ORIGINAL ARTICLE

Molecular Docking Analysis on Phytoconstituents of *Psoralea corylifolia* seeds against Mutant Beta Toxin *Staphylococcus aureus*

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ABSTRACT

Phytochemical analysis of cow urine extracts of Psoralea corylifolia seeds were analyzed by quantitative methods using Liquid Chromatography – Mass spectroscopy (LC-MS). The compounds of seeds from LC-MS analysis and this structure were retrieved from PubChem databases. The phytocompounds are analyzed for drug – likeness as Lipinski's rule. Molecular docking analysis of phytocompounds from Psoralea corylifolia seeds against the protein of crystal structure of beta toxin from Staphylococcus aureus F277A, P278A mutant with bound calcium ions (PDB ID: 3146). The interaction of protein and ligand reveals docking scores in all ligands. The highest docking scores reveals by Psoralidin, Corylidin, Bavachin, Neobavaisoflavone, Corylinal and Corylifol A. The present study reveals that Psoralea corylifolia seeds are acting as alternate medicine for treating beta toxin and various skin infections. **KEYWORDS:** Cow uring Psoralea corylifolia seeds docking S auraus

KEYWORDS: Cow urine, Psoralea corylifolia seeds, docking, S. aureus

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INTRODUCTION

The medicinal herb *Psoralea corylifolia* L. is on the verge of extinction. It is widely distributed in India, China, and Pakistan's Himalayan regions [1, 2]. And the *Psoralea* genus is native to North America [3]. Because of its ability to cure leprosy, *P. corylifolia* is also known as 'Kusthanashini,' or leprosy killer. It has a wide range of applications since it is an integral component of both the allopathic and conventional medical systems in different parts of the world. Psoriasis, leucoderma, and vitiligo are all treated with it in traditional Chinese medicine and Indian systems of medicine such as Ayurveda, Siddha, and Unani [4].

The plant is assumed to be warm in Chinese medicine, so it is used to treat kidney and spleen problems. Regardless, the plant's seeds are used as a diuretic, laxative, anti-parasitic, aphrodisiac, and competing remedy. Psoriasis, eczema, leukoderma, alopecia, and inflammation have all been treated with the seed paste [5, 6].

Even though seeds contain the majority of bioactive compounds of medicinal interest, *Psoralea corylifolia* seeds have been the subject of research. Psoralen, Isopsoralen, Bakuchiol, Bakuchicin, Bavachin, Isobavachin, Bavachinin, Bavachlcone, Isobavachalcone, Neobavachalcone, Corylifol A, B, C, D, E, Corylifolin, Corylifolinin, and other bioactive compounds exist [5, 7].

Bakuchi seed powder is mixed with cow's urine and Haratala Bhasma (yellow arsenic) in a 4:1 ratio for leucoderma. Leucoderma lesions are treated with this paste. External application of bakuchi seed powder combined with buttermilk is used to treat scabies and ringworm infestations [8, 9, & 10]. Bakuchi was combined with other herbs such as *Phyllanthus emblica* Linn. and *Acacia catechu* in a polyherbal extracts decoction that was recommended for treating leucoderma. As stated earlier, the seeds of *Psoralea corylifolia* have long been used as a medicinal agent in both Chinese and Ayurvedic medicine systems. Some of its biological activities have been recorded as antibacterial [11, 12], antiviral [13], antifungal [14, 15], anticancer and apoptotic [16], protective [17, 18, & 19].

Staphylococcus aureus is a highly important bacterium that causes infections in people all over the world. In healthy people, it causes a 30% infection rate. Despite the fact that it is asymptomatic, it can be lethal in immune-compromised patients. *Staphylococcus aureus* produces numerous cell surfaces and secreted virulence factors that allow it to cause a wide range of human illnesses, from mild boils to fatal toxic shock syndrome and necrotizing pneumonia. Certain strains of *Staphylococcus aureus* contain beta toxins [20, 21]. In humans, Staphylococcus aureus infections usually start with colonization of the mucus membrane or the skin. It produces toxins and cytolysins (leukocidins) that affect RBCs, epithelial cells in large numbers, and the immune system. Cytolysins include alpha, beta, gamma, and delta toxins. Exotoxins are beta poisons, and sphingomyelinase is a neutral enzyme [22].

The goal of this study was to identify the bioactive compounds in cow urine extracts of *Psoralea corylifolia* seeds, as well as to conduct a molecular docking review of the phytocompounds discovered in order to investigate molecular interactions.

MATERIAL AND METHODS

COLLECTION AND PROCESSING OF SEEDS SAMPLES:

The seed of *Psoralea corylifolia* was collected in the local folk medicine market in Cuddalore District, Tamil Nadu. After the collection of seeds, it was ground coarsely by using Morter and Pestle. The ground seed samples are sieved and stored for further processes.

PREPARATION OF EXTRACT:

10g of seeds powder of *Psoralea corylifolia* was mixed with 100 ml of fresh cow urine and incubated for 3 days. After incubation, the extract was filtered through Whatman No.1 filter paper. The filtered extract was used for further analysis.

LC-MS ANALYSIS:

The quantitative phytochemical analysis of cow urine extracts of *Psoralea corylifolia* seeds by the hyphenated technique of Liquid Chromatography-Mass spectrometry analysis. Result analysis of compounds by peak value.

IDENTIFICATION OF PHYTOCONSTITUENTS:

The spectrum of LC-MS analysis unknown components were compared with the spectrum of the known components stored in Wiley9 library and PubChem databases.

PASS PREDICTION:

PASS prediction is an online tool to predict the biological activity of compounds. PASS prediction analysis of these bioactive compounds obtained from LC-MS analysis. By using PASS prediction online tool (http://www.way2drug.com/PASSOnline/), Anti-bacterial activity of cow urine extracts of *Psoralea corylifolia* seeds.

MOLECULAR DOCKING ANALYSIS:

DOCKING ANALYSIS:

The molecular docking study aimed to determine the most derived target protein-ligand complex structure. The AutoDock Vina protocol with BIOVIA Discovery studio visualization was used to determining the active binding modes between the ligands and the target proteins. The parameters of the attributes are defining by the run ligand-receptor site. The algorithm uses protein-ligand interaction energy, Hydrogen bonds; binding energies were used to quantify the affinity of ligand binding. The docking energy is stated in Negative values. Higher negative energy values indicated the higher binding affinity of protein and ligand.

RETRIEVAL OF TARGET PROTEIN:

The protein of crystal structure of beta toxin from *Staphylococcus aureus* F277A, P278A mutant with bound calcium ions of 3i46 was obtained from RCSB Protein Data Bank. And the UNIPROT ID of 3i46 was A7LAI8 (http://chlorine.atomistry.com/pdb3i46.html).

LIGAND GENERATION:

For ligand generation, LC-MS analysis of Cow urine extracts of *Psoralea corylifolia* seeds compounds was used for molecular docking. The database of obtained compounds from Pubchem and the 3D structures of identified compounds were downloaded in SDF file format. Then that file was converted into a PDB file for further analysis by using Open Babel software. The compounds are used for the prediction of ligand properties such as pH, Molecular weight, Hydrogen bonds, acceptors, logP values and Refractive index. These compounds were screened for drug – likeliness according to Lipinski's rule of five. The drug – likeliness of Lipinski's rule of five was predicted by using online (scfbio-iitd.res.in).

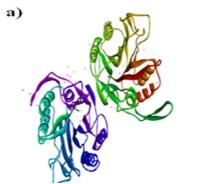
RESULTS

The phytoconstituents present in cow urine with *Psoralea corylifolia* seeds were analyzed through Liquid Chromatography-Mass Spectrometry (LC-MS). Results obtained from the LC-MS analysis and names of the compounds, molecular formula, logP value, Hydrogen bond donor count, Hydrogen bond acceptor count were retrieved from PubChem databases are in Table 1 and Graphical presentation in Fig 3.

PASS Prediction:

All the compounds are predicted biological activity through the PASS prediction online tool. And it is observed that the Antibacterial activity of *Staphylococcus aureus* and other various microorganisms. **Molecular Docking analysis:**

For docking analysis with 18 compounds retrieved from Pubchem databases and Standard drugs such as Methicillin and Cefazolin. All these 20 compounds are docked with the 3I46 protein retrieved from the RCSB PDB databank. The docking studies of Beta toxin of Staphylococcus aureus (3146) of binding active site were analyzed by using the CASTp online server. After identification of protein active binding site, molecular docking was analyzed by using Autodock vina MGL tools. In Autodock vina protein is loaded with macromolecules, and waters are removed. Then hydrogen polar bonds are added manually and add charges. Then macromolecule files are saved as PDBQT. Ligand files are input and saved as PDBQT files. Grid box are formed in centre grid are X = 4.139, Y = 6.845 and Z = -5.199. And size X = 20, Y = 20 and Z = -5.199. 20. Then configuration file was made by using all the details correctly. Command prompts are run by using data. After the file was generated, it was split by using Vina split. Then it is analyzed by using BIOVIA Discovery studio software used for protein and ligand interactions and publication-quality images ^[23]. After protein and ligand docking analysis, interactions of protein-ligand sites (amino acid), the phytocompounds of cow urine extracts of *Psoralea corylifolia* seeds against crystal structure of Beta toxin of Staphylococcus aureus F277A, P278A mutant with bound Calcium ions (3146) shows the binding activity of all the ligand. In this analysis of ligand interactions with Staphylococcus aureus having the highest interactions are shown in Table 2 and Fig 4.



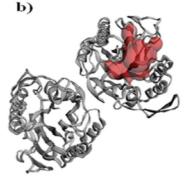


Fig 1: (a) Structure of 3I46 - crystal structure of beta toxin from *Staphylococcus aureus* F277A, P278A mutant with bound calcium ions. (b) CASTp – 3I46 active site.

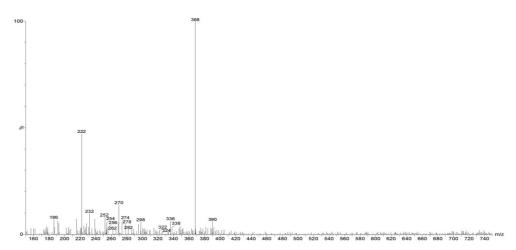


Fig 2: LC-MS analysis of Cow Urine extracts of *Psoralea corylifolia* seeds

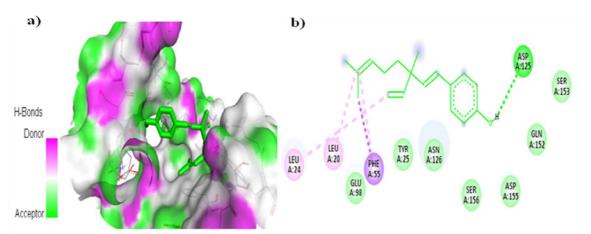


Fig 3: a) Ligand Interaction and b) 2D binding interaction of Bakuchiol derivatives with active site of 3I46 receptor.

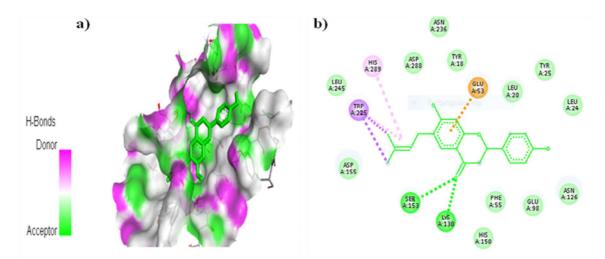


Fig 4: a) Ligand Interaction and b) 2D binding interaction of Bavachin derivatives with active site of 3I46 receptor.

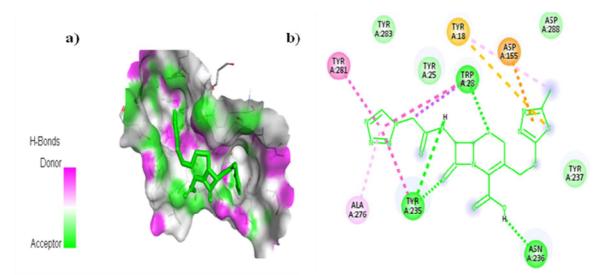


Fig 5: a) Ligand Interaction and b) 2D binding interaction of Cefazolin derivatives with active site of 3I46 receptor.

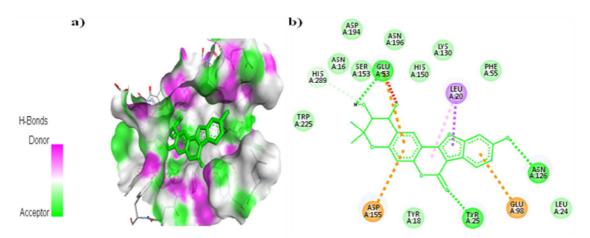


Fig 6: a) Ligand Interaction and b) 2D binding interaction of Corylidin derivatives with active site of 3I46 receptor.

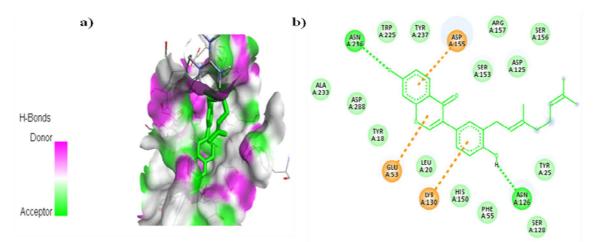


Fig 7: a) Ligand Interaction and b) 2D binding interaction of Corylifol A derivatives with active site of 3146 receptor.

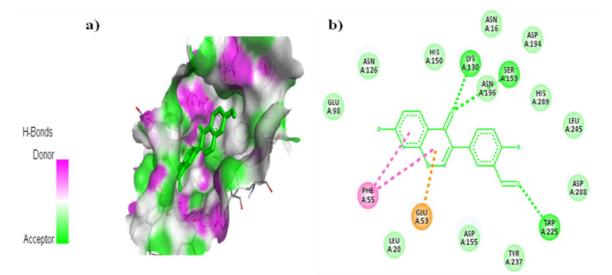


Fig 8: a) Ligand Interaction and b) 2D binding interaction of Corylinal A derivatives with active site of 3146 receptor.

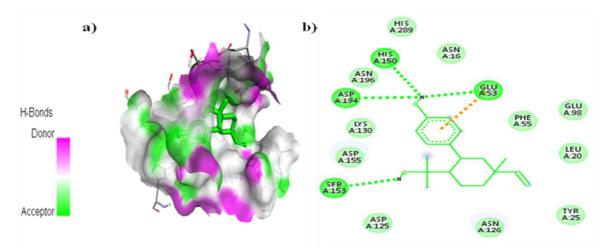


Fig 9: a) Ligand Interaction and b) 2D binding interaction of Cyclobakuchiol – C derivatives with active site of 3I46 receptor.

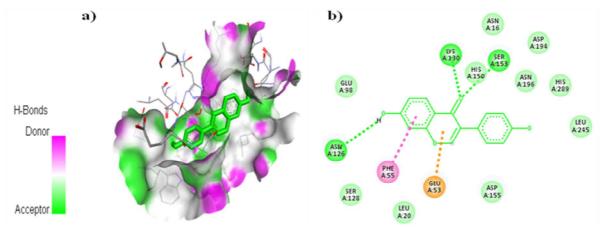


Fig 10: a) Ligand Interaction and b) 2D binding interaction of Daidzein derivatives with active site of 3I46 receptor.

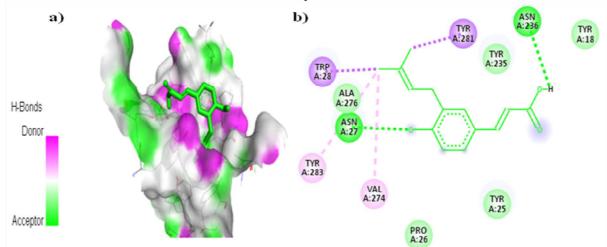


Fig 11: a) Ligand Interaction and b) 2D binding interaction of Drupanin derivatives with active site of 3146 receptor.

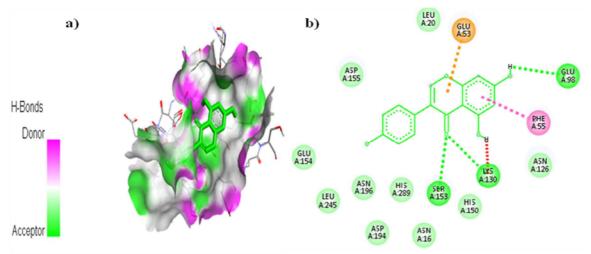


Fig 12: a) Ligand Interaction and b) 2D binding interaction of Genistein derivatives with active site of 3I46 receptor.

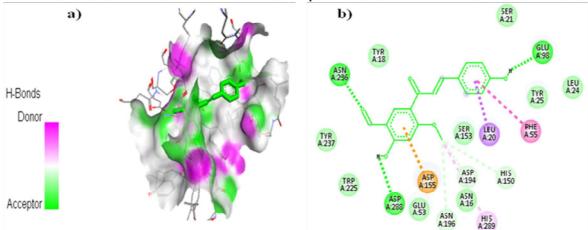


Fig 13: a) Ligand Interaction and b) 2D binding interaction of Isoneobavachalcone derivatives with active site of 3I46 receptor.

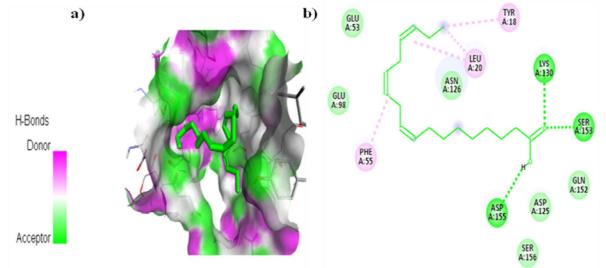


Fig 14: a) Ligand Interaction and b) 2D binding interaction of Linolenic acid derivatives with active site of 3I46 receptor.

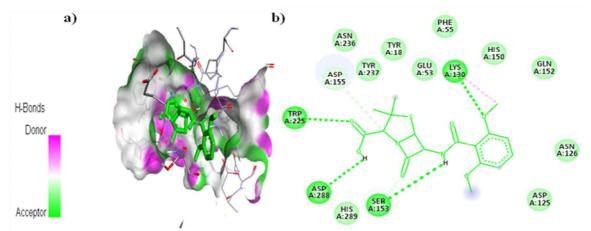


Fig 15: a) Ligand Interaction and b) 2D binding interaction of Methicillin derivatives with active site of 3I46 receptor.

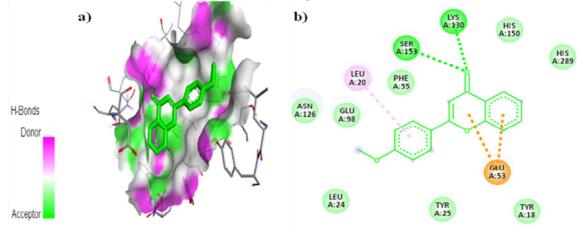


Fig 16: a) Ligand Interaction and b) 2D binding interaction of Methoxyflavone derivatives with active site of 3I46 receptor.

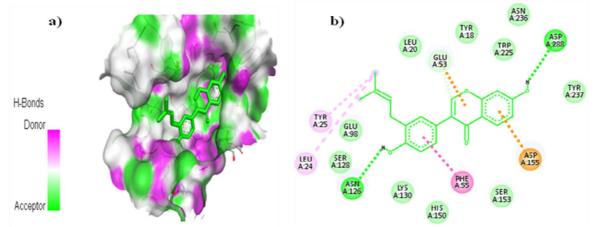


Fig 17: a) Ligand Interaction and b) 2D binding interaction of Neobavaisoflavone derivatives with active site of 3I46 receptor.

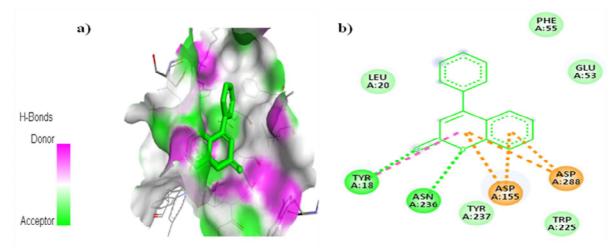


Fig 18: a) Ligand Interaction and b) 2D binding interaction of Phenylcoumarin derivatives with active site of 3146 receptor.

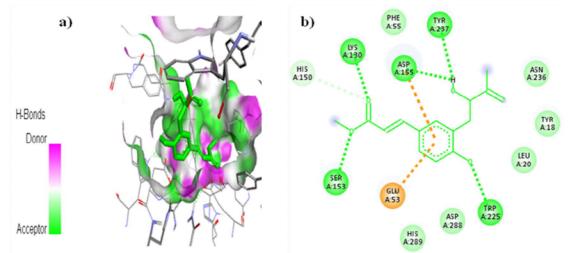


Fig 19: a) Ligand Interaction and b) 2D binding interaction of Plicatin-A derivatives with active site of 3I46 receptor.

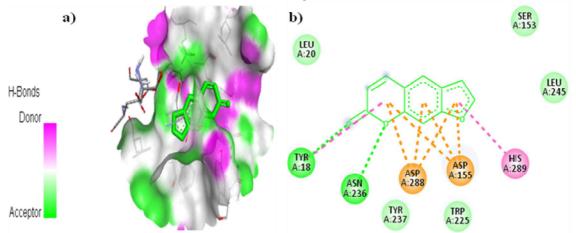


Fig 20: a) Ligand Interaction and b) 2D binding interaction of Psoralen derivatives with active site of 3I46 receptor.

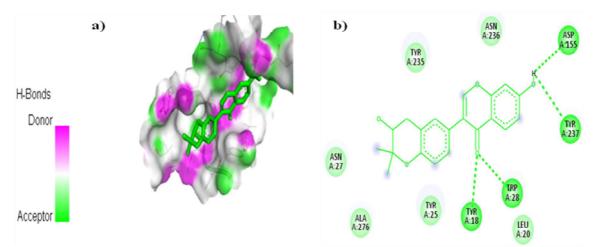


Fig 21: a) Ligand Interaction and b) 2D binding interaction of Psoralenol derivatives with active site of 3I46 receptor.

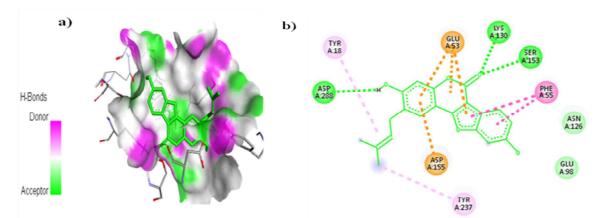


Fig 22: a) Ligand Interaction and b) 2D binding interaction of Psoralidin derivatives with active site of 3I46 receptor.

S.No	Compounds	PubChem	Molecular	Molecular Weight	HBD	HBA	logP
	Names	CID	formula	(g/mol)			
1.	Corylidin	5316096	C ₂₀ H ₁₆ O ₇	368.3	3	7	2
2.	C-Phenylcoumarin	613729	$C_{15}H_{10}O_2$	222.24	0	2	3.1
3.	Psoralen	6199	C ₁₁ H ₆ O ₃	186.16	0	3	2.3
4.	Drupanin	6440361	$C_{14}H_{16}O_3$	232.27	2	3	3.4
5.	Methoxyflavone	71793	$C_{16}H_{12}O_3$	252.26	0	3	3.5
6.	Daidzein	5281708	$C_{15}H_{10}O_4$	24.24	2	4	2.5
7.	Bakuchiol	5468522	C ₁₈ H ₂₄ O	256.18	1	1	6.1
8.	Plicatin - A	15730631	$C_{15}H_{18}O_4$	262.3	2	4	2.7
9.	Genistein	5280961	$C_{15}H_{10}O_5$	270.24	3	5	2.7
10.	Cyclobakuchiol - C	101956380	C ₁₈ H ₂₆ O ₂	274.4	2	2	4.5
11.	Linolenic acid	5280934	C ₁₈ H ₃₀ O ₂	278.4	1	2	5.9
12.	Corylinal	44257227	C ₁₈ H ₃₀ O ₂	282.25	2	5	2.5
13.	Isoneobavachalcone	5318608	C17H14O5	298.29	2	5	3
14.	Neobavachalcone	5320053	C ₂₀ H ₁₈ O ₄	322.4	2	4	4.4
15.	Bavachin	14236566	C ₂₀ H ₂₀ O ₄	324.4	2	4	4.1
16.	Psoralidin	5281806	C20H16O5	336.3	2	5	4.7
17.	Psoralenol	5320772	C20H18O5	338.4	2	5	2.8
18.	Corylifol - A	25056407	C25H26O4	390.5	2	4	6.3

T-bl- 1.	Describe of Com		LC-MS analysis
Table I:	Results of Com	bounds from	LU-MIS analysis
10.010 1.		poundo nom	

Table 2: Molecular Docking Analysis							
Ligand	Docking Score	Interacting Residues	Distance	Category	Туре		
	(kcal/mol)		(Å)				
Bakuchiol	-5.5	ASP125	2.37	Hydrogen	Conventional		
		PHE55	3.89	Bond	Pi-Sigma		
		LEU20	4.90	Hydrophobic	Alkyl		
		LEU24	5.14	Hydrophobic	Alkyl		
		PHE55	4.75	Hydrophobic	Pi-Alkyl		
				Hydrophobic			
Bavachin	-8.2	LYS130	2.32	Hydrogen	Conventional		
		GLU53	3.27	Bond	Carbon		
		ASP155 ASP288 PHE55	4.51	Hydrogen	Pi-Anion		
		HIS289 LEU20 TYR25	4.76	Bond	Pi-Anion		
			5.69	Electrostatic	Pi-Pi Stacked		
			5.12	Electrostatic	Pi-Pi T shaped		
			4.65	Hydrophobic	Alkyl		
			5.42	Hydrophobic	Pi-Alkyl		
			5.72	Hydrophobic	I I-AIKYI		
Cofor-li-	((TDD20	2.25	Hydrophobic	Converties 1		
Cefazolin	-6.6	TRP28	2.35	Hydrogen	Conventional		
		TYR235	2.72	Bond	Conventional		
		TYR235	3.05	Hydrogen	Conventional		
		ASN236	2.98	Bond	Conventional		
		ASP155	4.15	Hydrogen	Pi-Anion		
		TRP28	3.85	Bond	Pi-Sigma		
		TYR18	5.93	Hydrogen	Pi-Sulfur		
		TYR281 ALA276	4.55	Bond	Pi-Pi T-shaped		
			4.71	Electrostatic	Pi-Alkyl		
				Hydrophobic	5		
				Other			
				Hydrophobic			
				Hydrophobic			
Corylidin	-8.3	TYR25	2.19	Hydrogen	Conventional		
Corynam	-0.5	ASN126	2.37	Bond	Conventional		
		GLU53	2.04	Hydrogen	Conventional		
				Bond			
		HIS289	2.94		Carbon		
		GLU98	4.52	Hydrogen	Pi-Anion		
		ASP155	4.81	Bond	Pi-Anion		
		LEU20	3.94	Electrostatic	Pi-Sigma		
				Electrostatic			
				Electrostatic			
				Hydrophobic			
CorlifolA	-7.2	ASN236	2.26	Hydrogen	Conventional		
		ASN126	2.12	Bond	Conventional		
		LYS130	4.52	Hydrogen	Pi-Cation		
		GLU53	4.30	Bond	Pi-Anion		
		ASP155	3.84	Electrostatic	Pi-Anion		
				Electrostatic			
				Electrostatic			
Corylinal	-7.3	LYS130	2.26	Hydrogen	Conventional		
Soryman	1.0	SER153	2.20	Bond	Conventional		
			2.05				
		TRP225		Hydrogen	Conventional		
		GLU53	3.64	Bond	Pi-Anion		
		PHE55	5.94	Hydrogen	Pi-Pi Stacked		
				Bond			
				Electrostatic			

Table 2: Molecular Docking Analysis

				Hydrophobic	
Cyclobakuchiol C	-5.7	SER153	2.67	Hydrogen	Conventional
		GLU53	2.97	Bond	Conventional
		HIS150	2.71	Hydrogen	Conventional
		ASP194	3.08	Bond	Conventional
				Hydrogen	
				Bond	
				Hydrogen	
				Bond	
Daidzein	-7.1	LYS130	2.05	Hydrogen	Conventional
		SER153	2.68	Bond	Conventional
		ASN126	2.84	Hydrogen	Conventional
		GLU53	3.71	Bond	Pi-Anion
		PHE55	4.69	Hydrogen	Pi-Pi Stacked
				Bond	
				Electrostatic	
				Hydrophobic	
Drupanin	-6.0	ASN27	2.64	Hydrogen	Conventional
Drapanni	0.0	ASN236	2.67	Bond	Conventional
		TRP28	3.76	Hydrogen	Pi-Sigma
		TYR281	3.63	Bond	Pi-Sigma
		VAL274	5.08	Hydrophobic	Alkyl
		TYR283	4.66	Hydrophobic	Pi-Alkyl
		1111203	4.00	Hydrophobic	FI-AIKYI
				Hydrophobic	
Genistein	-7.0	LYS130	2.36		Conventional
Genistein	-7.0			Hydrogen	
		SER153	2.73	Bond	Conventional
		GLU98	2.93	Hydrogen	Conventional
		GLU53	3.64	Bond	Pi-Anion
		PHE55	4.70	Hydrogen	Pi-Pi Stacked
				Bond	
				Electrostatic	
				Hydrophobic	
Isoneobavachalcone	-6.3	ASN236	2.09	Hydrogen	Conventional
		GLU98	1.79	Bond	Conventional
		ASP288	2.16	Hydrogen	Conventional
		HIS150	3.55	Bond	Carbon
		ASP194	3.46	Hydrogen	Carbon
		ASN196	3.61	Bond	Carbon
		ASP155	4.14	Hydrogen	Pi-Anion
		LEU20	3.66	Bond	Pi-Sigma
		PHE55	5.56	Hydrogen	Pi-Pi Stacked
		HIS289	5.28	Bond	Pi-Alkyl
				Hydrogen	
			1	Bond	
			1	Electrostatic	
			1	Hydrophobic	
			1	Hydrophobic	
				Hydrophobic	
			2.42	Hydrogen	Conventional
Linolenic Acid	-4.5	LYS130	2.42	ingalogen	
Linolenic Acid	-4.5	LYS130 SER153	2.42	Bond	Conventional
Linolenic Acid	-4.5	SER153	2.01	Bond	Conventional Conventional
Linolenic Acid	-4.5	SER153 ASP155	2.01 2.32	Bond Hydrogen	Conventional
Linolenic Acid	-4.5	SER153 ASP155 LEU20	2.01 2.32 5.28	Bond Hydrogen Bond	Conventional Alkyl
Linolenic Acid	-4.5	SER153 ASP155	2.01 2.32	Bond Hydrogen	Conventional

				Hydrophobic	
				Hydrophobic	
Methicillin	-6.5	LYS130	2.41	Hydrogen	Conventional
		TRP225	2.67	Bond	Conventional
		SER153	3.03	Hydrogen	Conventional
		ASP288	2.77	Bond	Conventional
		SER153	3.18	Hydrogen	Carbon
		ASP155	3.44	Bond	Carbon
		LYS130	5.36	Hydrogen	Alkyl
		210100	0.00	Bond	
				Hydrogen	
				Bond	
				Hydrogen	
				Bond	
				Hydrophobic	
Methoxyflavone	-6.4	LYS130	2.25	Hydrogen	Conventional
meuloxyllavolle	-0.4	SER153	2.25	Bond	Conventional
		GLU53	3.90 5.24	Hydrogen Bond	Pi-Anion
		LEU20	5.34		Pi-Alkyl
				Electrostatic	
Nachara ' C	0.0	ACN1207	2.64	Hydrophobic	
Neobavaisoflavone	-8.0	ASN126	2.64	Hydrogen	Conventional
		ASP288	2.66	Bond	Conventional
		GLU53	3.33	Hydrogen	Carbon
		ASP155	4.07	Bond	Pi-Anion
		PHE55	4.52	Hydrogen	Pi-Pi Stacked
		LEU24	5.18	Bond	Alkyl
		TYR25	5.07	Electrostatic	Pi-Alkyl
				Hydrophobic	
				Hydrophobic	
				Hydrophobic	
Phenylcoumarin	-6.7	TYR18	2.61	Hydrogen	Conventional
		ASN236	2.52	Bond	Conventional
		ASP155	4.09	Hydrogen	Pi-Anion
		ASP288	4.56	Bond	Pi-Anion
				Electrostatic	
				Electrostatic	
PlicatinA	-5.7	LYS130	2.08	Hydrogen	Conventional
		SER153	2.63	Bond	Conventional
		TYP225	2.34	Hydrogen	Conventional
		ASP155	2.70	Bond	Conventional
		TYR237	2.46	Hydrogen	Conventional
		HIS150	3.61	Bond	Carbon
		GLU53	4.80	Hydrogen	Pi-Anion
				Bond	-
				Hydrogen	
				Bond	
				Hydrogen	
				Bond	
				Electrostatic	
Psoralidin	-8.4	LYS130	2.54		Conventional
r soi aiiulli	-0.4			Hydrogen	
		SER153	2.86	Bond	Conventional
		ASP288	2.76	Hydrogen	Carbon
		GLU53	3.90	Bond	Pi-Anion
		ASP155	4.53	Hydrogen	Pi-Anion
		PHE55	4.55	Bond	Pi-Pi Stacked

		TYR18	5.33	Electrostatic	Pi-Alkyl
		TYR237	4.96	Electrostatic	Pi-Alkyl
				Hydrophobic	
				Hydrophobic	
				Hydrophobic	
Psoralen	-6.2	TYR18	2.84	Hydrogen	Conventional
		ASN236	2.59	Bond	Conventional
		ASP155	4.43	Hydrogen	Pi-Anion
		ASP288	4.58	Bond	Pi-Anion
		HIS289	5.14	Electrostatic	Pi-Pi T-shaped
				Electrostatic	
				Hydrophobic	
Psoralenol	-6.6	TYR18	2.26	Hydrogen	Conventional
		TYR28	2.09	Bond	Conventional
		ASP155	2.09	Hydrogen	Conventional
		TYR237	2.88	Bond	Conventional
				Hydrogen	
				Bond	
				Hydrogen	
				Bond	

DISCUSSION

The physicochemical properties of all phytocompounds were analyzed by using Lipinski's rule of druglikeness. The crystal structure of beta toxin from *Staphylococcus aureus* F277A, P278A mutant with bound calcium ions (3146) and the ligand of all phytoconstituents were analyzed by docking and the protein-ligand interactions are revealed the highest binding activities. Analysis docking ligands against *Staphylococcus aureus* shows highest docking scores are Psoralidin (-8.4 kcal/mol), Corylidin (-8.3 kcal/mol), Bavachin (-8.2 kcal/mol), Neobavaisoflavone (-8.0 kcal/mol), Corylinal (-7.3 kcal/mol) and Corylifol A (-7.2 kcal/mol). Docking scores are better than standard antibiotics. It shows the interaction of protein-ligand with various categories such as hydrogen bonds, electrostatic, hydrophobic and types as conventional, Pi – Alkyl, Alkyl, Pi – Anion, Sulfur, Pi – Pi stacked. Docking studies of protein and ligand show amino acid residues such as LYS 130, ASP 155, ASP 288, SER 153, TYR 18, TYR 237 and GLU 53. The outcome was determined that the phytoconstituents of cow urine extracts of *Psoralea corylifolia* seeds can be used as an alternative medicine for various skin infections.

CONCLUSION

Psoralea corylifolia seeds are used for many biological activities such as Anti-bacterial, Anti-fungal, Anti-psoriatic, etc. Seeds are mixed with cow urine and ground as paste and used for leucoderma in the ancient period of India. The present docking studies concluded that the phytocompounds present in the seeds of *Psoralea corylifolia* having great effects to treat *Staphylococcus aureus* infections. Further studies will be carried out for analyzing various biological activities.

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CONFLICT OF INTEREST

There is no conflict of interest.

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