacterial properties of *Sida acuta* leaves. The growth of the Mtb H37RV strain suppressed the growth of *Sida acuta* leaves by at least 90% at the quantities examined using the Microplate alamar blue assay (MABA).^[26] The determination of the Minimum Inhibitory Concentration (MIC) was made. After examining various solvent extracts from the leaves of the *Sida acuta* plant, it was discovered that petroleum ether extract exhibited the highest level of activity, with a Minimum Inhibitory Concentration (MIC) of 0.8µg/ml. This was succeeded by the chloroform extract, which

demonstrated a moderate level of activity with a MIC of 1.6µg/ml. The least active extract was the methanolic extract, which had a MIC of 3.12µg/ml. The results of individual extracts were shown in Fig 8 and table: 8 shows standard values of Antitubercular drugs. The extract performed best against standard drugs such as Isoniazid (1.6µg/ml), Ethambutol (1.6µg/ml), Pyrazinamide (3.125µg/ml), Rifampicin (0.8µg/ml), and streptomycin (0.8µg/ml), respectively. The test results for *sida acuta* plant extracts was shown in Table: 9. According to the findings, this *Sida acuta* plant possesses a high concentration of active principles and good antibacterial activity. This extract of petroleum ether, chloroform, and methanol exhibits effective inhibition because of their high concentration of active ingredients. In this work, we show that *Sida acuta* leaf extracts are efficient against the mycobacterium

**Figure 8: MABA Assay test res.****Table 8: Test results for *Sida acuta* plant extracts.**

S. No	Sample (<i>Sida acuta</i> plant leaves Extract)	100 µg/ml	50 µg/ml	25 µg/ml	12.5 µg/ml	6.25 µg/ml	3.12 µg/ml	1.6 µg/ml	0.8 µg/ml
01	Petroleum ether extract-in petroleum	S	S	S	S	S	S	S	R
02	Chloroform extract-inchloroform	S	S	S	S	S	S	S	R
03	Methanol extract-inmethanol	S	S	S	S	S	S	R	R

Note: S-Sensitive, R-Resistant

CONCLUSION

Mycobacterium tuberculosis is transmitted between individuals through respiratory route and it mainly affect the lungs and any tissues. The treatment is always extensive because of Mtb differ in metabolic activity. In this study an *In-silico* used to find a possible antagonism against the Mtb 5V3Y and 3AF3. It shows an extraordinary binding between the anti-tubercloid proteins and phytoconstituents of *Sida acuta*. To assess their physiochemical properties and other relevant pharmacokinetic parameters for selected phytoconstituents of *Sida acuta* were analysed and screened by using computational tools like ADMET analysis. The compounds shows an excellent oral-bioactivity by obeying an Lipinski's rule. The present study is the first report of the anti-mycobacterial activity of chemical components and extract of leaves of *Sida acuta*. Preliminary phytochemical screening showed the extract of the leaves of *Sida acuta* possessed activity against *Mycobacterium tuberculosis* H37Rv which was determined by Alamar Blue assay *In-vitro* evaluation. The methanol extract contains numerous bioactive compounds and exhibited a promising activity. The results of this study can be used as additional data for future therapeutic intervention as isolating the specific compounds which is responsible for the anti-tubercloid activity and utilization of *Sida acuta*.

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Ethics

Ethics Committee Approval: Not applicable.

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