Research Article

In Silico Docking analysis of Mycobacterium tuberculosis potential targets AftB and EmbA with selected phytochemicals

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ABSTRACT

Mycobacterium tuberculosis, the causative agent of tuberculosis (TB) in humans, is a devastating infectious organism that kills approximately two million people annually. The current suite of antibiotics used to treat TB faces two main difficulties: (i) the emergence of multidrug-resistant (MDR) strains of *M. tuberculosis*, and (ii) the persistent state of the bacterium, which is less susceptible to antibiotics and causes very long antibiotic treatment regimes. It is a disease that cannot be cured through conventional remedies. Phytochemicals have played a vital role in the discovery of drugs against infectious diseases. In the current study, homology model of the targets were designed. Thirty three ligand molecules (basically secondary metabolites) which were commonly present in the plants were docked with the selected potential target of *Mycobacterium tuberculosis*, AftB and EmbA. The primary docking analysis was performed through *i*GemDock which is then validated through AutoDockVina docking software. The active sites were also predicted through the Ligand$^+$ tool. Among all the phytochemicals palmarin had a significant inhibitory activity with both the receptors. Binding pocket for both the targets were predicted (**AftB-**THR 474, ASP 522, SER 524, PHE 525, LEU 526, ARG 585 and **EmbA**- PRO 918, ASN 924, ARG 926, VAL 1057) forming hydrogen bonds at a very low energy value, thus forming a stable complex. Palmarin had excellent conformations showing the flexible behaviour of the ligand. The total energy of the receptor and ligand complexes has also been calculated.

Keywords: Tuberculosis, multidrug-resistant strains, *i*GemDock, palmarin.

INTRODUCTION

Tuberculosis (TB) is caused by an etiological agent *Mycobacterium tuberculosis* which is a second leading cause of morbidity and mortality all over the world. It has been estimated that in the year 2015, total of 10.4 million peoples were affected with tuberculosis bacterium which comprises around 3.5 million incidence in women and one million cases in children [1]. In the year 1993, tuberculosis was stated as global public health emergency [2]. According to the fact sheet 2016 of World Health Organisation (WHO), the disease was curable but the emergence of extensive drug resistant (XDR) and multi drug resistant (MDR) strains of Mycobacterium; has become a major concern in the treatment of tuberculosis [3]. The treatment of tuberculosis is becoming more challenging, it requires accurate and early diagnosis, screening of drug resistance and an effective DOTS (directly observed therapy, short-course) treatment regimens for the duration of six months and follow up support. There is an urgent need for the development of new and more effective drugs that may shorten the duration of the treatment. TB requires a four-drug regimen: isoniazid, ethambutol, pyrazinamide and rifampicin for the first two months which is then followed by rifampicin and isoniazid for another four months. These standard anti-TB drugs are available in the market that cure people from tuberculosis, but because of the improper use of antibiotics, many new strains of bacterium have been evolved that are showing resistance towards the extremely effective medications, i.e. isoniazid and rifampicin. Some drugs like gatifloxacin, moxifloxacin, rifapentine etc. are in late clinical trials but from the last three decades no new drug has been released in the market for the treatment of tuberculosis [4]. There is a dire need for a sterilising drug that may shorten the duration of chemotherapy and can combat against MDR and XDR TB.The unique structure and chemical composition of *Mycobacterium tuberculosis* cell wall deserves special attention, it is associated with the pathogenicity and also an attractive drug target for several anti-tubercular agents. Its cell wall is rich in lipid (over 60%) and is responsible for impermeability and in some extent resistant to many antibiotics [5]. EmbA is amycobacterial arabinosyl transferase, which is encoded by emb genes, which plays essential role in the biogenesis of mycobacterial cell wall and is a known target of etambutol. Ethambutol causes interruption in the synthesis of arabinan polymers [AG and LAM (lipoarabinomannan)], resulting ininhibition of arabinosyl transferases [6, 7, 8]. AftB is an arabinofuranosyl transferase which plays a crucial role in addition of the terminal β(1 --$>$2)-linked Araf residues and accounts for the synthesis of the arabinan domain of LAM

(Lipoarabinomannan). Biochemical precursor of lipomannan acts as immune modulator that modifies the host immune response [9]. Previous studies have suggested that AftB can be used as a potential new drug target [10]. In the present study, we have investigated and screened out some selected phytochemicals that may be possible drug candidates against potential therapeutic targets in *Mycobacterium tuberculi* (Table 1).

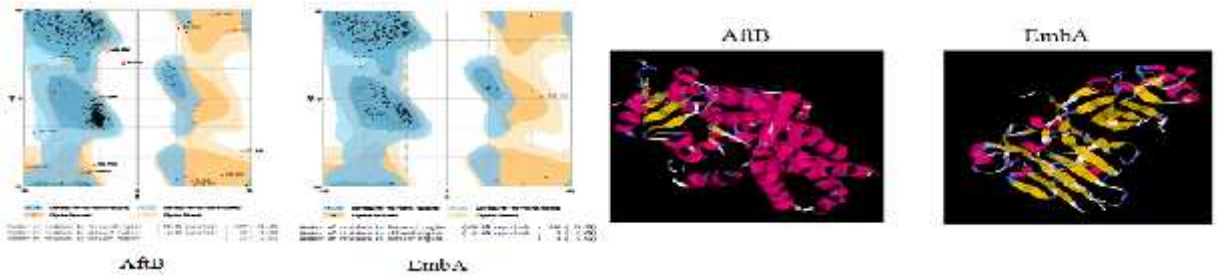

Figure1: Ramachnadran plot and three dimensional structures of the proteins. Black dots representing the amino acids and dark blue region representing the favourable zone

Table 1: Selected targets for the docking analysis

TARGETS	REMARKS	TARGET ID	Target	Drugs Available [11]
EmbA	Known target for ethambutol	PDB Not available	Cell Wall Biosynthesis	Ethambutol, Isoniazid,BTZ-043, BTZ-O43, PBTZ-169, SQ109,Delamanid, PA-824,TBA-354
AftB	Suggested as a potential target			

Material and methods

The potential drug targets and phytochemicals were identified from the literature search. The three dimensional structure of the protein and ligand were required for the docking study.

Homology modeling of the target protein: No records of tertiary structure of the protein were found in any of the structural database of protein. The target proteins were then modelled through homology modelling server Phyre (http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index) and RaptorX (http://raptorx.uchicago.edu/) by using primary sequence with accession no. ANZ84579.1 (AftB) and AOE38270.1 (EmbA). The generated homology models were then validated through Ramachandran Plot by using Rampage.

Ligand Preparation

The photochemical and drug compounds were retrieved from the Zinc and Pubchem database [12, 13]. Mol2 file was downloaded from these databases and the compounds were then converted to .pdb format through open babel software [14]; as docking software takes .pdb format as an input. These compounds were then scanned through Lipinski's filter (http://www.scfbio-iitd.res.in/software/drugdesign/lipinski.jsp#anchortag) and the molecules that qualify the Rule of Five were used for the study [15].The ligand used in the present study has all the properties of drug likeness (Table 2).

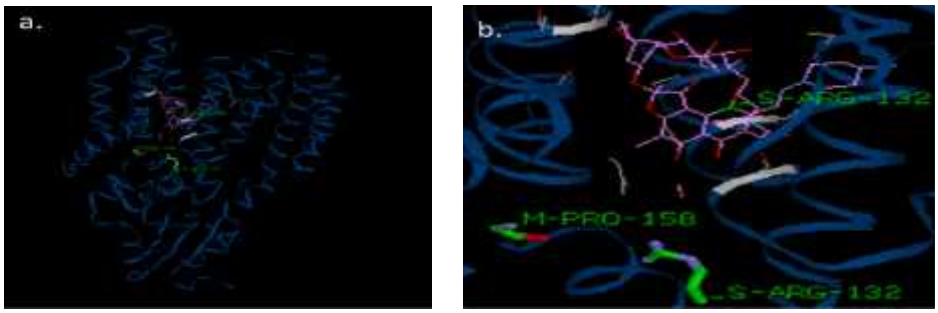

Figure 2 Visuals of docking interaction steps of palmarin ligand molecule with AftB protein.

Table 2: Lipinski's filter analysis of phytochemical ligands

S.No.	CHEMICAL CONSTITUENTS	ID	MOLECULAR WEIGHT	H-BOND DONOR	H-BOND ACCEPTOR	logP
1.	(+)-CATECHIN	ZINC_119983	290	5	6	1.54609
2.	2S-NARINGENIN	ZINC_156701	272	3	5	2.50989
3.	4-HYDROXYBENZALDEHYDE	ZINC_156701	122	1	2	1.20470
4.	ACACETIN	ZINC_3871358	284	2	5	2.72259
5.	ALLICIN	ZINC_1530846	163	1	1	2.09790
6.	ALLIIN	ZINC_1531038	178	4	3	-2.37590
7.	ALLYL PROPYL DISULFIDE	ZINC_2038819	148	0	0	2.96379
8.	APIGENIN	ZINC_3871576	270	3	5	2.41959
9.	BENZOQUINONE	ZINC_895247	108	0	2	0.25060
10.	CAJANIN	ZINC5998758	300	3	6	2.42819
11.	CAPROIC ACID	ZINC_1529230	115	0	2	0.31660
12.	CASTICIN	CID 5315263	374	2	8	2.71389
13.	GENISTEIN	ZINC18825330	270	3	5	2.11408
14.	KAEMPFEROL	ZINC_3869768	286	4	6	2.30530
15.	LAURIC ACID	ZINC_1529498	199	0	2	2.65719
16.	LUTEOLIN	ZINC_18185774	286	4	6	2.12520
17.	NIACIN (NICOTINIC ACID)	ZINC_1795	122	0	3	-0.55490
18.	N-TRANS-FERULOYLTYRAMINE	ZINC_901461	313	3	5	2.47850
19.	PALMARIN	CID442068	389	0	7	1.25100
20.	PROTOCATECHUIC ACID	ZINC_13246	153	2	4	-0.53870
21.	PRUNETIN	ZINC18847044	284	2	5	2.72259
22.	PSORALEN	ZINC_120283	186	0	3	2.36500
23.	QUERCETIN	ZINC_3869685	302	5	7	2.01090
24.	QUINAZOLINE	ZINC_4291262	216	0	2	2.68262
25.	SALICYLIC ACID	ZINC_1554	137	1	3	-0.24430
26.	SCOPOLETIN	ZINC_57733	192	1	4	1.33300
27.	STEARIC ACID	ZINC_4978673	283	0	2	4.99779
28.	SYRINGIC ACID	ZINC_156386	197	1	5	-0.22710
29.	UMBELLIFERONE	ZINC_58111	162	1	3	1.32440
30.	VANILLIC ACID	ZINC_338275	167	1	4	-0.23570
31.	VANILLIN	ZINC_2567933	152	0	3	1.13014
32.	VANILLIN	ZINC_2567933	152	1	3	1.21330
33.	XANTHYLETIN	ZINC_338304	228	0	3	2.80299

Virtual Screening and Docking of Ligands

Strength of association or binding affinity between two molecules can be predicted by molecular docking techniques. In the current study, we have analysed 33 phytochemical compounds that have been suggested to possess potential antimicrobial activity. These phytochemicals were docked with the AftB and EmbA proteins. AftB and EmbA play an important role in cell wall synthesis so we have used it as a target. These proteins were also docked with the drug compounds against tuberculosis that are available in the market. The interaction analysis of these drug compounds was used as a control for the study to compare the result of interaction of protein and phytochemicals. Primary docking analysis was performed using iGEMDOCK, which uses empirical

scoring function and Generic Evolutionary Method for molecular docking. It has a graphical user interface that recognizes the pharmacological interactions and performs virtual screening. The docking simulation results were then validated through Autodock Vina and the interaction was visualised through Ligplot+ software.

Results and Discussion

Molecular docking and de novo drug designing have become essential tools in the drug designing process. Application of *in-silico* docking has received considerable attention because it has decreased the expense and time, by increasing the speed and efficiency in the drug discovery process [16]. Tuberculosis is a pandemic disease which is caused by *Mycobacterium tuberculosis*. Multidrug-resistant (MDR) and extensive drug resistance (XDR) strains have become a major concern in the treatment of tuberculosis. The pathogen of tuberculosis has been showing resistance towards some of the conventional drugs. In the present study, we have selected phytochemicals that have been already validated to have antimicrobial activity and the conventional drugs of tuberculosis as a control to analyze the binding affinity ligand to the protein.

For the docking analysis, the software needs a protein databank file format that is .pdb format of the protein and the ligand both. The tertiary structure was not available in any of the database so we generated the 3D structure through homology modelling by using Phyre2 webserver and the quality assessment of the structures were performed by using RaptorX server. The structures were then validated by RamPage Ramachandran Plot Assessment server. The tertiary structures generated through Phyre2 seem to have better stability than the Raptor X generated structures. AftB-ANZ84579.1 (Phyre2 template c5f15A) and EmbA-AOE38270.1 (Phyre2 template c3ptyA) were having 92.0% and 95.5% of the residues in the most favored region respectively; this shows that the modelled proteins are highly stable and can be used for further study (Table 3, Figure 1). Ligand molecules were downloaded from PubChem and Zinc database.

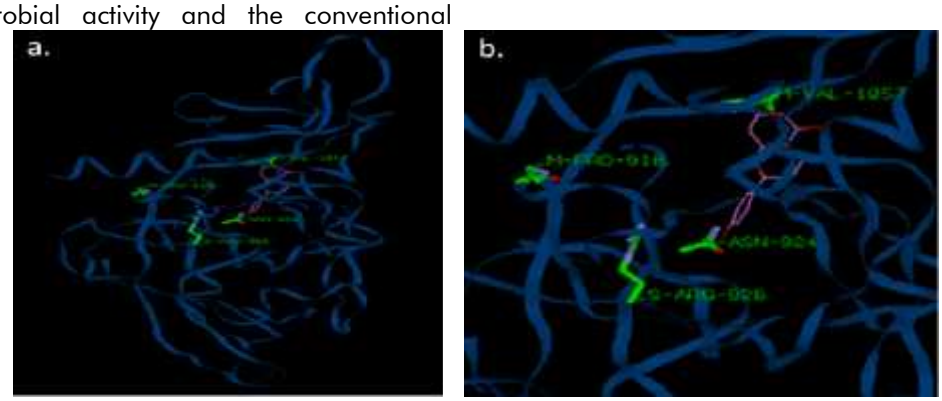

Figure 3. Visuals of docking interaction steps of palmarin ligand molecule with EmbA protein.

Table 3: Validation parameter and comparative analysis of the protein from Phyre2 and RaptorX through Ramachandran

Server		Ramachandran Plot	AftB ANZ84579.1	EmbA AOE38270.1
Phyre2	Template		c5f15A	c3ptyA
		Residues in the most Favored Region	92.0%	95.9%
		Residues in additionally allowed region	4.9%	2.6%
		Residues in generously allowed region	3.1%	1.5%
RaptorX	Template		5ezmA	3bywA
		Residues in the most Favored Region	91.6%	92.5%
		Residues in additionally allowed region	5.9%	4.2%
		Residues in generously allowed region	2.6%	3.3%

Primary protein ligand docking was performed through iGemDock, total thirty three ligands were docked against the two proteins AftB and EmbA. Eight anti-tuberculosis drugs- rifampicin, isoniazid, bedaquiline, delamanid, ethionamide, ethambutol, gatifloxacin, thiacetazone were used as a control for

the following study. The minimum binding energy of palmarin with AftB protein is -136.009 kcal/mol (Figure 2) and EmbA protein is -110.899 kcal/mol (Figure 3) which indicated that both were docked successfully with Palmarin [Table 4 and 5]. Palmarin was showing better interaction than the anti-tubercular drugs available in the market. It also showed better binding energy than the bedaquiline and delamanid, both these drugs are under clinical trial and have already been approved provisionally for the treatment of Drug Resistant TB [17]. The possible binding modes of selected phyochemicals at the target protein active sites have been shown in table 6. AftB protein residues THR 474, ASP 522, SER 524, PHE 525, LEU 526, ARG 585 and EmbA PRO 918, ASN 924, ARG 926, VAL 1057 protein residues was formed H-bond with palmarin ligand molecule.

Table 4: Energy values obtained through iGemDock during docking analysis of phytochemicals as ligand molecule and AftB as target protein and anti-tuberculosis drugs as a control

Compound	Energy	VDW	HBond
AftB- RIFAMPICIN-1.pdb	-97.5652	-88.1359	-9.42934
AftB-BEDAQUILINE-0.pdb	-97.2115	-93.8315	-3.37998
AftB-DELAMANID-0.pdb	-112.253	-98.7346	-13.5183
AftB-ETHAMBUTOL-0.pdb	-69.623	-59.123	-10.5
AftB-ETHIONAMIDE-0.pdb	-68.4753	-63.5532	-4.92209
AftB-GATIFLOXACIN-0.pdb	-86.3105	-75.3511	-10.0615
AftB-ISONIAZID-0.pdb	-79.1299	-41.4276	-37.7023
AftB-THIACETAZONE-1.pdb	-81.3858	-61.2378	-20.148
AftB-2S-NARINGENIN-0.pdb	-79.7473	-79.7473	0
AftB-4-HYDROXYBENZALDEHYD-0.pdb	-88.2165	-68.7911	-19.4254
AftB-ACACETIN-0.pdb	-84.2483	-84.2483	0
AftB-ALLICIN-1.pdb	-48.6798	-48.6798	0
AftB-ALLIIN-0.pdb	-57.8424	-57.8424	0
AftB-ALLYL PROPYL DISULFIDE-1.pdb	-46.2158	-46.2158	0
AftB-APIGENIN-0.pdb	-79.5353	-79.5353	0
AftB-BENZOQUINONE-1.pdb	-49.1763	-49.1763	0
AftB-CAJANIN-1.pdb	-85.6504	-66.2466	-19.4038
AftB-CAPROIC ACID-1.pdb	-56.3401	-37.9823	-18.3578
AftB-CASTICIN-1.pdb	-92.565	-75.5196	-17.0454
AftB-CATECHIN-1.pdb	-93.6594	-66.4119	-27.2475
AftB-FERULIC Acid-0.pdb	-102.06	-86.5486	-12.1807
AftB-FERULOYLTYRAMINE-0.pdb	-88.6349	-85.8084	-2.82646
AftB-GENISTEIN-0.pdb	-98.6536	-80.8576	-17.796
AftB-KAEMPFEROL-1.pdb	-93.0901	-62.9584	-30.1317
AftB-LAURIC ACID-0.pdb	-66.3896	-53.6876	-12.702
AftB-LUTEOLIN-0.pdb	-90.6852	-77.3705	-13.3147
AftB-NICOTINIC ACID-0.pdb	-67.7459	-40.0834	-27.6625
AftB-PALMARIN-1.pdb	-136.009	-108.782	-27.2266
AftB-PROTOCATECHUIC ACID-0.pdb	-70.0168	-55.117	-12.5257
AftB-PRUNETIN-1.pdb	-82.6418	-69.1832	-13.4586
AftB-PSORALEN-1.pdb	-82.1856	-72.2544	-9.93123
AftB-QUERCETIN-0.pdb	-97.9868	-79.3004	-18.6864
AftB-QUINAZOLINE-1.pdb	-72.3087	-60.6434	-11.6653
AftB-SALICYLIC ACID-1.pdb	-68.3034	-39.1915	-29.1119
AftB-SCOPOLETIN-0.pdb	-78.5441	-55.9798	-22.5643
AftB-STEARIC ACID-1.pdb	-83.5451	-70.8885	-12.3314
AftB-SYRINGIC ACID-1.pdb	-70.0199	-44.4374	-25.5825
AftB-UMBELLIFERONE-1.pdb	-80.5775	-55.8552	-24.7223
AftB-VANILLIC ACID-0.pdb	-71.0508	-59.215	-8.38663
AftB-VANILLIN-0.pdb	-70.7336	-48.3258	-22.4078

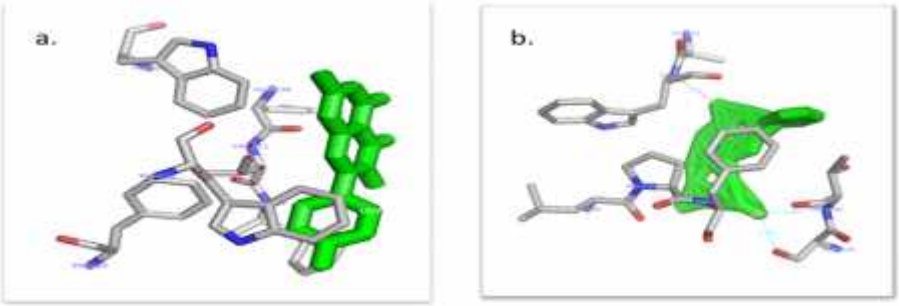

Figure 4. Visuals of docking interaction steps of palmarin ligand molecule with (a.) AftB and (b.) EmbA.

Table 5: Energy values obtained through iGemDock during docking analysis of phytochemicals as ligand molecule and EmbA as target protein and anti-tuberculosis drugs as a control

Compound	Energy	VDW	HBond
EmbA-RIFAMPICIN-0.pdb	-98.1699	-80.7946	-17.3753
EmbA-BEDAQUILINE-0.pdb	-90.6367	-87.1168	-3.51986
EmbA-DELAMANID-0.pdb	-105.125	-101.283	-4.10288
EmbA-ETHIONAMIDE-1.pdb	-65.3871	-47.8871	-17.5
EmbA-ETHAMBUTOL-1.pdb	-70.4931	-58.8448	-11.6483
EmbA-GATIFLOXACIN-0.pdb	-85.6877	-80.5495	-5.13816
EmbA-ISONIAZID-0.pdb	-72.943	-48.8778	-24.0652
EmbA-THIACETAZONE-1.pdb	-80.7604	-61.3258	-19.4346
EmbA-2S-NARINGENIN-1.pdb	-77.7834	-77.7834	0
EmbA-4-HYDROXYBENZALDEHYD-0.pdb	-92.2324	-82.216	-10.0164
EmbA-ACACETIN-0.pdb	-80.4204	-80.4204	0
EmbA-ALLICIN-0.pdb	-45.6825	-45.6825	0
EmbA-ALLIIN-0.pdb	-52.438	-52.438	0
EmbA-ALLYL PROPYL DISULFIDE-0.pdb	-46.0031	-46.0031	0
EmbA-APIGENIN-0.pdb	-77.3713	-77.3713	0
EmbA-BENZOQUINONE-0.pdb	-47.5377	-47.5377	0
EmbA-CAJANIN-1.pdb	-85.6516	-57.3452	-28.3064
EmbA-CAPROIC ACID-0.pdb	-52.5862	-36.1561	-14
EmbA-CASTICIN-1.pdb	-83.9902	-65.0207	-18.9695
EmbA-CATECHIN-1.pdb	-103.457	-87.3606	-16.096
EmbA-FERULIC ACID-0.pdb	-81.3048	-76.4845	-4.82032
EmbA-FERULOYLTYRAMINE-1.pdb	-97.5699	-77.5503	-20.0196
EmbA-GENISTEIN-0.pdb	-90.8176	-63.9319	-26.8857
EmbA-KAEMPFEROL-1.pdb	-94.0116	-63.6201	-30.3915
EmbA-LAURIC ACID-0.pdb	-62.9623	-44.9006	-13.7452
EmbA-LUTEOLIN-0.pdb	-84.1977	-67.236	-16.9617
EmbA-NICOTINIC ACID-1.pdb	-60.4057	-46.5951	-13.8106
EmbA-PALMARIN-1.pdb	-110.899	-93.2554	-17.6434
EmbA-PROTOCATECHUIC ACID-0.pdb	-80.0941	-43.9031	-34.4904
EmbA-PRUNETIN-0.pdb	-81.5443	-71.2005	-10.3438
EmbA-PSORALEN-1.pdb	-72.8609	-58.5704	-14.2905
EmbA-QUERCETIN-1.pdb	-99.4995	-66.4917	-33.0078
EmbA-QUINAZOLINE-0.pdb	-75.0691	-64.5691	-10.5
EmbA-SALICYLIC ACID-1.pdb	-70.8002	-45.3818	-23.4108
EmbA-SCOPOLETIN-0.pdb	-76.9022	-58.0087	-18.8935
EmbA-STEARIC ACID-1.pdb	-70.5732	-59.8511	-9.5
EmbA-SYRINGIC ACID-1.pdb	-75.0082	-59.4227	-16.3797
EmbA-UMBELLIFERONE-0.pdb	-66.9088	-51.6977	-15.2111
EmbA-VANILLIC ACID-0.pdb	-80.9871	-55.7457	-23.5536
EmbA-VANILLIN-1.pdb	-72.0226	-55.6367	-16.3859
EmbA-XANTHYLETIN-0.pdb	-75.1337	-66.1825	-8.95124

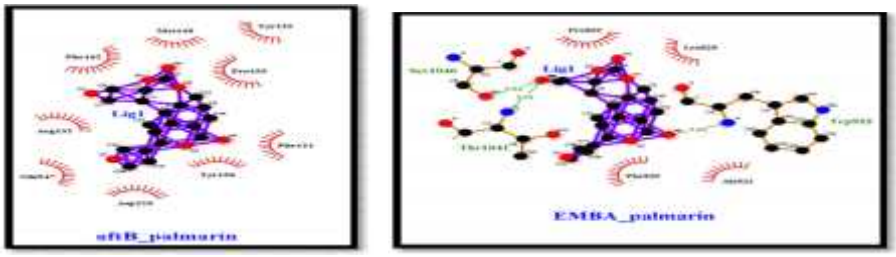

Figure 5. Interaction sites of amino acids with AftB and EmbA with selected phytochemicals generated through Lig+.

Table 6: Interaction analysis of amino acids with AftB and EmbA with selected phytochemicals. H-S signifies hydrogen bond with sidechain; H-M signifies hydrogen bond with the main chain

Anti-tubercular Compounds	Interaction with AftB	Interaction with EmbA
Bedaquiline	H-M MET 357	H-M GLU 845
Catechin	H-M LEU 473 -2.5	H-M GLY 844 -2.6
	H-S THR 474 -2.5	H-S ASN 847 -2.5
	H-S ASP 522 -4.7	H-M SER 949 -3.8
	H-M SER 524 -2.8	H-M PRO 950 -2.5
	H-M LEU 526 -2.6	H-M 952 GLN -5
	H-S ARG 585 -2.5	
Delamanid	H-S SER 223 -4.7	H-S LYS 816 -3.1
	H-S SER 224 -5	
Ethionamide	H-M PRO -3.5	H-M SER 842 -3.5
		H-M GLY 844 -3.5
		H-M GLU 845 -3.5
		H-M SDN 846 -3.5
		H-S ASN 847 -3.5
Gatifloxacin	H-S ARG 201 -4.1	
	H-M ALA 249 -3.5	
Isoniazid	H-M ASP 472 -6.9	H-M GLY 844 -2.8
	H-M LEU 473 -3.5	H-S ASN 847 -2.7
	H-S THR 474 -6	H-M LEU 848 -7
	H-S ASP 522 -7	
	H-M TYR 523 -3.3	
	H-M LEU 526 -3.5	
	H-S TYR 592 -7.6	
Palmarin	H-S THR 474 -2.4	H-M PRO 918 -3.5
	H-S ASP 522 -5	H-S ASN 924 -3.5
	H-M SER 524 -2.7	H-0S ARG 926 -3.5
	H-M PHE 525 -5.7	H-M VAL 1057 -3.5
	H-M LEU 526 -7	
	H-S ARG 585 -3.7	
Rifampicin	H-S SER 223 -2.4	H-S ARG 1038 -13.9
	H-S SER 224 -4.5	
Quercetin	H-S ARG 415 -1.7	H-M LEU 781 -2.8
	H-M ASP 472 2.5	H-M GLY 814 -5.6
	H-M SER 524 -3.5	H-M PHE 830 -3.5
	H-M PHE 525 -3.4	H-M THR 1041 -6
	H-M LEU 526 -3.3	
	H-S ARG 585 -4.3	
Kampferol	H-S ARG 415 -8.7	H-M GLY 814 -7
	H-M ASP 472 -2.5	H-M PHE 830 -3.5
	H-S ASP 522 -10	H-S SER 1040 -2.5
	H-M SER 524 -3.5	H-M THR 1041 -6
	H-S ARG 585 -5.5	

To validate the docking analysis done by iGemDock, we performed the docking study of the proteins with the selected phytochemicals using AutoDock Vina. AutoDock Vina also calculated the binding free

energies of these interactive molecules to find the best binding mode. The calculated free-energy of binding for palmarin is -12.2 kcal/mol (Figure 2). Docking results shows that palmarin can enter the substrate-binding region of the active site (Table 7). The interaction analysis of the AftB and EmbA with the ligand Palmarin was obtained through the Ligplot+ software, the representation of the possible docking site is displayed in figure 4. Finally, the results demonstrated clearly that Palmarin accurately interacts with AftA and EmbA protein targets.

Table 7: Tabulated free energy (vdW, Hydrogen bonding energy, and electrostatic energy) of docked poses of Delamanid, Palmarin, Kaempeferol, Casticin, Catechin obtained from Autodock Vina.

Subunits	AftB	EmbA
Delamanid	-9.9	-6.7
Palmarin	**-12.2**	-8.9
Kaempeferol	-8.1	-5.7
Casticin	-8.0	-6.4
Catechin	-8.1	-8.5

Conclusion

Multi drug resistant tuberculosis (MDR-TB) and extensively drug-resistant tuberculosis (XDR-TB) are a major concern that threatens tuberculosis control. Several researches are going on the development of anti-tuberculosis drugs, but since three decades there have been no new drug launched in the market. Drug discovery in itself is a time consuming and expensive process, but by using the computational methods we can increase its speed and efficiency [16]. The rapid increase in pharmaceutically relevant macromolecular structures that are accessible, de novo drug designing and protein-ligand docking have become important tools to support the drug designing process. In the current study, we have selected two proteins Aftb and EmbA, their docking analysis were performed. Phytochemical palmarin exhibited better docking energy as compared with other phytochemicals and known anti-TB drugs. Thus, this study can prove to be beneficial in the development of new and efficient anti-TB drugs.

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