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A computational approach for the identification of anti-HIV phytocompound(s) with respect to T-cell receptor through molecular docking

Daisy. P*[1], Rajalakshmi. M[1], Lilly.V[2], Anusta. S[1]

[1]*PG & Research Department of Biotechnology & Bioinformatics, Holy Cross College, Tiruchirappalli*
[2]*PG & Research Department of Zoology, Holy Cross College, Tiruchirappalli*

ABSTRACT

The most common secondary immunodeficiency is Acquired Immunodeficiency Syndrome or AIDS, which results from infection with the Human Immunodeficiency Virus 1 (HIV1). HIV preferentially infects T-cells, attacking the very system that protects us from viruses. Each T-cell has its own type of T-cell receptor, which recognizes its own type of peptide. There is no cure for immunodeficiency disorders. Therapy is aimed at controlling infections and, for some disorders, replacing defective or absent components These drugs attempt to inhibit the process that the virus goes through to kill T- lymphocytes. The medicinal plants and compounds isolated from them is concerned, it is relevant to note that by simply looking to the recent literature, several reports have been published in which plant extracts have been claimed to exhibit anti-HIV-1 activity. 11 phytocompounds were chosen to evaluate anti-HIV activity. These 11 phytocompounds were analyzed with Lipinski's properties and ADMET properties using Accord Excel 6.1. Molecular docking was performed between phytocompounds and T-cell receptor using Discovery Studio 2.1. The Ig-like domain of T-cell receptor was analyzed using PROSITE database. The phytocompounds saponin, catechin, costunolide, eremanthin, dihydroxy gymnemic triacetate, gymnemic triacetate, polysaccharide and terpenoid have hydrogen bond interaction with T-cell receptor except gymnemic diacetate. Of these nine phytocompounds, catechin and eremanthin have produced a minimal energy value with a maximal libdock score and also the hydrogen bond interaction. But the phytocompound catechin alone interacted with Ig-like domain of the T-cell receptor and it might be involved in the prevention of further T-cell infection by HIV. Therefore, catechin could be considered as an excellent clinically relevant oral drug in preventing AIDS.

Keywords: AIDS, Molecular docking, Lipinski's and DMET properties, T-cell receptor, catechin.

INTRODUCTION

Secondary immunodeficiencies are far more common than primary immunodeficiencies, which are, by definition, caused by genetic defects affecting cells of the immune system [1]. Acquired

Immunodeficiency Syndrome (AIDS), resulting from infection by Human Immunodeficiency Virus (HIV), is the best known secondary immunodeficiency largely because of its prevalence and its high mortality rate if not treated.

The majority of HIV infections are caused by HIV-1 because HIV-2 is a less common strain even though it is up to eight times less transmissible and pathogenic than HIV-1[2, 3]. The main HIV targets are CD4 T-lymphocytes, but other cell expressing CD4 in the surface such as monocytes, macrophages, dendritic cells or CD8+ T-lymphocytes are susceptible to infection [4, 5].

T-cell receptors on the surface of T-cells bind tightly to viral peptides displayed in MHC. Each T-cell has its own type of T-cell receptor, which recognizes its own type of peptide. The CD4 antigen is an integral membrane glycoprotein of human helper/inducer T lymphocytes that serves as the receptor for the human immunodeficiency virus (HIV) [6]. HIV preferentially infects T-cells, attacking the very system that protects us from viruses. Without treatment, the virus steadily attacks T-cells, depleting the immune system. When the number of T-cells gets too low, the infected individual progresses into AIDS[7].

The life cycle of the human immunodeficiency type-1 virus (HIV-1) is one of the major targets for the development of pharmaceutical compounds of great interest in biomedicine, considering the fact that HIV-1 infection causes AIDS. Accordingly, significant efforts have been made in the recent past to identify molecules inhibiting the different biological steps of the HIV-1 life cycle [8, 9, 10]. The important steps in HIV-1 infection are virus–cell attachment, gp120-CD4 binding, gp120-coreceptor binding, viral fusion, viral assembly and disassembly, reverse transcription, nuclear import of the pre-integration complex, proviral integration, viral transcription, processing of viral transcripts and nuclear export, assembly of new virions. In addition to HIV-1 proteins, several cellular factors are involved in HIV replication [11,12].

The current therapeutic approach is based on the combined use of different molecules, such as AZT (zidovudine), enfuvirtide (the first fusion inhibitor), tenofovir (a reverse transcriptase inhibitor), atazanavir (a protease inhibitor), tipranavir (another protease inhibitor) [13]. The appearance of azidothymidine (AZT) in 1985 was the first drug that inhibited HIV replication and controlled the infection. Almost ten years later, the introduction of the Highly Active Antiretroviral Therapy (HAART) – a combination of three or more drugs that act against HIV – reduced the mortality and morbidity of the disease, leading AIDS to come to be considered a chronic illness in developed countries.

The activity of anti-HIV plants extracts is comparable or even better than commonly used anti-HIV drugs, including AZT and Enfuvirtide. An example of such studies is that reported on the comparative *in-vitro* effects of AZT and extracts of *Ocimum gratissimum, Ficus polita, Clausena anisata, Alchornea cordifolia, Elaeophorbia drupifera* against HIV-1 and HIV-2 infections. Interestingly, they found that some plant extracts were more active than AZT in inhibiting HIV-1 life cycle [14].

Despite the fact that the molecular target(s) of the biological action of several anti-HIV substances, including alkaloids (O-demethyl-buchenavianine,papaverine), polysaccharides

(acemannan), lignans (intheriotherins, schisantherin), phenolics (gossypol, lignins, catechol dimers such as peltatols, naphthoquinones such as conocurvone) and saponins (celasdin B, Gleditsia and Gymnocladus saponins), has not been fully elucidated, the molecular targets of several isolated compounds from medicinal plants have been identified [15].With the help of the Computer-aided drug design (CADD), the molecular targets of phytocompounds can be predicted and the anti-HIV activity of phytocomounds could be evaluated.

The medicinal plants and compounds isolated from them is concerned, it is relevant to note that by simply looking to the recent literature, several reports have been published in which plant extracts and compounds have been claimed to exhibit anti-HIV-1 activity by inhibiting several HIV-1 life cycle steps. For instance, triterpenes inhibit virus absorption, but also virus–cell fusion and reverse transcription. But there is report stating the anti-HIV activity of the phytocompounds against the T-Cell receptor by gp120-CD4 binding.

The present study is aimed to evaluate the anti-HIV activity of phytocompounds against the T-Cell receptor by gp120-CD4 binding through *in-silico* approach. The compounds isolated using bioassay guided fractionation are chosen for the study. They are novel saponin (*Eugenia jambolana*) possessing antibacterial activity [16]; catechin (*Cassia fistula*) possessing antidiabetic activity [17]; costunolide (*Costus speciosus)* possessing antidiabetic activity [18] and antioxidant activity [19]; eremanthin (*Costus speciosus)* possessing antioxidant activity [19]; novel dihydroxy gymnemic triacetate possessing antidiabetic activity [20], novel gymnemic diacetate & novel gymnemic triacetate (*Gymnema sylvestre)* ; gallic acid (*Terminalia bellerica)* possessing antidiabetic activity [21]; polysaccharide (*Tinospora cordifolia)*; novel terpenoid possessing antidiabetic activity [22] and lupeol (*Elephantopus scaber).*

MATERIALS AND METHODS

2.1.ChemSketch

ACD/Chemsketch is a chemical drawing software package from Advanced Chemistry Development Inc. designed to be used alone or integrated with other applications. ACD/Chemsketch is the powerful all-purpose chemical drawing and graphics package from ACD/Labs developed to help chemists quickly and easily draw molecular structures, reactions and schematic diagrams, calculate chemical properties, design professional reports and presentations.

2.2.Accord Excel

Accord for excel use the Accord Chemistry Engine to handle chemical structures and incorporates a number of add-ins to perform chemical calculations. The Accord Chemistry toolbar provides an alternative method of accessing Accord commands and also provides access to additional display operations and functions short-cuts. The ADMET (Absorbtion, Distribution, Excretion, Metabolism, Toxicology) properties were calculated for the phytocompounds using Accord excel.

2.3.Protein Data Bank (PDB)
Source: www.rcsb.org
The PDB is the single, global archive for information about the 3D structure of biomacromolecules and their complexes, as determined by X-ray crystallography, NMR spectroscopy and cryo-electron microscopy, and includes more than a few Nobel Prize winning structure. T-cell receptor was downloaded from Protein data bank with the specific resolution and the PDB id is 2X70.

2.4.Docking – Discovery Studio
Accelrys Discovery Studio (2.1) is a life science modeling and simulation suite of application focused on optimizing the drug discovery process. The mechanism for ligand placement is based on fitting points. Fitting points are added to hydrogen bonding groups on the protein and ligand. A molecular mechanics like scoring function which includes terms of hydrogen bonds is employed by DS to rank the docked posses. The docking algorithm was also accessed in order to know the binding sites and the number of rotatable bonds of the ligand.

2.5.Protein preparation
The ligands and crystallographic water molecules were removed from the protein, and the chemistry of the protein was corrected for missing hydrogen. Crystallographic disorders and unfilled valence atoms were corrected using alternate conformations and valence monitor options. Following the above steps of presentation, the protein was subjected to energy minimization using the CHARMm forcefield.

2.6.Ligand preparation
The three dimensional structures of phytocompounds were drawn by Chemsketch software and saved in .sk2 format to download in Discovery studio 2.1. Hydrogen bonds were added and the energy was minimized using CHARMm force field. Lipinski's properties like molecular weight, log P and number of Hydrogen-bond donors and acceptors for the active principles were noted.

2.7.PROSITE
Source: www.expasy.org/prosite/
PROSITE is a database of protein families and domains. It is based on the observation that, while there is a huge number of different proteins, most of them can be grouped, on the basis of similarities in their sequences, into a limited number of families. a protein signature can be used to assign a newly sequenced protein to a specific family of proteins and thus to formulate hypotheses about its function. Ig-like domain profile was analysed for T-cell receptor using PROSITE domain database.

RESULTS

The NMR structure of the phytocompounds isolated from medicinal plants namely A) saponin B) catechin C) costunolide D) eremanthin E) dihydroxy gymnemic triacetate F) gymnemic diacetate G) gymnemic triacetate H) gallic acid I) polysaccharide J) terpenoid K) lupeol are presented in Figure-1. Figure-2 shows the three dimensional structures of the chosen phytocompounds developed by chemsketch 12.0 software. Table-1 describes the Lipinski properties like molecular weight, log p, number of hydrogen bond donors and acceptors for the

active compounds. Table-2 depicts the ADMET (Absorbtion, Distribution, Excretion, Metabolism, Toxicology) properties of the compounds.

Figure-1: NMR structure of phytocompounds A) saponin B) catechin C) costunolide D) eremanthin E) dihydroxy gymnemic triacetate F) gymnemic diacetate G) gymnemic triacetate H) gallic acid I) polysaccharide J) terpenoid K) lupeol

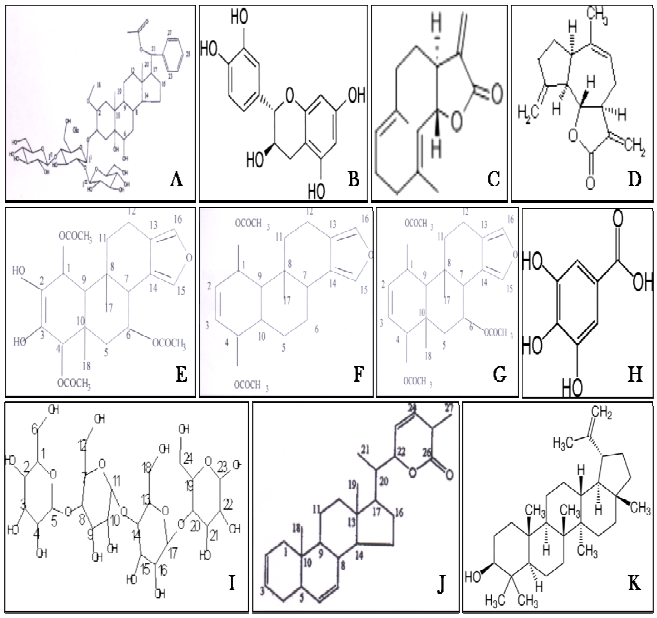


Figure-2: Three dimensional molecular structure of phytocompounds A) saponin B) catechin C) costunolide D) eremanthin E) dihydroxy gymnemic triacetate F) gymnemic diacetate G) gymnemic triacetate H) gallic acid I) polysaccharide J) terpenoid K) lupeol

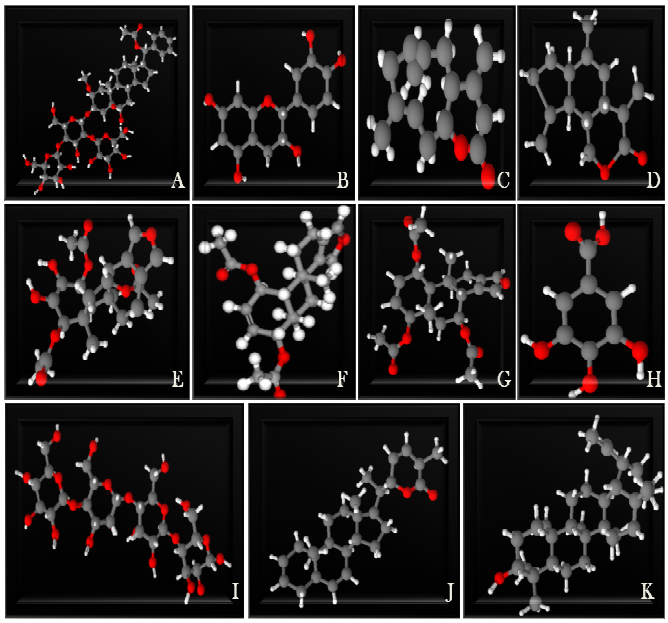


Table-1: Lipinski properties of active phytocompounds.

S.No	Compound	Hydrogen bond donors (<=5)	Hydrogen bond acceptors (<=10)	Molecular weight (<=500) [g/mol]	Alog P (<=5)
1	saponin	12	21	973.191	-0.187103
2	catechin	5	6	290.29	2.1127
3	costunolide	0	0	232.3181	3.3
4	eremanthin	0	2	230.30222	2.6
5	dihydroxy gymnemic triacetate	2	9	462.54	0.7009
6	gymnemic diacetate	0	5	358.47	3.102
7	gymnemic triacetate	0	7	430.54	2.7509
8	gallic acid	4	5	170.11954	0.7
9	polysacchride	3	11	454.50912	-1.5
10	terpenoid	0	2	394.65	6.3443
11	lupeol	1	1	426.801	8.0281

Table-2: ADMET properties of phytocompounds

S.No	Compound	Aqueous solubility	Blood brain penetration level	CYP450 2D6	Hepatatoxicity	HIA	Plasma Protein binding level
1	saponin	2	4	0	1	3	0
2	catechin	2	1	0	1	0	1
3	costunolide	2	1	0	1	0	1
4	eremanthin	2	1	0	1	0	0
5	dihydroxy gymnemic triacetate	3	1	0	0	1	0
6	gymnemic diacetate	2	2	0	0	0	0
7	gymnemic triacetate	2	3	0	0	0	0
8	gallic acid	4	3	0	0	0	0
9	polysacchride	1	1	0	0	3	0
10	terpenoid	1	1	0	0	1	0
11	lupeol	0	4	0	0	3	2

Figure-3: Structure of a) T-cell receptor retrieved from PDB database b) T-cell receptor with sphere definition and binding site for docking c) T-cell receptor with the specific domain (Ig like domain) d) T-cell receptor and its domain without sphere.

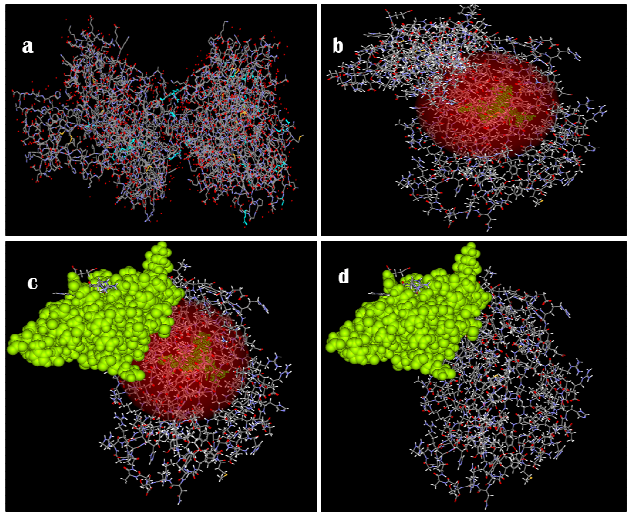


Figure-3 displays the various forms of T-cell receptor. 3a is representing the three dimensional structure of T-cell receptor retrieved from PDB (Protein Data Bank) database with the resolution of 2Å. The prepared protein structure for docking is shown in figure-3b which is included with the removal of water molecules from the protein along with the addition of hydrogen atom. Then, the protein was subjected to energy minimization using CHARMm forcefield followed by defining sphere in red color and its binding site in green color. The protein with its specific Ig-like domain is shown in green color in figure-3c. The protein with its specific domain without defined sphere is shown in figure-3d.

Figure-4: Interaction of drug-receptor complexes. The docked complexes are a) saponin b) catechin c) costunolide with T-cell receptor.

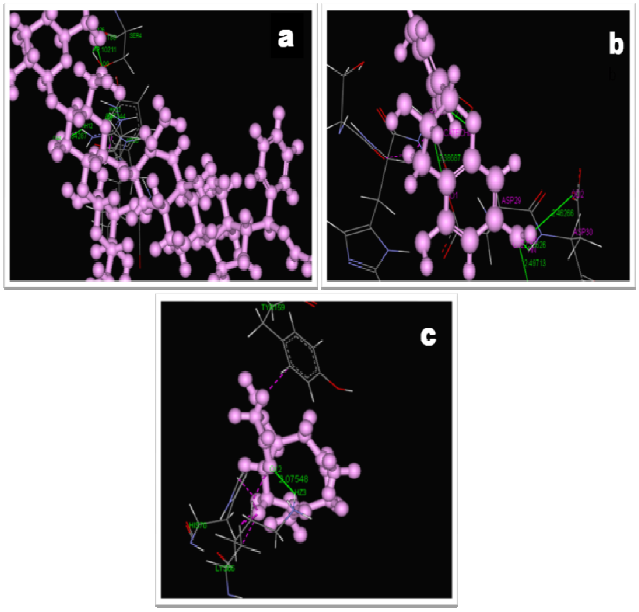


Figure-5: Interaction of drug-receptor complexes. The docked complexes are a) eremanthin b) dihydroxy gymnemic triacetate c) gymnemic diacetate with T-cell receptor.

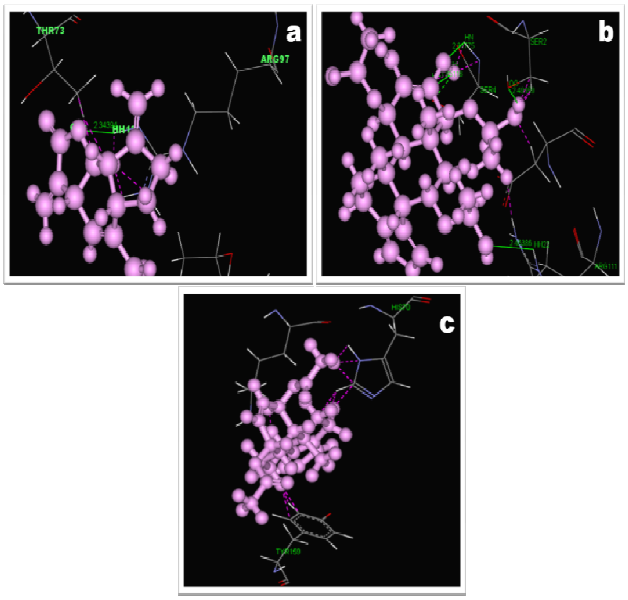
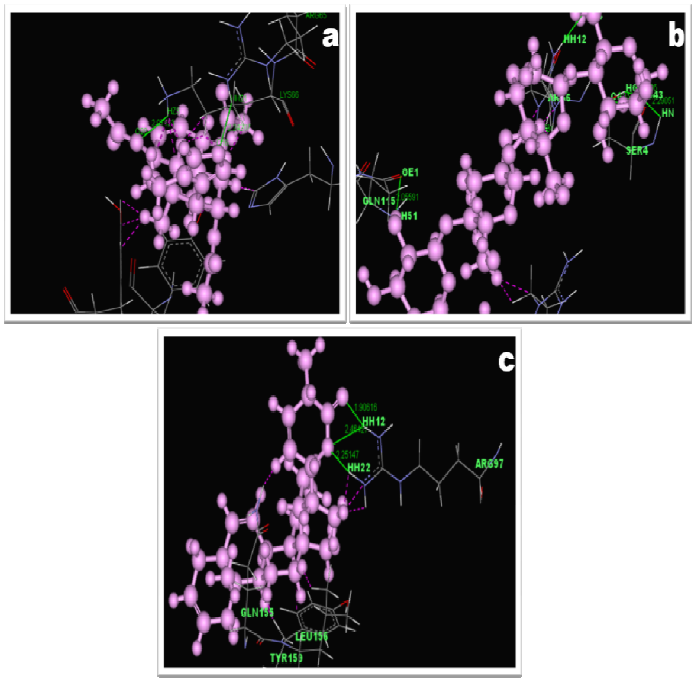


Figure-6: Interaction of drug-receptor complexes. The docked complexes are a) gymnemic triacetate b) polysaccharide c) terpenoid with T-cell receptor.



The results of interaction between T-cell receptor with the phytocompounds (a) saponin, (b) catechin, (c) costunolide are shown in figure-4, with the phytocompounds (a) eremanthin, (b) dihydroxy gymnemic triacetate, (c) gymnemic diacetate are shown in figure-5 and with the phytocompounds (a) gymnemic triacetate, (b) polysaccharide, (c) terpenoid are shown in figure-6. The green dot lines denote the hydrogen bonds. All the amino acid residues which involved in molecular interactions are displayed as lines and the ligands are displayed as ball and sticks in pink color.

The observed results of the drug-receptor interaction for the phytocompounds saponin, catechin, costunolide, eremanthin, dihydroxy gymnemic triacetate, gymnemic diacetate, gymnemic triacetate, polysaccharide, terpenoid are tabulated in Table-3.

The domain for the T-cell receptor was identified from position 185-271 as Immunoglobulin (Ig)-like domain profile from PROSITE database motifs are resulted in figure-7. The domain position from 185-271 taken from PROSITE database is displayed in green color and the compound catechin is displayed in pink color is presented in figure-8. The amino acid tryptophan 209 is interacted with the compound catechin.

Table 3: Results of drug-receptor interactions

S.No	Compounds	Docking pose	Docking Scores		Receptor- ligand Hydrogen bonds			
		Absolute energy	Libdock score	Total no.of hydrogen bonds7 Contacts	Amino acid & Position	Atom in amino acid	Atom in Ligand	Bond length
1.	saponin	100.52	130.832	4/2	ARG-6 ARG-6 SER-4 SER-4	HH12 HH22 OG HG	O44 O37 H126 H126	2.34284 2.47344 2.10211 2.18802
2.	catechin	37.524	82.991	5/3	ASP-29 ASP-29 TRY209 SER-4 SER-4	OD2 HN HH HG OD1	H29 O12 O12 O H34	2.46266 2.35626 2.49713 2.15254 2.38687
3.	costunolide	55.382	74.823	1/5	LYS-66	H23	O12	2.07548
4.	eremanthin	39.768	64.856	1/5	ARG-97	HH12	O12	2.34394
5.	dihydroxy gymnemic triacetate	100.959	81.71	5/8	SER-4 SER-4 SER-4 SER-2 ARG-11	HG HN H48 OG HH22	O19 O19 O34 H61 O32	2.15938 2.31775 2.85116 2.49159 2.46386
6.	gymnemic diacetate	74.651	77.684	0/9	-	-	-	-
7.	gymnemic triacetate	100.03	97.215	2/10	LYS-66 ARG-65	HZ3 HH21	O20 O16	2.07123 2.24207
8.	polysacchride	64.873	132.351	6	AGR-6 SER-4 SER-4 SER4 AGR-6 GLN-115	H84 HN HG OG HE OE1	HH12 O43 O43 H85 H63 H51	2.5316 2.29051 1.61596 1.931 1.51734 2.05595
9.	terpenoid	62.575	93.243	3	ARG-97 ARG-97 ARG97	HH12 HH12 HH22	O30 O25 O25	1.90616 2.46427 2.25147

Figure-7: Domain analysis of T-cell receptor.

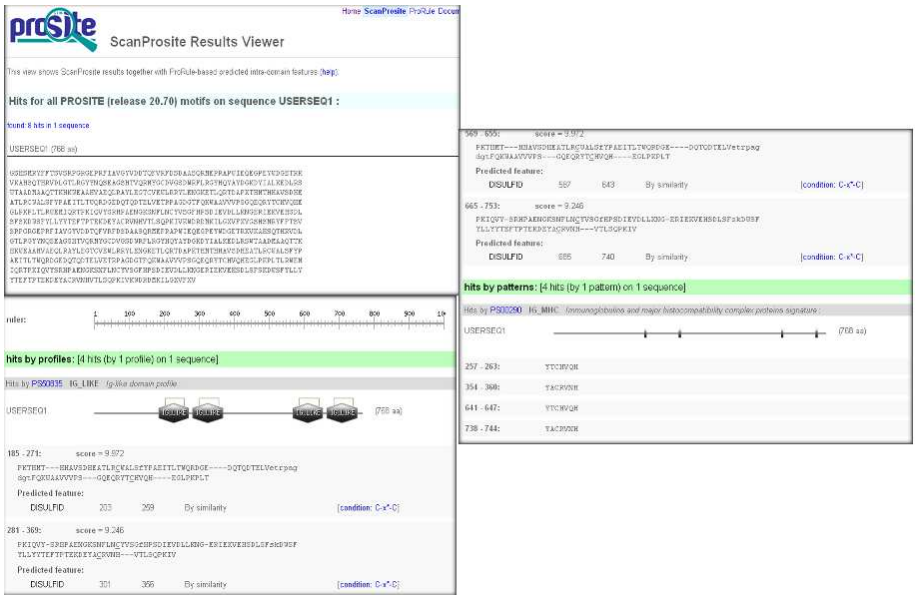
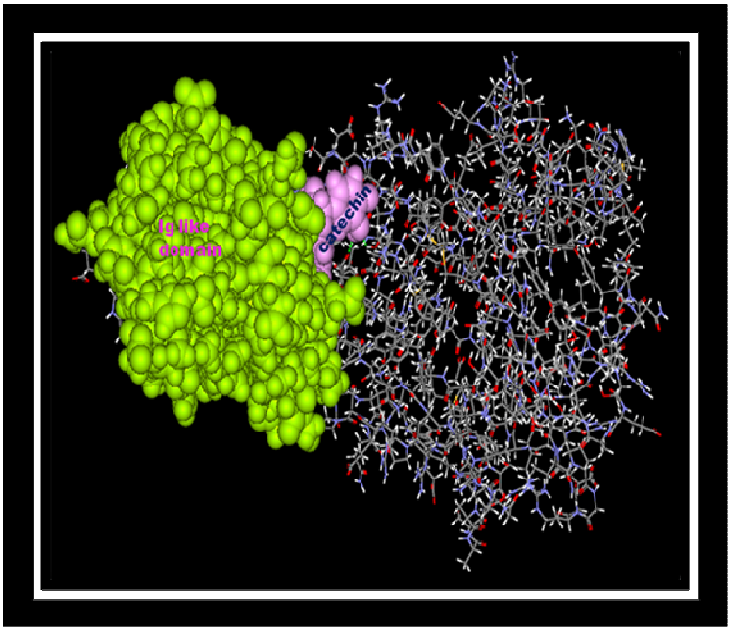


Figure-8: Ig like domain in T-cell receptor bounded with compound catechin.



DISCUSSION

Molecular Docking continues to hold great promise in the field of computer based drug design which screens small molecules by orienting and scoring them in the binding site of a protein. As a result novel ligands for receptors of known structure were designed and their interaction energies were calculated using the scoring functions [23]. Number of reports citing successful application of CADD in developing specific drugs in different therapeutic areas is expanding rapidly. The most well known factor is the “Lipinski’s rule of five” which was derived empirically from the analysis of the World Drug Index on the properties that maximize (satisfy) an oral drug candidate’s probability of surviving clinical development.

Christopher A. Lipinski formulated Lipinski’s rule of five to evaluate drug likeness, or determine if a chemical compound with a certain pharmacological or biological activity has properties that would make it a likely orally active drug in humans [24]. The rule is important for drug development where a pharmacologically active lead structure is optimized step-wise for increased activity and selectivity, as well as drug-like properties as described by Lipinski’s rule. Lipinski’s rule says that in general an orally active drug has no more than one violation of following criteria i.e. has no more than 5 hydrogen bond donors, not more than 10 hydrogen bond acceptors, molecular weight under 500 dalton, Partition coefficient A Log P less than 5.

In the present study, the phytocompound saponin violates all the four properties; polysaccharide violates the hydrogen bond acceptors, molecular weight and A Log P properties; terpenoid and lupeol violate only A Log P property. The other phytocompounds including catechin, costunolide, eremanthin, dihydroxy gymnemic triacetate, gymnemic diacetate, gymnemic triacetate and gallic acid are satisfying the Lipinski properties.

Drug likeness studies are a clear attempt to understand the chemical properties that make molecules either successful or possibly expensive clinical failures. Similarly the contribution of molecular properties which influence ADMET(absorption, distribution, metabolism, excretion and toxicology) are recognized alongside therapeutic potency as key determinants of whether a molecule can be successfully developed as a drug [25]. ADMET properties which include aqueous solubility, blood-brain penetration level, cytochrome 450(CYP450), hepatotoxicity, human intestinal absorption (HIA) and plasma protein binding levels.

According to Cheng and Merz, 2003 [26], aqueous solubility aids to predict the solubility of each compound in water at 25°C and it has seven different levels falls between 0-6. If the aqueous solubility of the compounds falls between the level 0-2 indicates low solubility, level 3 indicates good solubility, level 4 indicates optimal solubility and level 5 indicates high solubility. Earlier reports were suggested that, low solubility is detrimental to good and complete oral absorption, and so the early measurement of this property is of great importance in drug discovery [27, 28]. In connection with this context, as phytocompounds saponin, catechin, costunolide, eremanthin, gymnemic diacetate, gymnemic triacetate are observed to have low solubility, these compounds must have good and complete oral absorption.

As Egan and Lauri, 2003[29], cited, blood-brain barrier penetration level helps to predict the blood-brain penetrating efficacy of the phytocompounds after the oral administration and it has different levels ranging from 0-4. If the blood-brain barrier penetration level of the phytocompounds falls between 0&1, it shows the high penetrating efficacy, level 2 shows medium penetrating efficacy, level 3 shows low penetrating efficacy and level 4 shows undefined penetrating efficacy. In the present study, it is observed that the phytocompounds catechin, costunolide, eremanthin, dihydroxy gymnemic triacetate, polysaccharide and terpenoid are having high blood-brain penetrating capacity and as suggested by De Lange and Danhof, 2002[30], these compounds could reach their molecular target easily.

Susnow and Dixon, 2003[31], reported that, Cytochrome 4502D6(CYP450) model predicts CYP2D6 enzyme inhibition using 2D chemical structure of compound and it has 2 levels namely 0 for non-inhibitor and 1 for inhibitor. In the present study, all the 11 phytocompounds have found to be non-inhibitors and are unfavorable to inhibit CYP2D6 enzyme when they undergo metabolism via the cytochrome P450 (CYP) enzymes.

Human Intestinal Absorption (HIA) predicts the intestinal absorption of drugs after oral administration which falls into 4 levels of absorption from 0-3. As Egan and Lauri, 2002[32], suggested, the phytocompounds catechin, costunolide, eremanthin, gymnemic triacetate, gymnemic diacetate, gallic acid of the present study could be predicted to have a good absorption since they fall into the level of 0 and the other compounds are predicted to have a poor intestinal absorption.

According to Dixon and Merz, 2001[33], the plasma protein binding level predicts whether a compound is likely to be highly bound to carrier proteins in the blood. In the present study, all the 11 phytocompounds have a binding capacity to cross the membrane and bound to the plasma protein.

Dixon and Villar, 1999[34], described that hepatotoxicity aids to predict potential organ toxicity for a wide range of structurally diverse compounds and it has 2 levels namely 0 for non-toxic and 1 for toxic. Kennedy, 1997[35], stated that, toxicity is responsible for many compounds failing to reach the market and for the withdrawal of a significant number of compounds from the market once they have been approved. Based on this context, the phytocompounds saponin, catechin, costunolide, eremanthin of the present study should have been withdrawn from further investigation. But Daisy *et al.*, 2010[17] established that catechin is non-toxic and and Eliza *et al*., 2010[19] established the costunolide and eremanthin are also non-toxic to liver on streptozotocin-induced diabetic rats. Taken this into consideration they were involved for further investigation along with the other compounds which are found to be non-toxic and unfavorable to cause dose-dependent liver injuries.

Virupakshaiah *et al.*, 2007[36], defined that docking is the process of fitting together of two molecules in 3-dimensional space. Docking allows the scientist to virtually screen a database of compounds and predicts the strongest binders based on various scoring function. It explores ways in which two molecules such as drug and receptor together and dock to each other well. The molecules binding to a receptor, inhibits function, and acts as a drug.

Verlinde and Hol, 1994[37], suggested that when a drug binds to a target in molecular modeling and molecular design software, the lower the energy value the higher is the affinity of the drug. In this view, it is clear from the results (table-4) that catechin and eremanthin must have a higher affinity towards the receptor, since they produce a lower energy value while interacting with the receptor. A high libdock score is suitable for better protein-ligand interaction [38]. In this regards, the two phytocompounds saponin and polysaccharide should be defined to have a better docking interaction because of their high libdock score. But due to their higher energy value, they are not considered to have a better interaction. At the same time, catechin and eremanthin are comparatively having a higher libdock score. So, their docking interactions are evaluated further.

According to Trapani *et al.*, 1992[39], hydrogen bonding is most likely an essential requirement for many drug-receptor interactions. A single hydrogen bond is relatively weak and would not be expected to support a drug-receptor interaction alone, but when multiple hydrogen bonds are formed between drugs and receptors, as is typically the case, a significant amount of stability is conferred upon the drug-receptor interaction. In this context, it is wise to confirm from table-4 the interaction between catechin and receptor conferred a significant amount of stability when compared to eremanthin because catechin produced five hydrogen bond interactions with the residues ASP29 (2 hydrogen bonds), TRY209 and SER4 (2 hydrogen bonds) of the receptors whereas eremanthin produced only one hydrogen bond interaction.

Jiri Novotny *et al.*, 1986[40] stated that T-cell polypeptide chains are organized into immunoglobulin (Ig)-like domains consisting of multistranded antiparallel β-sheet bilayers. In the present study, when the T-cell receptor was subjected to domain analysis using PROSITE database, the Ig (Immunoglobulin)-like domain was identified from the position 185-271 in T-cell receptor. Interestingly, one of the five hydrogen bond of catechin with the T-cell receptor is at the residue TRY209 which is present in the Ig-like domain (185-271). This confirms that catechin is directly interacted with the Ig-like domain which in turn might block the T-cell

receptors. Furthermore, as David Goodshell, 2005[7] suggested this blocking of T-cell receptors might be involved in the prevention of further T-cell infection by HIV or prevention of the infected individual to progress into AIDS.

CONCLUSION

The protein-ligand interaction plays a significant role in structural based drug designing. In the present study, the phytocompound catechin has satisfied Lipinski's properties and also it has favorable ADMET properties. The interaction between T-cell receptor and catechin results minimal energy value and maximal libdock score with good hydrogen bond interaction. Furthermore, the phytocompound catechin interacts with Ig-like domain and it may protect the T-cell infection by HIV or prevent the infected individual to get progress in AIDS. Therefore, it could be predicted that the phytocompound catechin possesses anti-HIV activity by blocking the T-cell receptor and it can be developed into a potent oral drug for AIDS. Further *in-vivo* and *in-vitro* approaches are required to elucidate the molecular mechanisms of this activity.

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