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Research Article

COMPUTATIONAL INVESTIGATION OF ANTICANCER DRUGS AGAINST POTENTIAL MOLECULARTARGETS IN COLON CANCER

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ABSTRACT

Cancer is a class of disease, culpable for abnormal growth of cells. Colon cancer is a chronic intestinal cancer that accounts for 10% of cancer-related fatalities in all around the world. Recently it is established that MSH6 protein target contribute to elevated glioma and colon cancer sensitivity. The toxicological impact of various therapies remains a subtle question whether to recommend a drug/compound for invitro and clinical assessment or not. Majority of anticancer therapies approved by higher governing authorities elicit strong adverse and toxic responses upon administration, hence hinder their exploitation in these types of cancer types. Therefore, an elaborate toxicological approach was adopted to screen anticancer equipped with immunomodulatory properties drugs library to procure low toxic drug candidates which were further docked against MSH6 receptor using PatchDock. Thirty compounds having anticancer nature and immune stimulating activities were selected, only nine anticancer compounds qualified based on minimal toxic response and further utilized as a potential ligand for docking studies. Upon interaction, the results were classified based on Hydrogen bonding, and minimal binding free energy. Capacitabine and luvocrine had an effective anticancer activity as Capacitabine two hydrogen bonds with MSH6 residues (GLN-132 and PHE-133) with the binding free energy of -27.26 kJ/mol and Luvocrine formed three hydrogen bonds with (CYS-88, LYS-145 and LEU-448) amino acid residues having -44.06 kJ/mol. Based on their interaction, these drugs could be proposed as a strong anticancer compound for invivo potency for future examination. The significance of the present study is clearly reflected by the identification of best inhibitor against colorectal cancer respectively.

INTRODUCTION

Colon cancer is the fourth most common incident cancer (after breast, lung, and prostate) and the second most common cause of cancer death. Colon cancer is essentially the only cancer that occurs with approximately equal frequency in men and women. Rates of colon cancer vary by race and ethnic status(Potter, Slattery, & Bostick, 1993). Diet and other modiable lifestyle factors play major roles in the development of colon cancer. Colon cancer may contain following risk through literature study obesity, physical inactivity, alcohol consumption, early adulthood cumulative cigarette smoking, higher red meat consumption, and no or low intake of supplemental folic acid(Author et al., 2000). In colon cancer, molecular causes studied regulation of the Wnt pathway is a well-defined early event. In a whole array of other malignancies Wntsignaling also seems to be deregulated, although its significance in tumourigenesis, in most tumors, several regulatory circuits are altered during multistage tumor progression. In recent years, it has become obvious that one of these, the Wntsignaling pathway, plays a central role in the etiology of colon cancer, and is deregulated in a range of other tumors(Oving & Clevers, 2002). Human colon cancer harbors a small sub fraction of tumor-initiating cells (TICs) that is assumed to be a functionally homogeneous stem-cell-like population driving tumor maintenance and metastasis formation. We found unexpected

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cellular heterogeneity within the TIC compartment, which contains three types of TICs. Extensively self-renewing long-term TICs (LT-TICs), Rare delayed contributing TICs (DC-TICs), Tumor transient amplifying cells (T-TACs)[3]. The isolation and characterization of tumorigenic colon cancer cells may help to devise diagnosed by novel diagnostic and therapeutic Procedures (Dieter et al., 2011).

Multidrug treatments are increasingly important in medicine and for probing biological systems. Although many studies have focused on interactions between specific drugs, little is known about the system properties of a full drug interaction network (Yeh, Tschumi, & Kishony, 2006). Toxicity evaluation is an extremely important process during drug development. Which is time-consuming and costly. To speed up such a process, a quantitative structure-activity relationship (QSAR) study was performed to develop a computational model for correlating the structures(Su, Lu, Du, Chen, & Niu, 2017). The toxicity of substances can be observed by (a) studying the accidental exposures to a substance (b) in vitro studies using cells/ cell lines (c) in vivo exposure on experimental animals. Toxicological screening is very important for the development of new drugs and for the extension of the therapeutic potential of existing molecules. The US Food and Drug Administration (FDA) states that it is essential to screen new molecules for pharmacological activity and toxicity potential in animals (Parasuraman, 2011). In silico toxicology is one type of toxicity assessment that uses computational methods to analyze, simulate, visualize, or predict the toxicity of chemicals (Raies & Bajic, 2016). For a time, drug toxicology analysis has employed the classification of Hodge and Sterner that stipulates six classes of acute toxicity determined by rat poisoning upon enteral drug administration and vapor inhalation: class 1 Extreme toxic, class 2 High toxic, class 3 Moderate toxic, class 4 Low toxic, class 5 Practically nontoxic, class 6 Relatively harmless(Berezovskaya, 2003). In our study we identified the drugs through literature articles and eliminate that drugs which are used for the cure of colon cancer. The drugs which are used for the treatment classified these drugs on the basis of their toxicity class. There are 6 classes of drug toxicity, which drug compound are lies in which toxicity class. On the basis of this we selected the drugs which lies on class 4, 5, and 6. After that we used this drugs for the control of colon cancer disease.

AIMS AND OBJECTIVE

- Identification and characterization of selected drugs, structure and toxicity.
- To identify and analyze the drug compounds that have lies on the toxicity class 4, 5, and 6.

MATERIAL AND METHODS

Disease Identification

Selection of MutS homolog 6(MSH6) Receptor Protein

The MutS Homolog 6 (MSH6) Protein online server Protein Receptor Protein database investigated its expression in colorectal cell cancer.For interactions between MUTS Homolog 6 (MSH6) test the interaction with other proteins with STRING.

Gene card

GeneCards (www.genecards.org) has been used for almost 15 years as the comprehensive and authoritative collection of human gene data records. A deep linked web disk, which includes protein coding, pseudo-gene, RNA code, genetic locus, a cluster, and non-classed genetic code of > 73000 human géne entries, is automatically extracted from over 80 digital sources. The landscape annotation tool is also displayed to assess gene function information status (Safran et al., 2010).

Sequence retrieval

- Uniprot database is used for the retrieval of protein amino acids sequences.

Uniprot

The SwissProt, TrEMBL and PIR registry joined to create the Universal Protein Knowledgebase (UniProt) collaboration to provide the scientific community with the exclusive, unified and authoritative platform for protein sequences and functional knowledge. The Uniprot NREF server (UniRef) includes descriptive knowledge base sub-sets that are ideal for effective analysis. The UniParc is updated daily from a wide number of public domain servers Uniprot Library (Consortium U, 2014).

Structure of lead molecule

We have selected reported anti-cancer medicines for colon cancer from our research. The drug structure is available now from the pubChem database.

PubChem Database

The Drug, Compound and BioAssayPubChem (https:/ pubchem.nlm.nih.gov) consists of three interlinked repositories. The substance database includes chemical information that are obtained by individual contributors to PubChem, and a single chemical structures derived from the substance database is contained in the Compound database. It also provides a brief of PubChem3D, a resource from three-dimensional theoretical structures of PubChem-based composites as well as PubChemRDF, a PubChem data formatted Resource Description Framework (RDF), to share, analyze, and integrate data with information in other databases (Kim et al., 2016).

Toxicity

Toxicity estimated by web database Protox using the statistical method Compounds that are common for category IV toxicity that we have opted to research further.A further ACD / I Lab database for structural changes is made up of the substances in the toxicity 1,11,111 to decrease more toxicity and to examine more.

Protox Server

ProTox web server is the first freely available prediction tool focused on chemical similarities and toxic fragments, which is efficient compared to the existing QSAR-based approaches. A advancement of ProTox databases is the implementation of a toxicity class predictor using resemblance and fragmentation

approaches and offering an insight into processes involved in the development of toxicity through warnings of potential toxicity targets (Drwal et al., 2014).

Molecular Docking

Molecular docking has become an exponentially developed form of medicaments discovery. The molecular docking technique is used to model the relationship between small and protein molecules at the atomic level , helping us to classify behavior by small molecules at the bonding point of the target proteins (Vijesh et al,. 2013).

PatchDock

PatchDockis ageometrical based molecular docking algorithm.It seeks to find transformations in docking that provide good complementary molecular shapes. Such improvements cause large interface areas as well as small amounts of steric collisions when applied. The main reason behind the high efficiency of Patch Dock is its accelerated transformations, powered by the fitting of local features and the quest for six-dimensional transformation settings by brute force (Schneidman et al., 2005).

Visualization

For visualization of interaction between the drugs targets by Discovery Studio. Discovery Studio visualizes proteins that have been targeted by drugs.

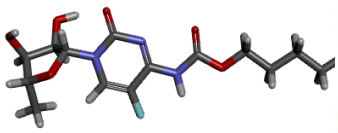
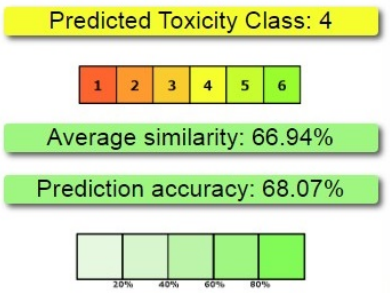
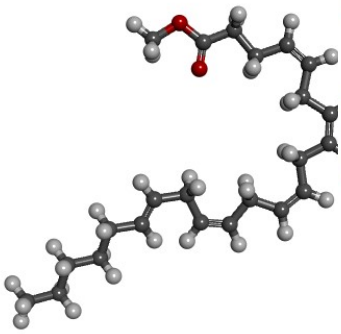
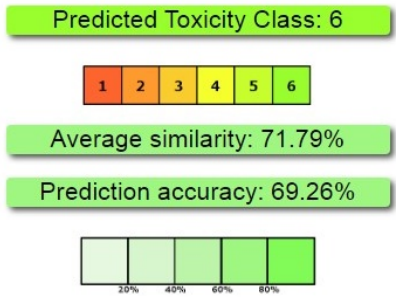
RESULTS & DISCUSSION

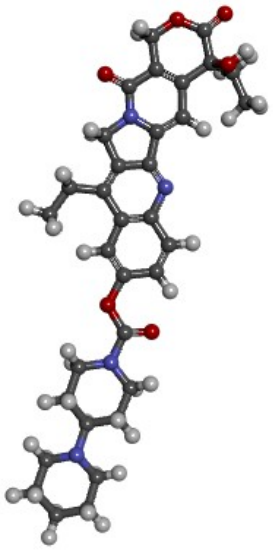
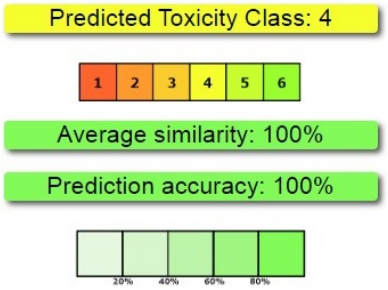
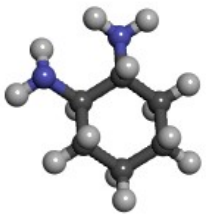
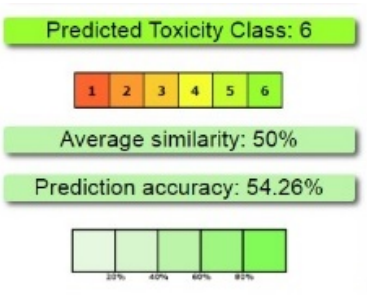
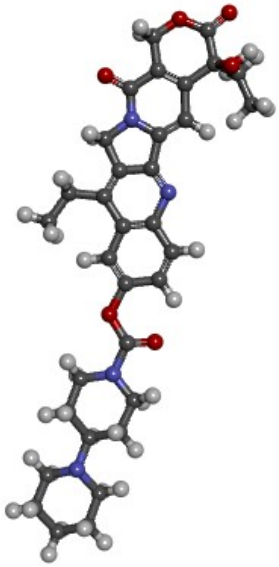
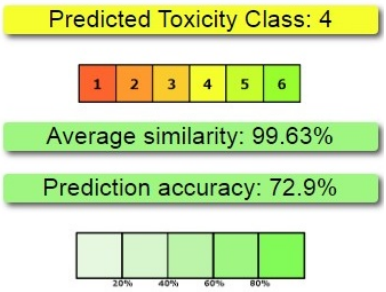
Selection of drug compound from the literature

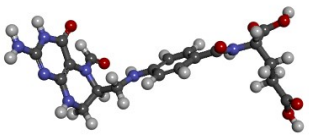
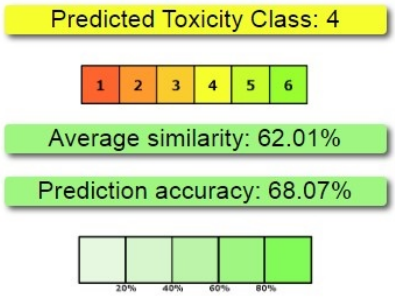
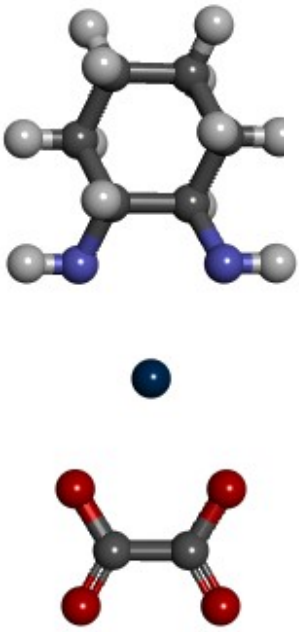
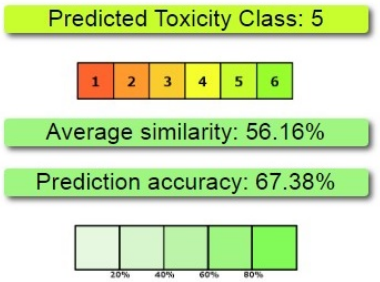
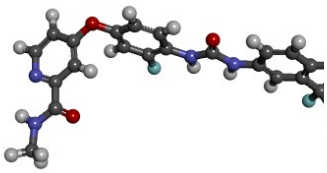
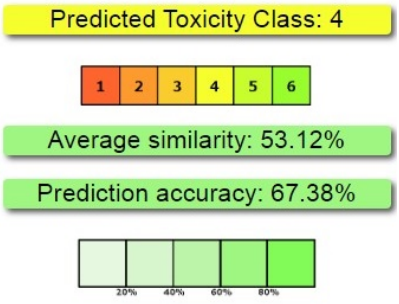
Succeeding the selection of the MutS homolog 6 (MSH6) structure, a novel inhibitor that directly suppresses the expression of this domain. Selection of MutS homolog 6 (MSH6) is based on a literature study and a selection of 16 lead compounds with different toxicity classes. Such lead compounds are often used on the basis of filters, such as the interaction of protein ligands, hydrogen bonds and energy reduction for further study. The data analysis shows that these recommendations are used in a variety of anti-cancer practices. The filter was applied to these leads and the normal toxicity class was selected which was involved in the anticancer activity.

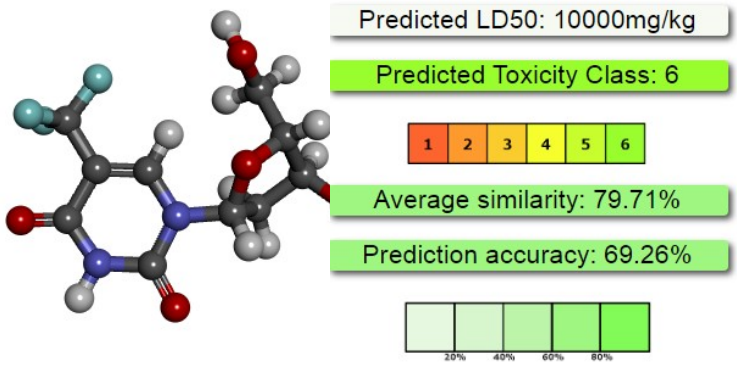
Toxicity

Toxicity is very important, as nine medications (Capectabine, Cetuximab, Compaster, Eloxatin, Irinotecan Hydrochloride, Leucovorin Calcium, Oxaliplatin, Regorafenib and Trifluridine) have been selected for advance therphy of colone cancer on toxicity bases. Toxicity is the key feature of any drug molecule, how toxic it is. Computationally we predicted toxicity via the ProTox server, our compound is in toxicity class IV, V and VI, which could be considered to be natural. A compound with a decreasing toxicity class is considered to be more toxic.

S.no:	Name	Compound Structure	Toxicity class
1	Capecitabine		
2	Cetuximab		

3	Compaster		
4	Eloxatin		
5	Irinotecan Hydrochloride		

6	Leucovorin Calcium		
7	Oxaliplatin		
8	Regorafeni		

9	Trifluridine	

Molecular docking

In hydrogen, vanderwaals and electrostatic bonding measures, the Patch Docking Software was used. Patch Dock supplied 100 configurations for each docking complex. The compounds have all been sorted by the lowest interface-delta-x energy (x-score), with the lowest score, but also with interactions with target residues. Depending on the lowest x score for each peptide protein complex, the best site was chosen. The Fire Dock service search finds these 10 best results. Docking complexes were visualized in Discovery Studio to explore electrostatic, HB and ΔG interactions. The active residues of interactive proteins, binding energies and hydrogen interactions are presented on Table 4.4 to better understand the interaction between peptides and target protein.

Table 4.4: List of whole selected peptides with different binding energies.

S.no	protein	ligand	Global Energy	Attractive VdW	Repulsive VdW	Hydrogen Binding	Solution number
1	MSH6	**Capecitabine**	-27.26	-17.74	11.88	-0.70	7
2	MSH6	**Cetuximab**	-26.33	-15.29	1.64	0.00	6
3	MSH6	Compaster	-25.64	-13.95	1.39	-4.05	6
4	MSH6	Eloxatin	-35.49	-16.89	5.95	-2.85	2
5	MSH6	**Irinotecan Hydrochloride**	-22.11	-14.41	19.94	-1.85	1
6	MSH6	**Leucovorin Calcium**	-44.06	-18.01	4.03	-3.28	9
7	MSH6	Oxaliplatin	-24.97	-13.45	1.73	-4.18	3
8	MSH6	**Regorafenib**	-27.89	-19.67	12.05	-4.12	9
9	MSH6	Trifluridine	-26.83	-16.67	8.81	-1.17	6

The assessment of the docking performancewasbuiled on the development of the HB counts between active protein remaning parts and lignds. Hydrogen interaction of anticancer drugs with target protein explored via the server, here is all nine drugs such as (Capectabine, Cetuximab, Compaster, Eloxatin, Irinotecan Hydrochloride, Leucovorin Calcium, Oxaliplatin, Regorafenib and Trifluridine) showed the association with the active residues of receptor.

Targets of Active domains docking

The performance of docking evaluation was focused on the composition of the HB counts between ligands and energetic protein remaining parts. Hydrogen interaction of anticancer drugs with target protein investigated via the application, all nine have been shown to be associated with active receptor residues.in learning binding interaction for the target protein energetic domain all chooses compound were used as ligands.; Capectabine, Cetuximab, Compaster, Eloxatin, Irinotecan Hydrochloride, Leucovorin Calcium, Oxaliplatin, Regorafenib and Trifluridine receptor interactions. As a result of docking,

both compounds have a high binding affection and their energy for binding is shown in Table 4.4.

Docking complexes of MUTS HOMOLOG 6(MSH6) with anticancer drugs

Pharmacophore Active Residue Models of MutS homolog 6(MSH6) Ligand Domain Receptor Polo box showed that Capecitabine, Cetuximab, Compaster, Eloxatin, Irinotecan Hydrochloride, Leucovorin Calcium, Oxaliplatin, Regorafenib and Trifluridine is hide in the binding area of MutS homolog 6(MSH6) Protein (Fig. 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 4.10, and 4.11).Overall findings demonstrated the best binding affinity in receptors and ligands. The receptor chain and ligand chain represent interactions with peptide residues in different colors in the docking complex. Apply force fields that help to attach peptide ligand to the receptor protein. The docking complexes of the domain MutS homolog 6 (MSH6) with anticancer drugs are shown in the figures.Chain of MutS homolog 6 (MSH6) polo box domain involved in association with selected whole peptides as shown in Fig. 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 4.10 and 4.11 Vander Waals interactions and ion interactions between the ligand receptor MutS homolog 6 (MSH6) are listed below.The Protein Receptor Active Residue Models of the MutS homolog 6(MSH6) ligand receptor showed that Capecitabine, Cetuximab, Compaster, Eloxatin, Irinotecan Hydrochloride, Leucovorin Calcium, Oxaliplatin, Regorafenib and Trifluridine is hide in the binding area of the MutS homolog 6(MSH6) protein (Fig. 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.4.9, 4.10, 4.11).Total results showed that the receptor and ligand have the best binding affinity and this model explained the receptor hydrophobicity. In the docking complex amino acids of receptor protein represent the interplay of 10 full docking results peptides in different colors of the receptor chain and ligand chain. The results of peptides add the ligand peptide with the receptor protein by using the hydrophobicity region on whole receptor sides. The MutShomolog 6 (MSH6) hydrophobicity docking complex with the Capecitabine ligand is shown in this figure. MutS homolog 6 (MSH6) residues show hydrogen donor and acceptor interactions with selected whole peptides as shown in Fig. 4.3 . The interaction with Capecitabine ligand, as described in Fig. 4.3, showed in the chain A of MUTS HOMOLOG 6 (MSH6) protein. Vander waals interactions with ASP-A:135 residues with distance 2.34 formed Capecitabine ligand. PHE-A residue:133 and GLN-A:132 form traditional ligand-distance hydrogen bonds 6.81 and 4.9. Interacting with the receptor Capecitabine ligand shows hydrogen, Vander Waals and ionic interactions but also α-α interactions. The 2D MUTS HOMOLOG models 6 (MSH6)are shown in theFig 4.3.

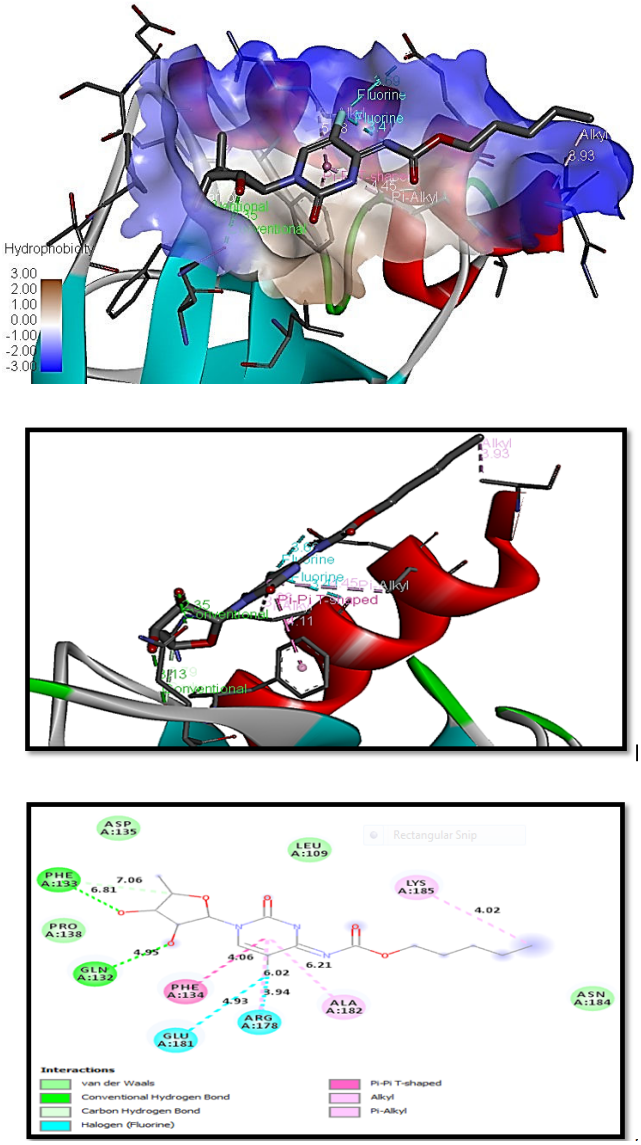
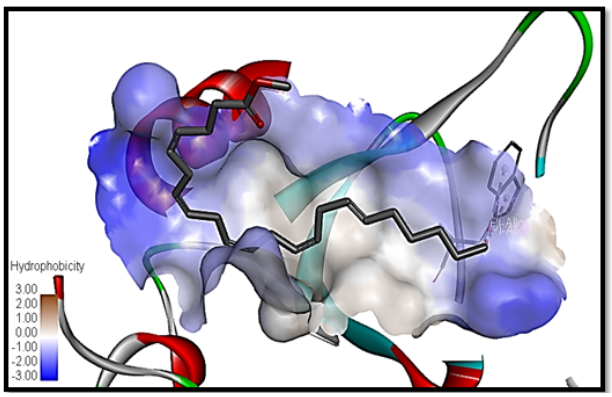


Figure 4.3: Hydrophobicity and Interaction Analysis of the MutS homolog 6(MSH6) receptor with capacitabine ligand.



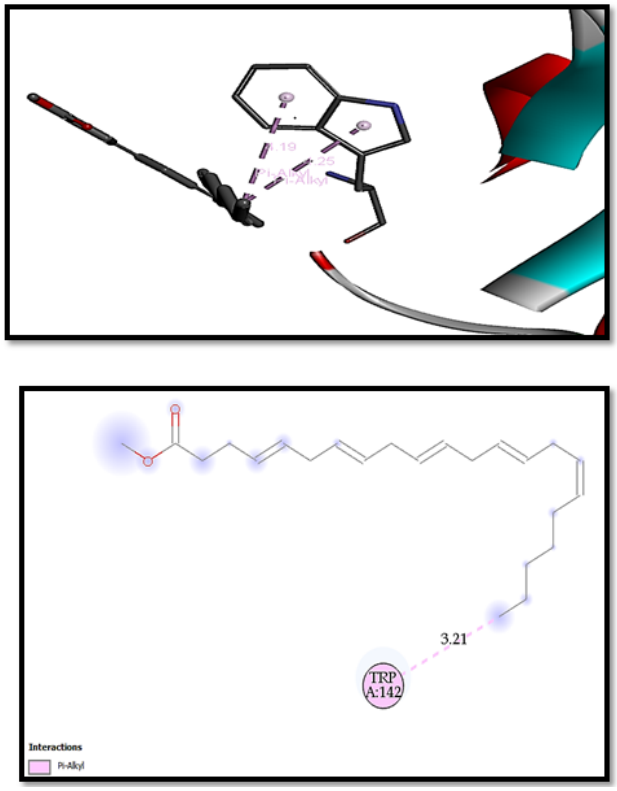
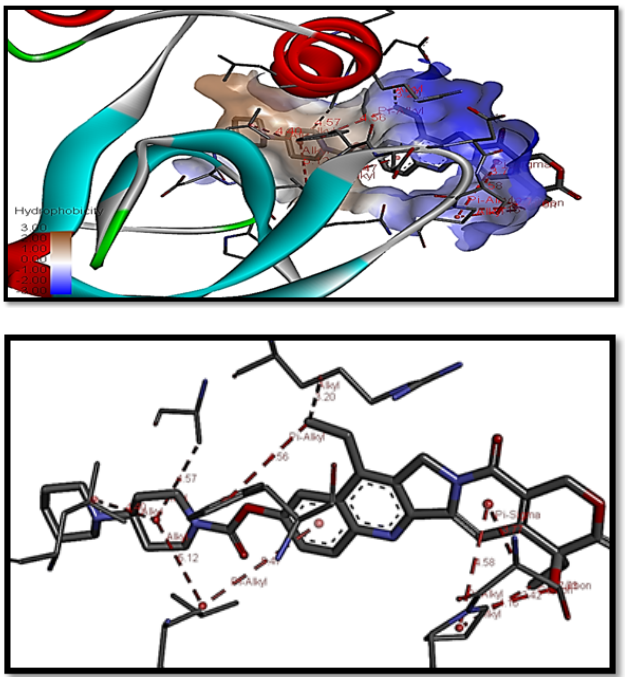


Figure 4.4: Hydrophobicity and Interactions analysis of MutS homolog 6(MSH6) receptor with cetuximab ligand.



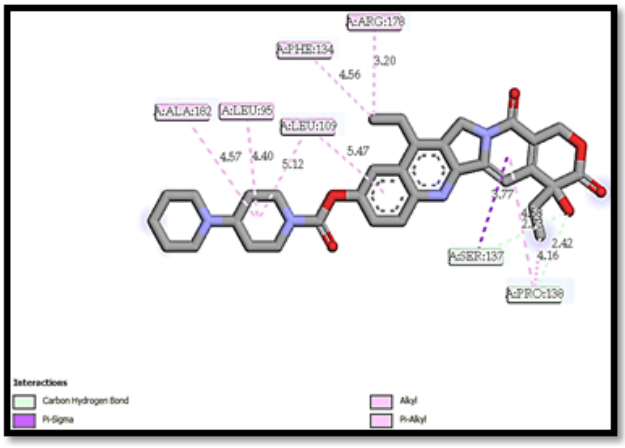


Figure 4.5: Hydrophobicity and Interactions analysis of MutS homolog 6(MSH6) receptor with compaster ligand.

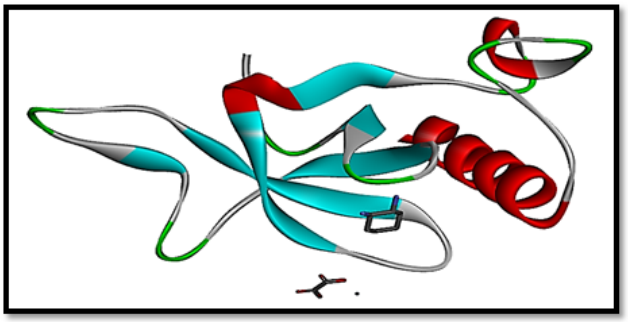


Figure 4.6: Hydrophobicity and Interactions analysis of MutS homolog 6(MSH6) receptor with eloxatin ligand.

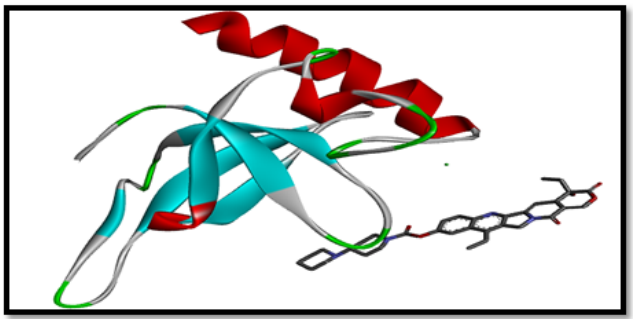
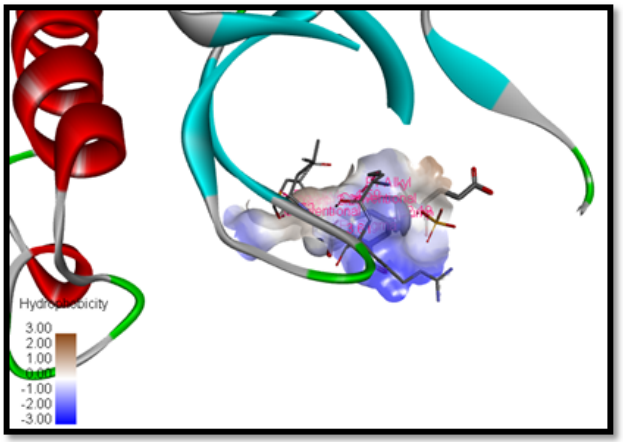


Figure 4.7: Hydrophobicity and Interactions analysis of MutS homolog 6(MSH6) receptor with Irinotean hydrochloride ligand.



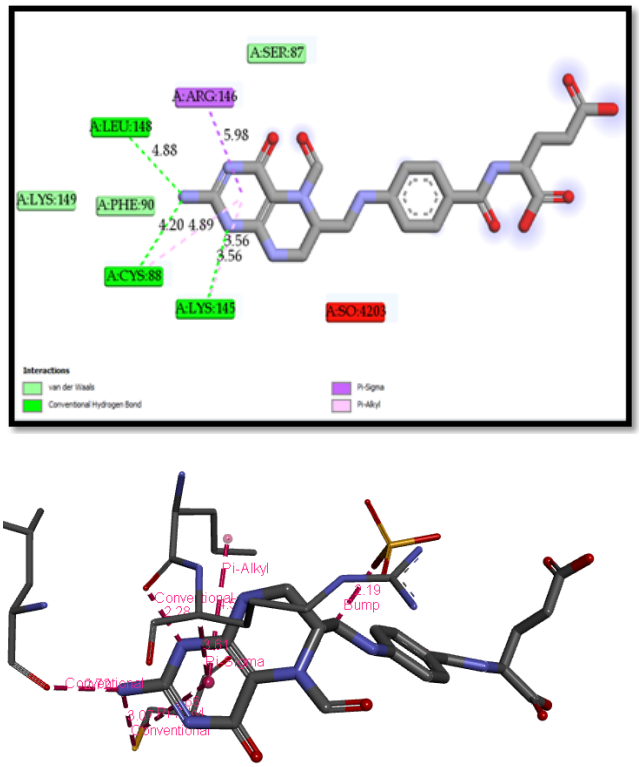


Figure 4.8: Hydrophobicity and Interactions analysis of MutS homolog 6(MSH6) receptor with **Leucovorin Calcium**ligand.

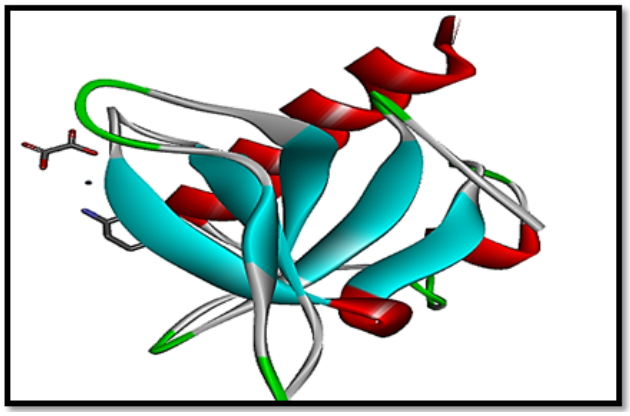


Fig 4.9: Hydrophobicity and Interactions analysis of MutS homolog 6(MSH6) receptor with Oxaliplatinligand.

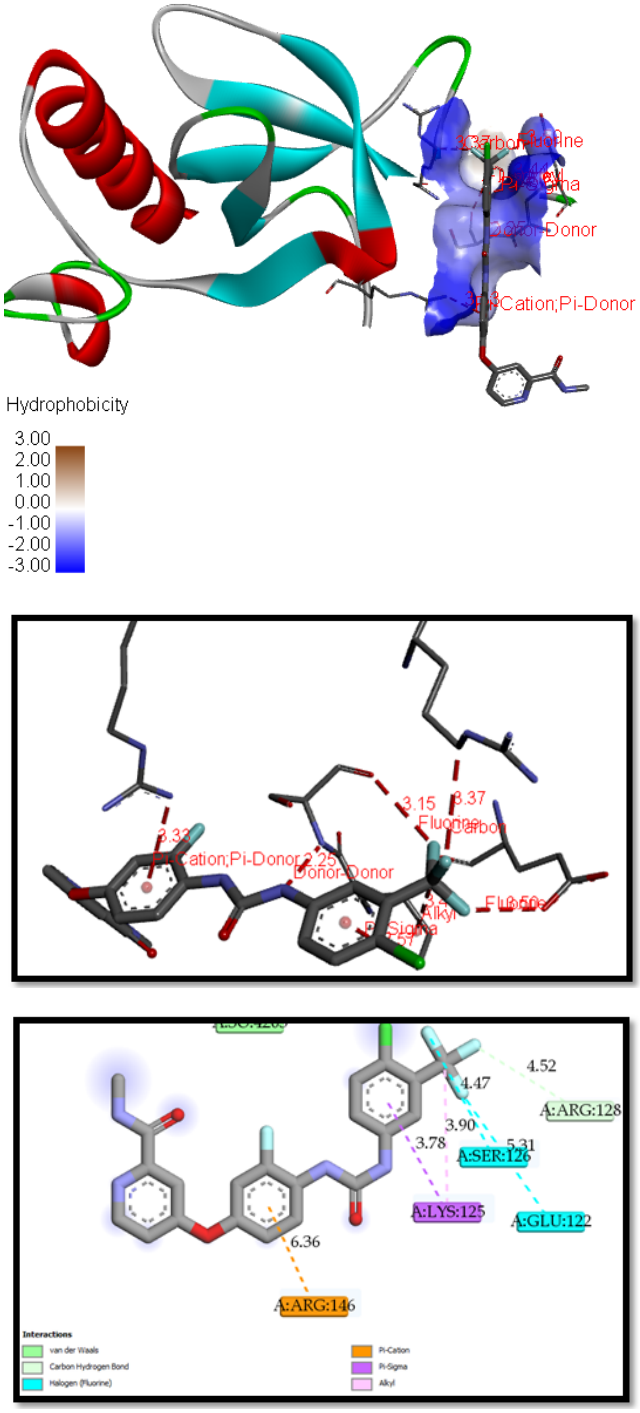
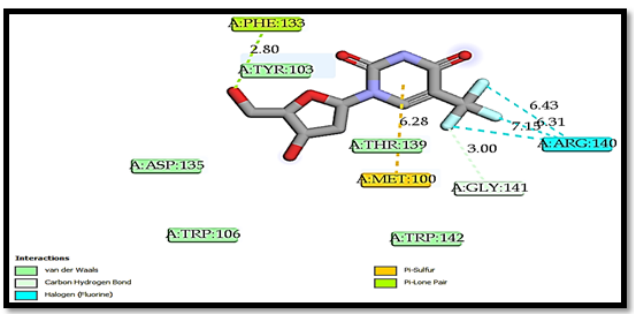
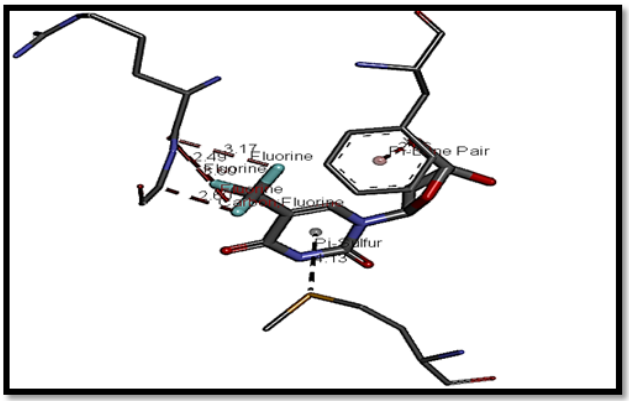


Figure 4.10: Hydrophobicity and Interactions analysis of MutS homolog 6(MSH6) receptor with Regorafenibligand.





Discussion

Good anticancer drugs are desperately needed in the fight against life-threatening cancer. Because of their promise, natural products have been used empirically since ancient times and their applications slowly grow. New potential molecules have created a medicines market, but due to lack of a concept of a natural model, drug candidates could not be synthesized. Plants need to be identified, since natural sources are adequate to extract model molecules (Demirezeret al., 2014). In this research we analyzed the action of nine different anti-cancers compounds. All selected compounds show significant binding affinity to the MSH6 protein, according to our research. The affinity of capecitabine is greater than that of other compounds docked by -2.21kcal / mol. The highest target of all compounds is known to be capecitabine (-28.26), Cetuximab (-26.33), Compaster (-25.64), Eloxatin (-35.49), IRC (-22.11), Leucovorin Calcium (-44.06), Oxaliplatin (-24.09) and Regorafenib (-27.89) and Trifluridine (-26.83). Hydrophobic and electrostatic interactions of MSH6 represent the best ligand energy and x results, but a few other parameters, including H-donor, H-acceptor and energy of Gibbs, have given low efficiency according to rule 5. The energy of Gibbs must be negative to medicines by law (Du et al., 2016).

In this test, capacitabine interaction with MSH6 created 5 HB in the ligand beginning with an energy range of -19 to -13, but binding affinity to more than one target was recorded in the previous research .. In their measurements and ratings of molecular docking, the measured capabin interactions were determined with active residues such as ASP-A: 135, PHE-A: 133 and GLN-A: 132, 2.34, 6.81, 4.9 (Senolet al., 2014). The average HB at distances of 2.34, 6.81 and 4.9; 3.20, 4.87 and 5.5 is found in Capitabine and Leuvocrine Calcium with site active residues, ASP-A:135, PHE-A:133, GLN-A:132; LEU-A:148; and LYS-A:148. The binding affinity with MSH6 leuvocrine is -4.02 kcal / mol of capitabine. This research was made by Wang et al . (2014), in which Surflex Dock module SYBYL-X 2.0 was used to dock the PPO-free ascorbic acid and 6 HB of ascorbic Acid and Amino Acid in active PPO-free binding energy with -4.63 kcal / mol. Ascorbic acid producing 3 HB with Glu-280 and Asn-281 PPO oxygen atoms is analyzed (wanget al., 2015). A analysis of the ascorbic acid composed of 3 or 4 HB with Ser-265 and the Glu230 recorded at a distance of 2Å. The current research stated that capacitabine and leuvocrine form calcium type 3HB, with active residues ASP A: 135, PHE-A: 133, GLN-A: 132; SER-A: 87; LEU-A: 148; and LYS-A: 148 with a binding affinity of -4,02 kcal / mol, but a prior analysis of the nokinsee et al. We also have good drug efficiency, since it has an IC50 value of more than 0.1mM with an energy binding of -4,83kcal / mol (Nokinseeet al., 2015).

The current research output examined that ascorbic acid has the ability to bind with variable residues of the different receptors; while ascorbic acid has demonstrated the highest binding affinity with respect to HB, ionic interaction, and Vander Waals interactions with all selected targets. Our study showed that capacitabine and calcium leuvocrine ligand binding free energy were correlated with each other, respectively -3.02kcal / mol and -4.02kcal / mol, but others are not interacted with MSH6 protein. Compared to the present work, previous research by Vanaja (2014) reported that capacitabine and leuvocrine calcium followed the best ADMET properties and QSAR definition, such as drug similarity, Acques solubility and scoring function, etc., and showed no mutagenic properties compared to other lead compounds. He had used AutoDockVina and Pymol to visualize the success being docked. He proposed that capacitabine and leuvocrine calcium, such as ASP-A: 135, PHE-A: 133, GLN-A: 132, SER-A: 87, LEU-A: 148, and LYS-A: 148, would have the best binding relationship with active target residues (Yellama and darsi, 2016).

Current performance has shown that the on-line study on the Molecular Dockserver by Kaempferol interacts with MSH6 through energy bindings of 0.70 kcal / mol up to -4.7 kcal / mol. (2012) reported that the Clitoriaternataekaempferol extract dotted with CDK2 protein displayed -5.28 kcal / mol bond power, 4.72 kcal / mol ligand energy and 515.461 surface interactions (Krithiga and Jayachitra, 2012). Specificity and affinity between the drug compound and the goal based on the shape and location of the contact surface of both partners (De-Azevedoet al., 2001). An earlier research showed that the fluorescence quenching and docking measurements bind kaempferol to bovine α-lactalbumin. We found that kaempferol is close to the Trp-60 and binds to the goal of 3 or 5 HB (Mohammadi and Moeeni, 2015). But, in this analysis we found that the active side residues MSH6 to 3 HB of leuvocrine and capacitabine calcium. The results showed that for different targets the interplay between capitabine and leuvocrine calcium patterns was variable. Awaluddin work projected a divergence with the current outcome, in which capacitabine and leuvocrine calcium not only developed hydrophobic associations with active amino acids ASP-A:135, PHE-A:133, GLN-A:132; SER-A:87; LEU-A:148; and LYS-A:148 but also shaped 3 H (Awaluddinet al., 2014).

According to a new review, capacitabine and leuvocrine calcium are involved in anticancer. We tested in vitro and in silicon that the capacitabine and leuvocrine calcium had comparable binding energies and, by molecular docking, the NF-Kb inhibitor docking and score functionality are proposed (Kadiogluet al., 2015). The study shows that the two studies on the variation of amino acid differed compared with the previous experiments, the capacitabine and leuvocrine calcium formed by 3HB with active residues ASP-A:135, PHE-A:133, GlN-A:132; SER-A:87; LEU-A:148 and LYS-A:148 (Daisy et al., 2009). The

determination of ADMET profiles of lead compounds is a major obstacle in designing drug schemes (Brito, 2011). However, due to low toxicity and pharmacokinetic propensities, most of the product fails in product development. ADMET properties in the drug design field are the first step in the discovery of affective lead compounds (Tsaiounet al., 2009). The ratio of opioid compound blood concentration to brain concentration (DBB) is the experimental BbB (Blood brain barrier). Drug discovery optimization is one of the main parameters and is achieved through information from BBB about drug spread (Alavijehet al., 2005; Abraham, 2004; Hurst et al., 2007). The compounds' capacity to function as a drug is established by ADMET properties of active compounds, including BBB drug diffusion, caco2, P-Glycoprotein substrates, human intestinal absorption and organic renal transport. A positive response is strongly supported for all selected substances. Fatty acids synthesizing, bile acids, carcinogenics, medicines, hormones and CYP 450 chemicals Cypo-cytochromic genome codes (CYP57). 75% of step I metabolism depends on CYP enzymes (Bibi, 2008). In terms of toxicity, many of the existing compounds have been found not toxic.

The affinity of the drug candidate to the target molecules was shown by the receptor-ligand complex's highest binding energy. The greatest binding affinity with MSH6 protein is seen in all the active ingredients that require chemicals to become drugs. Of the 9 selected compounds, only two showed major interactions with target proteins and were closely linked in the binding pocket. Current analysis found that all compounds, except capacitabines and leuvocrine calcium, were contravening rule5; only Capacitabine and leuvocrine calcium were passed through filters used in the study and met the criteria as a drug candidacy. Almost all compounds had significant interactions with both argenin and glutamine. A potential candidate for anti-cancer drugs could be Capecitabine and leuvocrine calcium. The number of additional compounds in contrast to HB or ionic interactions was the average amount of hydrophobic contact with active protein residues.

The best inhibitor for control points can be Capecitabine and calcium leuvocrine, as better ligand-receptor interactions, binding affinity, and stability showed. Our findings showed that the 5 screening compounds of Capacitabine and leuvocrine calcium have significant MSH6 inhibitory activity. Based on current findings, the capacitabine and leuvocrine calcium are involved in anti-cancer by blocking the MSH6 receptor. The findings strongly indicate that the promise of anti-cancer candidates is capacitabine and leuvocrine calcium. We selected the highest adverse energy binding energy complex Capacitabine and leuvocrine calcium -4,2 kcal / mol binding energy, and finally the capacitabine and leuvocrine were chosen as drug candidates from 9 natural compounds based on the Lipinski five-stranded law. Both compounds were highly affinity to the receptors because their negative energy was binding.

CONCLUSION

Based on docking interaction, we analyzed the anticancer compounds comprised of 16 compounds against MSH6 to identify drug candidates for colon cancer. Only nine anticancer compounds were selected as a ligand for the current study on the basis of adequate toxicity profile. On the basis of ligand-target values, hydrophobic and ionic interactions, each docked complex was analyzed. The docking interplay with target proteins only occurred for nine compounds. In comparison to nine compounds, only two compounds have the best interplay with the protein, all the selected target proteins formed ligand docking complexes.

This research rapidly creates more unexpected goal-based medicines. The product of this research is sometimes used as clinical tests. The drug aim-based medication outline showed the link between ligand and receptor particles for capacitabine and luvocrine medicines additionally. Communication of these medicines with other objectives and medicinal products shows their cooperation. The relationship of these medicines with other aims will open up new fields for the communication of medicines. Beginning with the discovery of the receptor, different drugs in industry can be used to meet such targets and to produce outstanding results. Minimum effort as medicines are less costly.

Capacitabine and leuvocrine meet the criteria for being a medicinal candidate on the basis of the analysis of results. We found that Capacitabine and leuvocrine have an efficient anticancer activity and can be proposed for future testing as a strong anticancer compound. Identification of the best colorectal cancer inhibitor clearly reflects the importance of the current study.

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