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In Silico Design Of Antimalarial Drug From *Catharanthus Roseus* (G. Don) Alkaloid Molecules against AMA1 Protein

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The emergence and spread of drug resistance in Plasmodium falciparum, the parasite causing the most severe form of malaria is a major threat to malaria control and elimination program around the globe. With Plasmodium falciparum having evolved widespread resistance against a number of previously widely used drugs, currently artemisinine and its derivatives are the cornerstones of first line treatment of uncomplicated malaria. Growing incidences failure reflects artemisinine resistance. Pharmacology approach in this study is being used against AMA1 protein which can be used as major target for drug due to its participation in erythrocytic infection stage. This protein is conserved in all plasmodium species. The AMA1-PLAF8 structure is modelled through homology modelling method and virtual screening against Catharanthus roseus fraction is carries out using Maetrso. Secologanin, Vindoline, tabersonine, Vincristine, Serpentine, Ajmalicine, Catharanthine and catechol were taken for screening. Secaloganine showed the best binding results with lowest binding energy (-7.815 Kcal/mol) and shortest bond length i.e. 1.80881?. This virtual screening investigation suggests that Secaloganin can be repurposed for malaria control and prevention.

Keywords: Apical Membrane Antigen 1 (AMA 1); Artemesinine resistance; Malaria; Molecular docking; XP Gscore.

Malaria keeps on causing unsuitably significant degrees of illness and demise, as archived in progressive versions of the World Malaria report. [1] As indicated by the most recent report, there were an expected 627000 lives lost in malaria 2020.[2] Malaria is preventable and treatable and the worldwide need is to lessen the weight of infection and demise while holding the drawn out vision of Malaria destruction.

The only malaria vaccine, RTS,S/AS01, initiates incomplete adequacy through enlistment of antibodies against the sequence (Asn-Ala-Asn-Pro) of the circumsporozoite protein (CSP). However, there are many antigenic determinants of Plasmodium against which either medications or antibodies are formed. [3] The different standards for antigen choice as well as medication definition are summed up in table.1.

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The current situation is confronting many difficulties in vector control and parasite disposal. One of the most significant challenges is drug obstruction in Plasmodium. While obstruction is regularly evaluated by drug adequacy concentrates on that uncover applicant point transformations, whose pervasiveness are checked. The genuine method of activity of obstruction is related with changes which are frequently less clear. Notwithstanding, a significant comprehension of the sub-atomic instrument hidden medication opposition can prompt the improvement of new synthetic mixtures that can re-establish drug productivity. Witnessing the need for antimalarial drug, there is need of virtual screening of some potential drug candidates to push them up for further trials.

Catharanthus roseus is an important medicinal plant of family Apocynaceae with 70 different types of alkaloids, steroids and chemotherapeutic agents which are effective as anticancerous, antimalarial and antimicrobial activity. Vinblastine and Vincristine are two important alkaloids that are being used widely to treat diabetes.[23] *Catharanthus roseus* (L.) G. Don contains terpenes and alkaloids which exhibits great pharmacological activities. [24] It has wide range of medicinal properties such as antioxidant, [25-27] anticancer, [28] antidiabetic, [29] antimicrobial,[30] antiulcer,[23] hypertensive,[24,31] wound healing, [31] hypolipidemic [27] and memory enhancement. [28,29] With virtual screening the objective is to explore antimalarial effect of various alkaloid fractions of the plant.

The potential drugs and their mechanism of action is summarized in table 2, however, the effect and targets of various drugs is summarized in table 3. There are no medications for sporozoite form; the causal prophylaxis drugs repress erythrocytic stage. The suppressive prophylaxis acting medications smother clinical infection beginning. Primaquine is the main medication which targets hyphozoites of *P.vivax* and *P.ovale* as well as gametocytes of Plasmodium.

Following treatments are used to treat uncomplicated *P. falciparum* malaria (2015) Treating children and adults with uncomplicated *P. falciparum* malaria (except pregnant women in their first trimester) with one of the following ACTs:

- artemether + lumefantrine
- artesunate + amodiaquine
- artesunate + mefloquine
- dihydroartemisinin + piperaquine
- artesunate + sulfadoxine-pyrimethamine (SP).

The current situation is confronting many difficulties in vector control and parasite elimination. One of the recent problems in malaria elimination is *Plasmodium* mutants. The mutation in Kelch protein resulted in resistance. To overcome such obstructions drug designing against target protein is been done to overcome future problem of resistance. As changes in the Kelch13 (PfK13) quality were distinguished as the vital sub-atomic markers and stayed to be key indicators of ART resistance. As far as drug delivery is concerned the most potential and safe target stage is invasion of Red Blood Cells. Regarding above fact and seeing the overview of *Plasmodium* infection in figure.1. Merozoite surface antigen 1,[8] Plasmodium falciparum erythrocyte membrane protein 1, [13] RIFIN, [15] Apical Membrane Antigen 1 are the most effective targets. However, AMA1 protein is chosen in this work because of its transmembrane nature and many unrevealed characters. [13]

This paper covers in silico designated drug adequacy against AMA1 protein quality and its viability to be utilized as medication in future for Malaria treatment.

METHODOLOGY

The FASTA grouping of *P. falciparum* for AMA 1 was recovered from the UniProt data set (https://www.uniprot.org/). The comparing UniProt ID explicitly for the *P. falciparum* strain utilized for this study was AMA1_PLAF8. The Protein sequence and 3D structure of PfK13 was derived from Uniprot data set.

Protein Modelling

Protein modelled through Homology modelling method through Swiss Model. The maximum homology was 97% with searched templates, the modelled prepared by choosing best matching template and best model selected on basis of lowest RMSD value and DOPE score. The model

Table 1. Plasmodium exposed surface antigens are:

S.No.	Protein ID	Protein name	Protein function
1.	IPR010901	Merozoite Surface 1, C-terminal	C-terminal region of merozoite surface protein 1 which helps in invasion of Red Blood Cells.[4]
2.	IPR010423	Ookinete Surface antigen, EGF domain	Pvs25 and Pvs28 antigenic proteins present on surface of Plasmodium.[5]
3.	IPR032761	*Plasmodium falciparum* erythrocyte membrane protein1, N terminal	Protein domain present on *Plasmodium falciparum* infected erythrocytes to adhere host endothelial receptors.[6]
4.	IPR003067	Plasmodium Circumsporozoite Protein	Surface antigen on surface of sprozoite of *Plasmodium* which is passes from mosquito vector to mammalian host.[7]
5.	PF12319	Tryptophan-Threonine-rich plasmodium antigen C terminal	C terminal of the surface antigen present on *Plasmodium.*[8]
6.	PF07462	Merozoite surface protein 1 (MSP1) C-terminus	Represent C terminal region of merozoite surface protein 1 which induces merozoite infection to Red Blood Cells.[9]
7.	IPR029210	*Plasmodium falciparum* erythrocyte membrane protein-1,N terminal segment	Protein domain present on *Plasmodium falciparum* infected erythrocytes to adhere host endothelial receptors.[10]
8.	IPR006373	Variant surface antigen Rifin	RIFIN Expressed on free merozoites as well as on infected erythrocytes contributing to antigenic variation capacity of the parasite.[11]
9.	IPR010784	Merozoite surface protein type	Merozoite invasion to erythrocytes involves multiple interaction with Merozoite Surface Protein.[4]
10.	PF15445	Acidic terminal segments, variant surface antigen of PfEMP1	These proteins help in evading host immune system by sticking to endothelial cells.
11.	PF06247	Pvs28 EGF domain	Group of okinete surface protein and induces immune responses in body
12.	IPR006499	Reticulocyte binding protein	These are reticulocyte binding protein which express Duffy antigen
13.	PF03805	Cytoadherence linked asexual protein	Induces binding of *Pf* to host endothelial cells
14.	PF15448	N terminal segments of *Plasmodium falciparum* erythrocyte membrane protein	This is a transmembrane protein that shares domains with molecules expressed on infected erythrocytes
15.	PF07133	Merozoite surface protein (SPAM)	It is a platform for binding to human erythrocytes by *Plasmodium falciparum*
16.	IPR003298	Apical membrane antigen 1	Expressed on invasive merozoite which are causative agent of malaria
17.	IPR026894	DNAJ containing protein, X domain	This domain is found in *Plasmodium falciparum* ring infected erythrocyte surface antigen and is shown to bind to spectrin and stabilize tetramer.[12]

18.	IPR024056	Apical membrane antigen 1 (AMA-1) domain superfamily	AMA-1 appears to be transported to the merozoite surface close to the time of schizont rupture.[13]
19.	IPR005553	Cytoadherence Linked Asexual Protein (CLAP)	CLAP is found to be associated in binding of *P.falcipaprum* infected erythrocytes to host endothelial cells.
20.	IPR010884	6-Cysteine (6-Cys) domain	6-Cys domain is found in *Plasmodium* proteins that are expressed in all stages of parasite life in both vertebrate and mosquito hosts.[14]
21.	PF02009	RIFIN (Repeated Interspersed families)	These are expressed on the surface of infected erythrocytes.[15]
22.	PS50095	PLAT (Polycystin-1, lipoxygenase and alpha toxin) domain profile	It is involved in protein-protein, protein-lipid interaction. In *P.falciparum* it is expressed on surface of gametocyte and interacts with mammalian triglyceride lipase.[16]
23.	PS50092	Thrombospondin type-1 (TSP1) repeat profile	It is present in circumsporozoite protein of Plasmodium.[17]
24.	PF15447	N terminal segments of PfEMP1	It is variable part of the variant surface antigen family *Plasmodium falciparum* and adhere to host endothelial receptors.[18]
25.	IPR043226	Neural cytotoxicity triggering receptor 3	It stimulates NK cells cytotoxicity.
26.	IPR009484	Protein of unknown function DUF1103	This family function is unknown.
27.	IPR014886	La protein, xRRM domain	La protein motifs are generally involved in binding to UUU-3'OH sequence of various RNA Polymerase III where xRRM domain induces conformational changes.[19]
28.	IPR034204	Subtilisin SUB1-like catalytic domain	It activates the merozoite surface protein allows it to bind to host erythrocyte membrane prior to egress.[20]
29.	PS50234	VWFA domain profile	Von Willebrand Factor (VWF) is a large multimeric protein required for normal hemostasis.[21]
30.	IPR036383	Thrombospondin type-1(TSP1) repeat superfamily	These are multimeric glycoprotein that function at cell surfaces and in extracellular matrix.[22]

structure was validated through Ramachandran plot.

Ligand Preparation

The small molecule library was built based on a wide range of experimental activity against *P. falciparum*. Molecular preparations such as the insertion of hydrogen bonds, 2D to 3D conversion, stereoisomers production, neutralisation of charged structures, or identification of most likely ionisation state at a user-defined pH, and the entire preparation were carried out using Maestro's LigPrep application.[32]

Protein preparation

Because the protein was simulated, the YASARA Energy Minimisation Server was used to perform an energy minimisation (Krieger et al. 2009)[33]. This minimised protein was then used in the Protein Wizard tool for further processing. Using Maestro's Glide application, the receptor grid with given grid coordinates of X = -20, Y = -10, and Z = 0 was produced with a box size of 36 × 36 × 36 Å. [33]

Molecular Docking

The produced ligand library was then docked with the protein grid using Glide's XP (extra precision) docking function, yielding an XP Glide score as a consequence. To rank docking poses and determine protein–ligand binding affinities, the XP Glide scoring function is utilised. Using a "funnel-type" method, the Glide algorithm searches for the ligand's position, orientation, and conformation in the enzyme's active site. [34] Maestro's Pose viewer & XP-visualizer software was used to analyse the output files.

Protein FASTA sequence

>QKY59679.1 AMA1

M K S S N T K M Q C I V K K L S L L A M P V V
I A A I L S L K I V P A G A A F V A F Q T D P P S S R G N R
R S S R G G R N Q Q A A G R Q A Q N E A E G T E R A G G R S
S S S K I I Q Q T P W T K Y M I K Y D I A R C H G

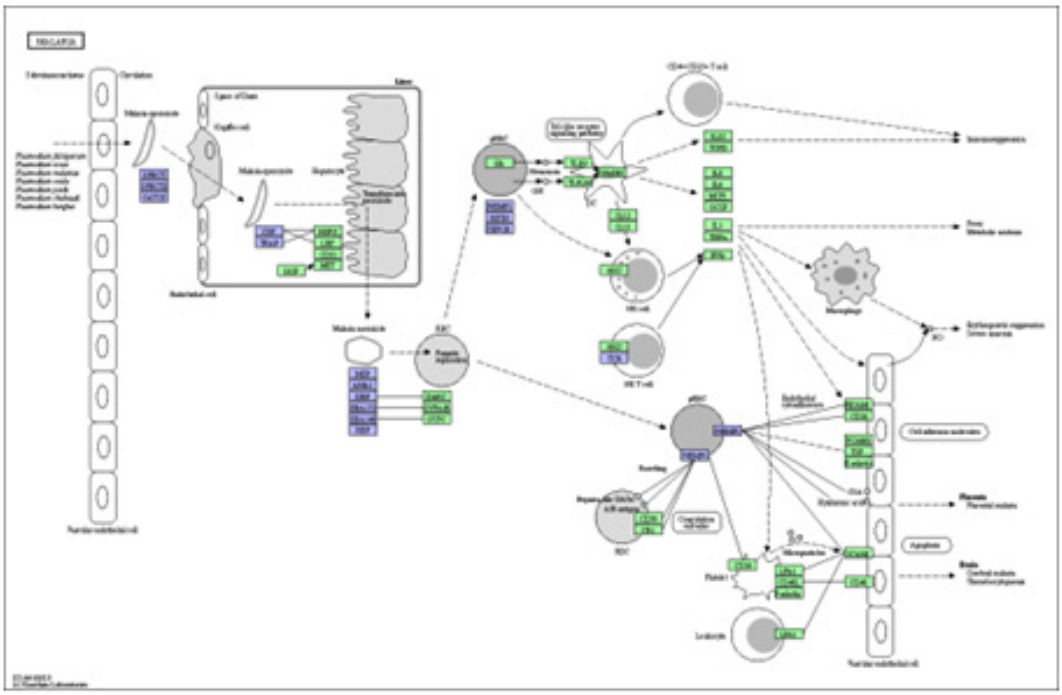


Fig. 1. Source: KEGG Malaria - Reference pathway - hsa pathogen

Table 2. Antimalarial drugs are classified on basis of its target

S. No.	Mode of action	Target Site		Type of drug
1.	Depending on stage of plasmodium it affects	Tissue Schizocidal	Primary Tissue forms	a. Sulfodoxine + Pyrimethinin b. Proguanil c. Atrovaquine d. Primaquine
			Latent Tissue Forms (Hyphozoites)	a. Primaquine b. Tafenoquine
		Blood Schizontocidal	Rapid action	a. Chloroquine b. Artemesinin derivative c. Quinine d. Mefloquine e. Atoquine f. Amodiaquine g. Lumefantrine
			Slow action	a. Proguanil b. Pyrimethamine + Sulfadoxine c. Clirdomycin
		Gametocidal		a. Artemesinin b. Primaquine c. Chloroquine and Quinine
2	Depending on clinical indications	Causal prophylaxis Suppressive prophylaxis		No drugs for sporozoite from, these drugs will inhibit pre-erythrocytic stage a. Chloroquine b. Mefloquine c. Doxycycline
		Clinical cure		a. Chloroquine b. Artemesinin derivative c. Quinine d. Mefloquine e. Atoquine f. Amodiaquine g. Lumefantrine d. Proguanil e. Pyrimethamine + Sulfadoxine h. Clirdomycin
		To prevent relpase		a. Primaquine
		Transmission to mosquitoes		a. Primaquine

SGIYVDMGGYEAIGGKHYRMPIGK NCPMSPIRDAIFGKWVSGACVALES
CPVMGKVINLASGADFLEPISADNP AFEEFVNSAEECASILFENSATDIDVD
RYRGLGFPETVLKHTGALAGALTGTANNA VDAEGYNEINELYSGLKNLQLKQIAFSLF
INLSPVSAEDLRKWGYKGNPV TNCAEYAN APMSKSAATAKLSKGVGKNWANYESNL
NIVPG SDTRTKYRYPFVYDGKDELCYVL GICRILSETPTCLIINAGSLAMTALGSPLESD
YSPMQYNQG SRYCDADGSLEEGPSSLLC AINFPCDIDTVGYVEPRTRNGENGESRFP
MKPYKSDLDAHLYYGSSRIDPKWDV VTTALSIKTLKCTKYVHSKYSESCGT

Table 3. Antimalarial drugsdivided on basis of groups

S.no.	Group	Type of drug	
1.	Quinoline derivative	a. Chloroquine b. Quinine c. Atroquine d. Primaquine e. Mefloquine f. Tefloquine	
2.	Artemesinin	Artemesinin derivative	a. Dihydroartemesinin b. Artemether c. Artesunate d. artether
		Synthetic	a. Arteolane
3.	Aryl alcohol derivative	a. Lumefantrine	
4.	Antifolates	a. Pyrimethamine b. Sulfodoxine c. Doprone d. Proguanil	
5.	Antimicrobials	a. Tetracyclin b. Clindamycin	

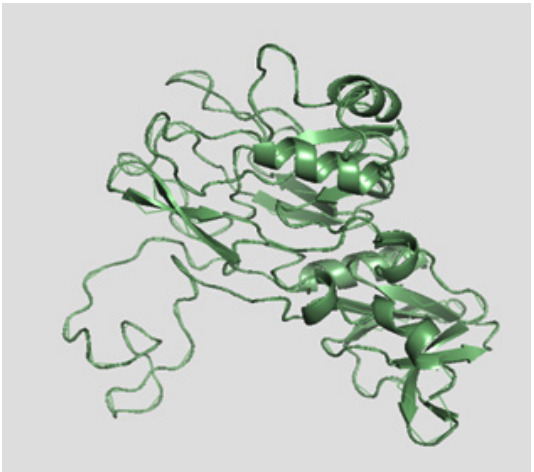


Fig. 2. Model prepared through modeller

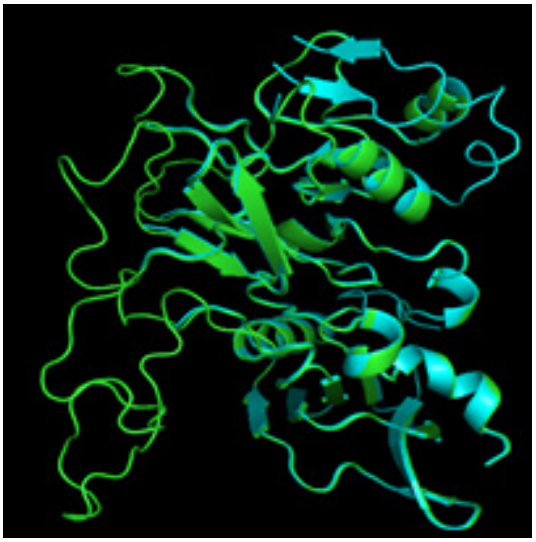


Fig. 3. Superimposing modelled structure with template 6n87

Table 4. XP Gscore and drug targets

S.no.	PDB	DRUG ID (PubChem)		XP GScore
1	Secologanin	ID:	CHEMBL1235867	-7.815
		Name:	SECOLOGANIN	
		Max Phase:	0 Research	
		Molecular Formula:	C17H24O10	
		Molecular Weight:	388.37	
		ChEMBL Synonyms:	Secologanin	
		Molecule Type:	Small molecule	
2	Vindoline	ID:	CHEMBL526546	-4.734
		Name:	VINDOLINE	
		Max Phase:	0 Research	
		Molecular Formula:	C25H32N2O6	
		Molecular Weight:	456.54	
		ChEMBL Synonyms:	Vindoline	
		Molecule Type:	Small molecule	
3	Ajmalicine	ID:	CHEMBL1604074	-6.23
		Name:	Ajmalicine	
		Max Phase:	0 Research	
		Molecular Formula:	C21H24N2O3	
		Molecular Weight:	352.43	
		Molecule Type:	Small molecule	
4	Serpentine	ID:	CHEMBL3559488	-6.286
		Name:	Serpentine	
		Max Phase:	0 Research	
		Molecular Formula:	C21H21N2O3+	
		Molecular Weight:	349.41	
		Molecule Type:	Small molecule	
5	Catharanthine base	ID:	CHEMBL2163793	-3.847
		Name:	CATHARANTHINE BASE	
		Max Phase:	0 Research	
		Molecular Formula:	C21H24N2O2	
		Molecular Weight:	336.44	
		ChEMBL Synonyms:	Catharanthine Base	
		Molecule Type:	Small molecule	
6	Vincristine	ID:	CHEMBL90555	-5.899
		Name:	VINCRISTINE	
		Max Phase:	4 Approved	
		Molecular Formula:	C46H56N4O10	
		Molecular Weight:	824.97	
		ChEMBL Synonyms:	Vincristine VINCRISTINE	
7	Tabersonine	ID:	CHEMBL2011511	-4.99
		Name:	TABERSONINE	
		Max Phase:	0 Research	
		Molecular Formula:	C21H24N2O2	
		Molecular Weight:	336.44	
		ChEMBL Synonyms:	Tabersonine	
		Molecule Type:	Small molecule	
8	Catechol	ID:	CHEMBL280998	-3.622
		Name:	CATECHOL	
		Max Phase:	0 Research	
		Molecular Formula:	C6H6O2	
		Molecular Weight:	110.11	
		ChEMBL Synonyms:	Pyrocatechol	

		Molecule Type:	Small molecule	
9	Artemesinin	ID:	CHEMBL567597	-3.226
		Name:	ARTEMISININ	
		Max Phase:	4 Approved	
		Molecular Formula:	C15H22O5	
		Molecular Weight:	282.34	
		ChEMBL Synonyms:	(+)-Artemisinin ARTEMISININ GNF-PF-5341 NSC-369397	
		Trade Names:	Artemisin	
		Molecule Type:	Small molecule	

YYYCSE EKSSYLSRLYQFLSNHSV KKAMAITAALLALIFAIYWVYRRLYT TKIRR EHEDYDRLMSKYEYDDVS HAVSEPEQQLKTD AYIWGEAAARPSDI TPVHLTKLN

RESULTS

Protein FASTA sequence downloaded from NCBI, BLASTp done with protein datasets. The maximum similarity was found to be 97% which suggests that homology modelling method can be used. Swiss Model software was used for searching best matched templates and best identical template was then used for preparing AMA1 model. 6n87 was found to be best match sequence and used as template for building model. Modeller was also used for building the model. Best model was selected among various models prepared on basis of DOPE score. The best model showed DOPE score -20753.71484 (Fig. 2). The modelled structured was validated by superimposing it with best match templates on basis of Root Mean Square Deviation (RMSD) which was found to be 1.65764 (Fig. 3). The structure was validated with Ramachandran plot, the plot statistics reveal that 82.6% of the residues of modelled structure were in favourable region and additional 15% were in allowed region. Only 0.7% of the residues were in disallowed region. More than 97% of the structure was in allowed regions which shows the modelled protein was good enough to carry out virtual screening. For virtual screening by using Glide's XP (extra precision) docking function. The results were analysed by Maestro's Pose viewer and XP-visualize software. YAARA energy minimization serevr was used to perform energy minimization. *Catharanthus roseus* alkaloid fraction molecules were used as ligands against the modelled protein. Secaloganin showed Hydrogen bonding with chain A and chain B with Lysine 149 and Glutamine 147 (Fig.5 A). The shortest length H- bond is formed with Lysine 149 of Chain A of bond length 1.80881 Å. Serpentine showed two H-bond with Lysine 149 with varied bond lengths (Fig.5 B). Ajmalicine showing H-bond with Porline 218 and Lysine 149 of chain A, while one more H-bond is formed between Lysine 149 of chain B (Fig.5 C). Vincristine is a known anticancerous compound showing H-bond with Lysine 215 and Glutamine 147 of chain A and B (Fig. 5 D) respectively. Tabersonin showing hydrophilic interactions with Leucine 187, Phenylalanine 196, proline 190 of chain B and proline 220, proline 218 and glutamine 148 of chain A (Fig. 5 E). Vindoline showing H-bond with Lysine 149 and Glutamine 147 of chain B (Fig. 5 F). Catharanthine showing H-bond with Leucine 221 (Fig 5 G). Catechol forming H-bond with Lysine 149 of chain a and Glutamine 147 of chain B (Fig. 5 H). Artemisinine which is known drug of malaria shows one H- bond with Lysine 149 of chain A (Fig. 5 I).

DISCUSSION

In this study alkaloid fraction of *Catharanthus roseus* were taken for docking against AMA protein. An extensive survey of literature related to *Catharanthus roseus* was conducted up to Janauary,2022. *Catharanthus*

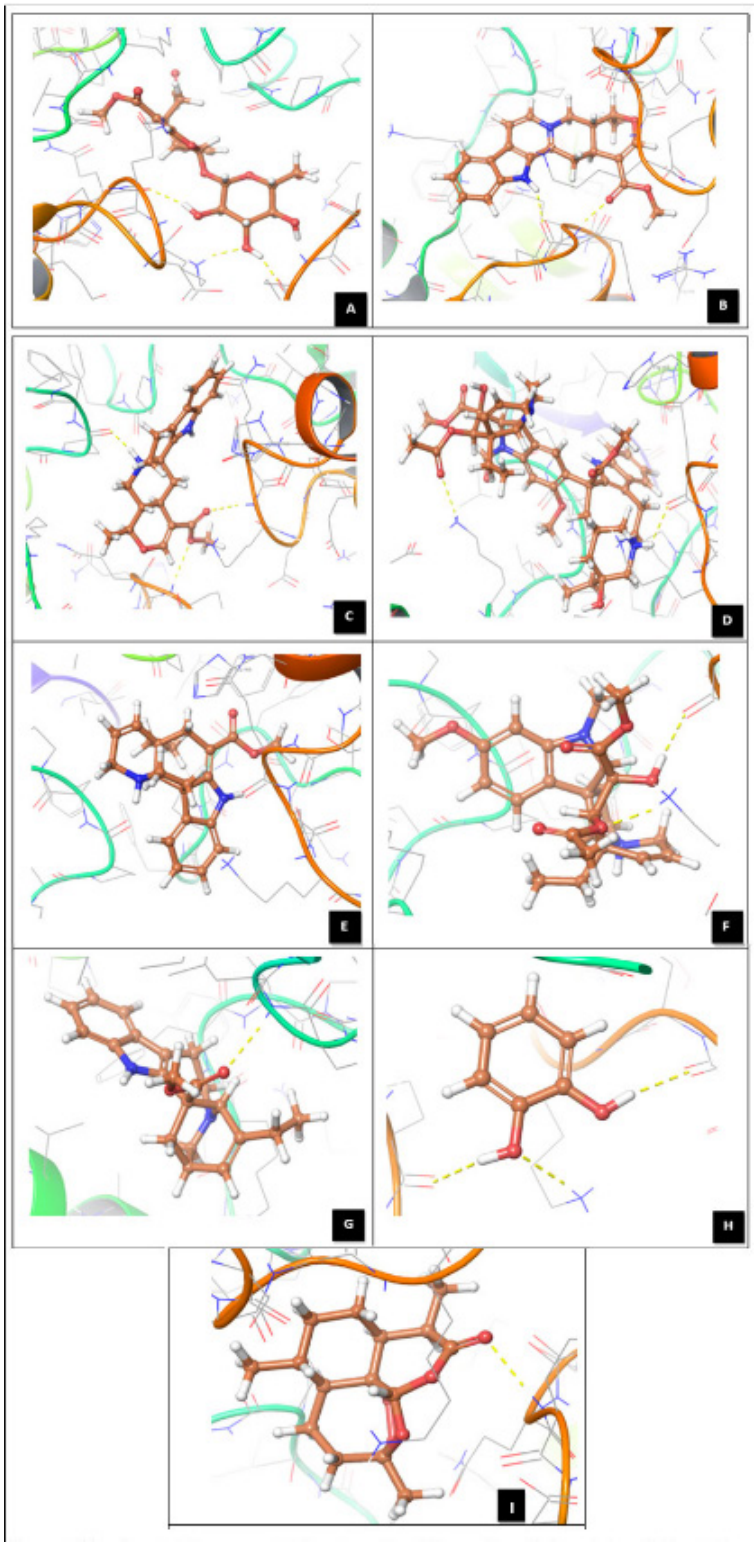
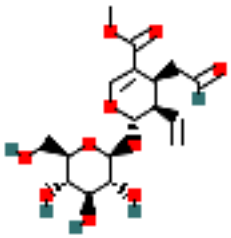
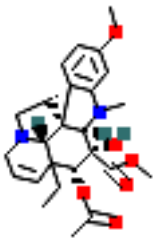
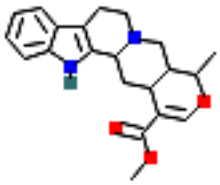
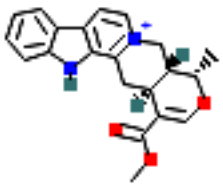
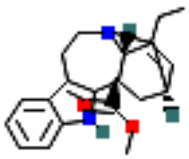
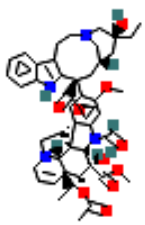
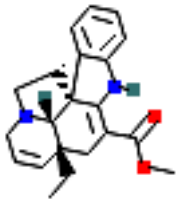
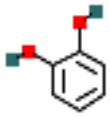
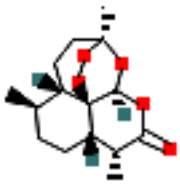


Fig. 4. Showing docking pose of A. Secologanin, B. Serpentine, C. Ajmalicine, D. Vincristine, E. Tabersonine, F. Vindoline, G. Catharanthine, H. Catechol, I. Artemisinine

Table 5. Structures of all compounds taken from PubChem

S.No.	Compound	Structure
1.	Secologanin	
2.	Vindoline	
3.	Ajmalicine	
4.	Serpentine	
5.	Catharanthine	
6.	Vincristine	

7.	Tabersonine	
8.	Catechol	
9.	Artemisinine	

roseus has been of prime importance in the traditional medicine systems and has wide therapeutic applications for many centuries. During phytochemical investigation total of 344 compounds including monoterpene indole alkaloids, bisindole alkaloids, flavonoids, phenolic acids and volatile were found active against many diseases in *Catharanthus* roseus.[35] AMA is a surface protein which is crucial for erythrocyte invasion of parasite, the AMA 1_PLAF8 structure is not revealed yet so protein modelling done through Swiss Model and structure validated by superimposing modelled protein with available templates. *Catharanthus roseus* is revealed for many therapeutic values but anti-malarial molecule is underinvestigation.[36] *Catharanthus roseus* leaf and flower extract is proved to inhibit parasite 66% Megha et al, 2017. However, when pharmacology of *Catharanthus roseus* leaves and flowers was done, majority of alkaloids fractions were revealed. The major molecules present in *Catharanthus roseus* leaf and flower extract are Secologanin, Vindoline, tabersonine, Vincristine,Serpentine, Ajmalicine,Catharanthine [37] and a little fraction of catechol is been observed which is phenolflavanoid. Virtual screening is been done through Maestro and protein was simulated by YASARA energy minimization software. In virtual screening the best XP Gscore is shown by Secaloganine i.e. -7.815 Kcal/ mol while that of artemisinine is -3.226 Kcal/mol which is a known drug. Artemisinine are derived from extracts of weet wormwood and are well established for the treatment of malaria, including highly drug resistant dtrains. Its efficacy also extends to phyllogenetically unrelated parasitic infections such as schistosomiasis. In modelled protein Lysine 149 in chain A is participating in Hydrogen bond formation with secaloganin, Serpentine, Ajmalicine. Vincristine, Catechol and atremisinine. Chain Glutamine 147 is participating in hydrogen bond formation with Secaloganine, Vinscristine, Vindoline and catechol. Chain A proline 218 is participating in Hydrogen bond formation with Ajmalicine . The shortest Hydrogen bond if formed between Ajmalicine and proline 218 (1.8492 ú), Chian A lysine 149 and Sepentine (1.82641 ú) and Secaloganin and ChainA Lysine 149 (1.80881 ú).

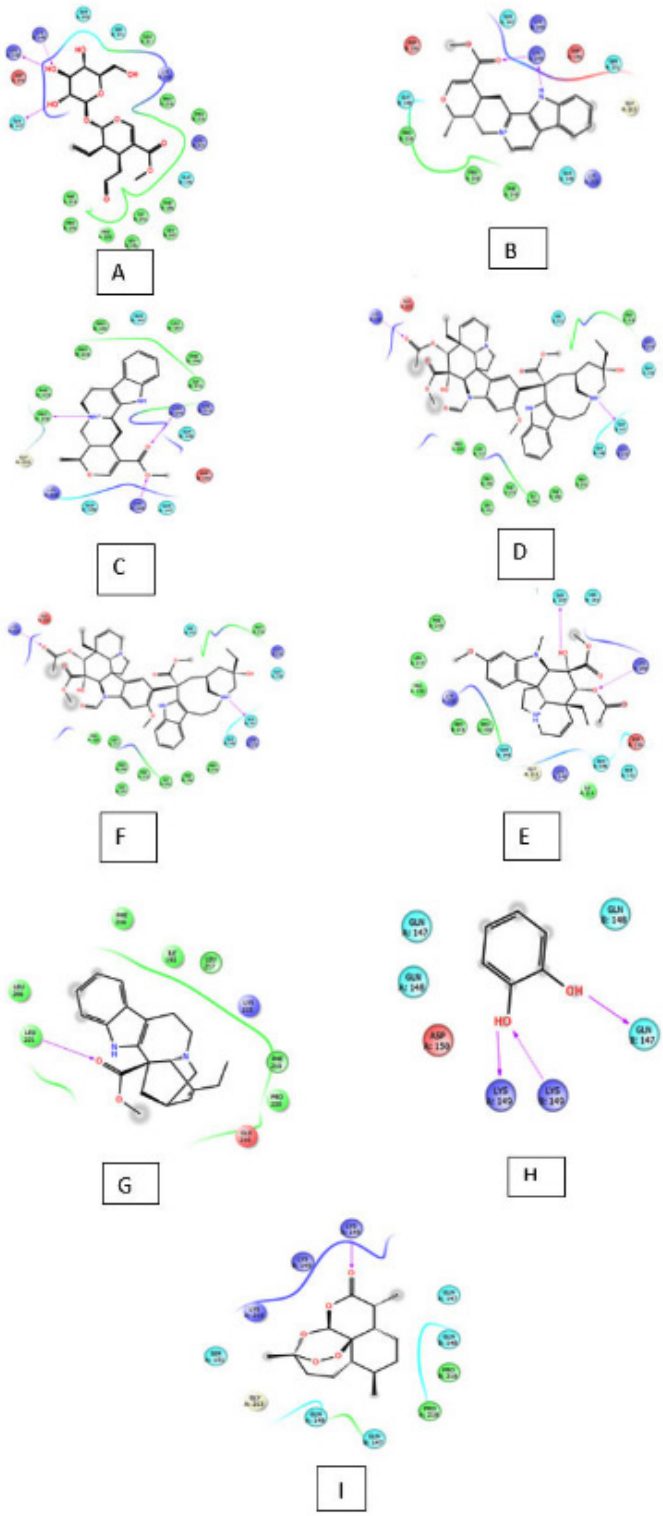


Fig. 5. Showing protein ligand binding of A. Secologanin , B. Serpentine, C. Ajmalicine, D. Vincristine ,E. Tabersonine , F.Vindoline G. Catharanthine, H. Catechol ,I. Artemisinine

Table 6. Details of the ligand protein interactions and participating amino acids

S. No.	Name of Compound	Participating residues	Bond length(ú)	Backbone/ Sidechain	Donar angle	Acceptor angle	Binding energy (Kcal/mol)
1.	Secaloganin	Chain A: LYS 149	1.80881	Backbone	162.125	159.578	-7.815
		Chain B: LYS 149	1.7705	Sidechain	129.785	150.832	
		Chain B :GLN 147	2.00271	Backbone	178.615		
2.	Serpentine	Chain A: LYS 149	1.82641	Backbone	171.464		-6.286
		Chain A: LYS 149	2.02224	Backbone	148.236		
3.	Ajmalicine	Chain A: PRO 218	1.8432	Backbone	131.325	162.126	-6.230
		Chain A: LYS 149	2.38055	Backbone	109.751		
		Chain B:LYS 149	2.12241	Backbone	145.232		
4.	Vincristine	Chain A: LYS 149	2.16061	Sidechain	168.287		-5.899
		Chain B: GLN 147	2.36326	Backbone	141.045	123.219	
5.	Vindoline	Chain B : GLN147	2.03706	Backbone	142.347	173.627	-4.734
		In chain B: LYS 149	1.911687	Sidechain	124.405		
6.	Tabersonine						-4.99
7.	Catharanthine base	LEU 221	2.09897	Backbone	153.093		-3.847
8.	Catechol	Chain A :LYS 149	2.003264	Backbone	158.85	149.116	-3.662
		Chain A :LYS 149	2.02838	Sidechain	119.466		
		Chain B :GLN 147	2.02045	Backbone	151.825	162.144	
9.	Artemisinine	Chain A :LYS 149	2.0194	backbone	108.321		-3.226

Tabersonine is making Hydrophillic interactions with the protein's Proline 190, Lutamine 147 pocket. Tabersonine is a monoterpenoid indole alkaloid with cytotoxic activity. It has a role as an antineoplastic agent and a metabolite.

CONCLUSION

The above data reveal that Secaloganine can be further taken explored as a drug molecule for antimalarial drug formulation, and chemoinformatics techniques can be used to future investigate the most stable form of the molecule in the future.

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This study did not involve human participants, and therefore, informed consent was not required.

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This research does not involve any clinical trials.

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Not Applicable

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