

Interaction of Cibacron Blue Attached Magnetic Polymers with Albumin Using Computational Tools

Cibacron Blue F3GA Baęlı Manyetik Polimerler ile Albumin Etkileşiminin Bilgisayarlı Ortamda İncelenmesi

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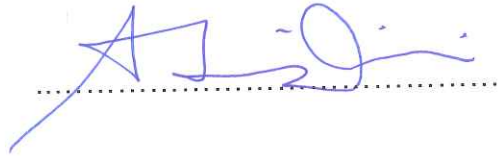
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21 / 06 / 2019


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SEÇKİN KILIÇ

ABSTRACT

Interaction of Cibacron Blue F3GA Attached Magnetic Polymers with Albumin Using Computational Tools

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Master of Science, Department of Chemistry

Supervisor: Prof. Dr. Adil DENİZLİ

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Human plasma contains a vast amount of human serum albumin (HSA). Almost 60% of human plasma protein contains HSA. Blood volume regulation based on colloid osmotic pressure is a vital role of serum albumins. In order to hide their hydrophobic nature, they can be seen transferring some low water-soluble molecules. These molecules consisted of some steroid hormones, some salts, free fatty acids, calcium, and some drugs. Low or high level of albumin almost always caused several diseases. Besides, albumin should be removed from blood plasma in some cases, since high abundancy of albumin hinders biomarkers in proteome studies. Affinity chromatography is a standard method, which used for protein purification and separation studies due to its specificity, selectivity. There are several affinity chromatography methods, such as dye affinity, immobilized metal chelated affinity, and affinity electrophoresis. Cibacron Blue F3GA (CBD), as a dye ligand, is one of the most used dyes amongst dye affinity chromatography. CBD is ideally suited for HSA purification for several years. However, even though CBD has many purification applications, there is not much research focused on the

interaction between CBD and HSA in molecular simulation. In this thesis, interactions between CBD and HSA were simulated via AutoDock molecular docking software in this study. Investigated possibilities resulted in six different conformations on different locations, which light the way to variable connectivity of CBD. Thus, it is determined that the most favorable binding is conformation 5, with its lowest binding energy, which is energetically favorable.

Keywords: Cibacron Blue, Human Serum Albumin, Molecular Docking, AutoDock Software

ÖZET

Cibacron Blue F3GA Bağlı Manyetik Polimerler ile Albumin Etkileşiminin Bilgisayarlı Ortamda İncelenmesi

Seçkin KILIÇ

Yüksek Lisans, Kimya Bölümü

Tez Danışmanı: Prof. Dr. Adil DENİZLİ

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İnsan serumu albümini (HSA), insan plazması içeriğinde en sık karşılaşılan proteindir. Bu haliyle kan içeriğindeki proteinlerinin %60'ını oluşturur. Yağ asitleri ve ilaç gibi farklı molekülleri kan içinde aktarmasının yanında en önemli görevlerinden biri, kan ile doku sıvıları arasında su miktarının dengelenmesini, yani ozmotik basıncı sağlamaktır. Albüminin eksikliği çeşitli metabolik hastalıklara yol açmakla birlikte, kanda bol miktarda bulunması da proteom analizlerinin kısıtlanmasına neden olmaktadır. Bu nedenlerle, albümin uzun yıllardır çeşitli yöntemlerle saflaştırılmakta veya kan ortamından uzaklaştırılmaktadır. Saflaştırma ve ayırma yöntemleri arasında en sıklıkla kullanılan yöntem afinite kromatografisidir. Afinite kromatografisi, belli bir moleküler yapıya ve yönlenmeye sahip immobilize ligand ve hedef molekül arasındaki seçici, spesifik ve tersinir etkileşimlere dayanan bir ayırma yöntemidir. Afinite kromatografisi, immobilize metal şelat afinite yöntemlerinden boya afinite kromatografisi, afinite kapiler elektroforez afinite çöktürme ve afinite membranlara kadar birçok alanda kullanılan yöntemlerin başında gelmektedir. Boyar madde Cibacron Blue (CBD) ise boya

afinite kromatografisinde en çok kullanılan boya ligandlardan birisidir. HSA saflaştırılması için CBD çok uyumlu bir boya liganddır. Ancak, CBD boya ligand içeren birçok afinite uygulaması olmasına rağmen, CBD ve HSA arasındaki etkileşimin bilgisayarlı ortamda incelendiği çok fazla araştırma bulunmamaktadır. Bu kapsamdaki tez çalışmasında, CBD ve HSA arasındaki etkileşimin değerlendirilmesi için moleküler kenetlenme yazılımı AutoDock kullanılmıştır. CBD ile yapılan moleküler kenetlenme çalışmaları, altı farklı konformasyonda CBD ve HSA arasında bir etkileşim olabileceğini ve HSA'nın farklı bağlanma bölgelerine ulaşabileceğini göstermiştir. Altı farklı konformasyonun bağlanma serbest enerjileri hesaplanmıştır. CBD'nin en uygun konformasyonunda ve enerjetik olarak en istenir sonuç, konformasyon 5 için belirlenmiştir.

Anahtar Kelimeler: Cibacron Blue, Human Serum Albumin, Moleküler Bağlanma, AutoDock Yazılımı

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I must express my heartfelt gratitude to my mother; with her generous support I overcome the obstacles in my life, and if my father processed his umwelt like in his old days, I believe that he would be proud as well.

Lastly, as in the words of Mustafa Kemal ATATÜRK, "Science is the most real guide for civilisation, for life, for success in the world. To search for a guide other than science is absurdity, ignorance and heresy."

Thank you all; unmentioned friends, colleagues, scientists for being in my life.

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SYMBOLS & ABBREVIATIONS

Abbreviations

BS1	Binding Site 1 of HSA
BS2	Binding Site 2 of HSA
BS3	Binding Site 3 of HSA
CBD	Cibacron Blue F3GA
HSA	Human Serum Albumin
PDB	Protein Data Bank
GUI	Graphical User Interface
MMTK	The Molecular Modeling Toolkit
UCSF	University of California, San Francisco
MD	Molecular Dynamics
MM	Molecular Mechanics
ADT	AutoDockTools
GA	Genetic Algorithm
Min	Minimization command
DockPrep	Dock preparation command
LBE	Lowest Binding Energy
MBE	Mean Binding Energy
Conf	Conformation
3D	Three-dimensional

1.INTRODUCTION

Human plasma contains a vast amount of human serum albumin (HSA). Almost 60% of human plasma protein contains HSA. Blood volume regulation based on colloid osmotic pressure is a vital role of serum albumins. In order to hide their hydrophobic nature, they can be seen transferring some low water-soluble molecules. These molecules consisted of some steroid hormones, some salts, free fatty acids, calcium, and some drugs. Hence there is rivalry amongst drugs for albumin binding sites. This situation affects the strength of the binding process. Low or high level of albumin almost always caused several diseases. Besides, albumin should be removed from blood plasma in some cases, since high abundancy of albumin hinders biomarkers in proteome studies.

A standard method for protein purification and separation studies is affinity chromatography due to its specificity, selectivity. There are several affinity chromatography methods, such as dye affinity, immobilized metal chelated affinity, and affinity electrophoresis. Among these, dye ligand affinity chromatography is one of the most common methods for protein purifications since it binds to macromolecules to be explicitly separated and reversibly. For a feasible scenario for HSA purification, Cibacron Blue F3GA is a relatively more available dye, which was an adsorbent built upon a sulfonated triazine structure of a dye, also usable in low purity conditions. Although CBD has many albumin purification applications, there is not much research focused on identifying the molecular interaction between CBD and HSA in molecular simulation.

Computational techniques strengthen their position because they are offering such results beyond experimental possibilities for areas such as functional site location, comparative modeling, binding site recognition in proteins, protein-ligand docking as well as protein-protein docking, and molecular dynamic.

Molecular docking is basically a method based on the journey to a stable complex via interaction of two or more molecules. Such complex's 3D structure can be computed with the usage of algorithms via binding properties of ligand and protein. The ability of interaction of such protein with small molecules is crucial in which

resultant dynamics could change for the favor of enhancement or inhibition of its biological function.

In this thesis, AutoDock v4.2.6 was used for docking ligands to identify active locations for specific targeting of binding sites on target proteins. UCSF Chimera software was used for minimization of structures then preparation for docking. This process minimizes the energy of molecule models. In order for the process to succeed, some atoms could be held fixed. For the source of the protein structure, ProteinDataBank (PDB) was used via UCSF Chimera. All conformations of CBD had a 10 run of GA with 150 as population size and 27000 maximum number of generations.

2.GENERAL INFORMATION

2.1.Albumin

Distinct properties of albumin, which was not a well-known protein at the time, recognized by Professor Ansell in 1839, had essential bodily purposes. In the Lancet he said, "albumen is doubtless one of the most important of the animal proximate principles; it is found not only in the serum of the blood but in lymph and chyle, in the exhalations from serous surfaces, in the fluid of cellular tissue, in the aqueous and vitreous humours of the eye, in many other animal fluids, albumin acts sometimes as an acid and a base and its powers of maintaining its combinations is so great albumin proportions are pretty nearly the same in all higher animals, the levels are nearly the same in the sexes and between the ages of 20 and 80". Therefore, for over 180 years, we have become known of some highly accurate description of serum albumin properties [1].

HSA has a single, polypeptide chain, which is non-glycosylated, containing amino acid residues with a total of 585. It has an amino-acid order which incorporates 17 disulfide bridges, consisting of Cys 34 and Trp 214. The other structural distinction of HSA is a unique pattern of double ribbons. Disulfide bridges hold jointly said loops [2]. HSA incorporates electrostatically different three massive domains, charge-pH properties, and denaturability. Figure 2.1 illustrates the three-ball and a container shape with amino acid order folding pattern and size of HSA [3]. There are three domains called DI for Domain I, DII for Domain II, and DIII for Domain III can be seen in Figure 2.1 from N terminal to C terminal, from left to right respectively. Each domain has its merits. Domain III has two high-affinity attachment sites mainly for fatty acid. However, Domain I and Domain II has central sites. Both situations remarkably increase conformational stability [3].

Human plasma contains a vast amount of HSA. Almost 60% of human plasma proteins consist of HSA. If immunoglobulin was counted, the total amount jumps to 80%. HSA can be found in tissues and some other parts in the body. HSA has a wide variety of physiological functions. Furthermore, it contributes significantly to colloid osmotic blood pressure in-vivo. Plus, HSA can be used to convey and

allocate many chemically diverse substances [4]. Those molecules have a very wide range of possibilities. Such as amino acids like cysteine, tryptophan, and tyrosine; bile acids, bilirubin, and long-chain fatty acids and hormones like aldosterone, cortisol, and testosterone are also among those substances. Accordingly, one must add metal ions like copper, calcium, chloride, magnesium, zinc, and several pharmaceuticals to the list as well [5].

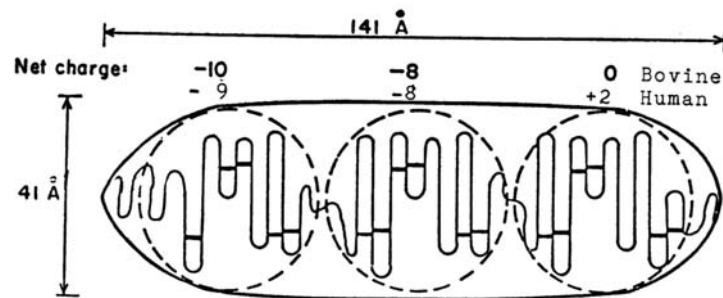


Figure 2.1. Three major domains accompanied by a disulfide-bonded alpha-helical subdomain of HSA are shown in the three-ball model [3].

2.2. Dye-Ligand Affinity Chromatography

In order to acquire purified proteins, there are several techniques to choose on. Yet dye-ligand affinity chromatography is increasingly valuable and a comparatively advantageous technique [6]. Table 2.1 shows some of the advantages. The triazine scaffold containing dyes have specific binding abilities [7-9]. Although all dyes are synthetic their classification of pseudo-specific affinity ligands doesn't change. In particular such dyes use mimicry while binding to proteins [10].

In contrast, commercially available dyes are not well equipped for usage right away; instead, they tend to have some various impurities which needed to be purified via chromatographic techniques [12, 13]. However, those techniques are necessary, only when immobilized dyes are used. Consequently, a small number of contaminants would be immobilized on the matrix, and they would be gone after washing [14-16].

Table 2.1. List of advantages of reactive dyes [11].

Economically and universally accessible
Immobilization efficiency
Avoids hazardous and toxic reagents in matrix activation
Stable against biological and chemical attack
Storage of matrix without activity loss
Reusable, withstand cleaning and sterilization
Ease of scaling
High capacity
Medium specificity

2.3.Magnetic Affinity Separation

Isolation and purification of enzymes from various biological sources is a crucial part of enzymology. Protein purification process generally a four-stage process, namely; recovery, concentration, purification, and formulation; hence, each have different objectives. Study of separation procedures enabling to obtain pure or substantially purified enzymes is significant. Production costs of proteins is a setback in some cases because they tend to carve out 30 – 80% of costs alone [17]. Advanced separation techniques are a necessity. Such techniques should be capable of treating solutions containing target enzyme(s) regardless of some small impurities and in the presence of large quantities of accompanying proteins and other low and high molecular weight compounds via both comprehensive and straightforward processes.

In biochemistry and biotechnology, target enzymes isolation is customarily carried out using all sorts of techniques like chromatography, electrophoretic, ultrafiltration, precipitation [18]. Among them, affinity chromatography is one of the most vital technique; which has a vast amount of successful laboratory scale applications in its inventory. Nonetheless, the main drawback of standard column affinity chromatography is the impossibility to handle samples containing

contaminating particulate material. Affinity chromatography does not work with contaminated materials or materials that have not already been purified. For these kinds of purposes, if a successful result is desired, a batch separation process for magnetic affinity adsorption can be used.

Magnetic separations represent extremely versatile separation processes enabling to isolate and purify peptides, proteins, nucleic acids, cells, viruses, environmental contaminants, and other target molecules directly from crude samples. Batch magnetic affinity separation of target enzymes can be performed straightforwardly and rapidly, with not many handling steps. The whole process of the enzyme purification method can be performed in a single test tube. Immobilized affinity ligand carrying magnetic carriers as well as magnetically responsive biopolymer particles having an affinity for the isolated enzyme or specifically designed magnetic molecularly imprinted polymer particles are mixed with an appropriate enzyme source. The separation process, which is usually very gentle to the target enzyme(s), can be carried out straight in impure samples. Such impurities have suspended solid material. Column chromatography techniques have the ability to broke up big protein complexes if magnetic separation techniques have been carefully established. Magnetic techniques can also be used for enzyme concentration from diluted solutions. In connection to magnetic properties of magnetic adsorbent substances, they can be selectively separated from such sample comparatively with ease. Whole blood, plasma, urine, milk, whey, food waste, and numerous other materials can be used to isolate target enzymes. However, the binding process does not occur right away. There is an incubation period to think of. Finally, magnetic particles and targets are bound after such a process. A magnetic separator is all that is needed for the removal of the complex with ease [19,20]. In addition to laboratory scale separations, these techniques can also find applications in larger-scale processes [21,22]. Several alternative approaches, such as separation in fluidized beds, which are already magnetically stabilized [17,23], or magnetic two-phase systems [24] were described.

Typical examples of published purification procedures document the effectiveness of magnetic affinity separation techniques. Recently published review papers on similar topic present up-to-date applications of magnetic separation procedures

and document continuing the importance of this experimental approach [17,25-29].

2.3.1. Materials and Apparatus

It is a straightforward process to use magnetic separators and do experiments. Rare-earth magnets such as NdFeB are the go-to choice for magnetic separators since they are widely available from a variety of sources worldwide. Commercial laboratory scale separators have disinfectant-proof materials as a difference from their consumer counterparts. On the other hand, racks have to accommodate different types of vessels. In order to separate larger volumes such as 500 – 1000 mL, flat ones are more appropriate.

Large volume magnetic separation systems for bottles of different volumes can be successfully used for both batch and flow-through magnetic separations [30]. A review paper put on word for separating magnetic particles with a diameter of ca 1 μm or larger [19]. Separation of nanoparticles and sub-micrometer sized particles possibly necessitate the involvement of other separators. Such need can be overcome with the usage of high gradient magnetic separators use steel balls or wool-packed columns. Columns later separated from the magnetic field, in order to particles to be retained in the matrix. A gentle vibration is nice to have [19,31].

Appropriate magnetically responsive affinity materials are used to capture the target enzyme from its source. Commercial [17,29] or laboratory prepared [29,32] magnetic materials are available in the market. That kind of materials can be seen in the market as magnetic particles. Such particles have been produced from various synthetic polymers (e.g., polystyrene), biopolymers (e.g., cellulose, chitin, chitosan, dextran), porous glass, or silica. Alternatively, such particles could be based on surface-modified (silanized) iron oxide (magnetite, maghemite, or ferrites) can be used. Magnetic particles usually carry appropriate functional groups (e.g., amino, carboxyl or thiol ones), which enable subsequent affinity ligand immobilization. Besides, activated magnetic particles are already obtainable from the market, which in turn enable direct binding of affinity ligands.

The breadth of magnetic particles mostly differs from ca 50 nm to approximately 10 μm [17, 19,33]. Nevertheless, millimeter range diameter having particles are

not impossible either [34]. Ideal properties of a magnetic adsorbent good enough for bioseparation proposes to comprehend a high binding capacity, low non-specific binding, and physicochemical robustness [29].

2.3.2. Magnetic Affinity Separation of Proteins

One of the two mainly used methods for magnetic affinity separation is the direct method. In this direct method, magnetic affinity adsorbent is added to the sample, which causes a tendency for binding of target compounds. Another method is the indirect method. However, in this method, the sample is being added a free affinity ligand. This action makes it possible for the target compound to interact with the ligand. As a result, magnetic particles catch the final complex. In both methods, magnetically separated and washed particles have been used, and then the target compounds are eluted. If ligands and the target do not have high affinity, the indirect method can also be used [19].

As stated above, magnetic affinity separation of enzymes is usually based on the interaction of the target enzyme(s) with an appropriate affinity ligand bound to the magnetic carrier. Useful inspiration for how to find an appropriate affinity ligand-target enzyme combination can be found in standard affinity chromatography. Typical affinity ligands comprehend natural and synthetic enzyme inhibitors (Table 2.2), reactive organic dyes (Table 2.3) and many other molecules such as substrates, antibodies, affitins, aptamers, chelated heavy metal ions, synthetic peptides, amino acids, drugs and some others (Table 2.4). Many procedures are available for binding the specific affinity ligand to an appropriate magnetic carrier; e.g., magnetic supports bearing amino groups can be easily activated by glutaraldehyde to enable binding of amino groups containing molecules. Alternatively, magnetically modified biopolymers such as chitin, chitosan, starch, alginate, or lignocellulose can be used for the same purpose (Table 2.5). A simple magnetic modification of affinity adsorbents used for standard affinity chromatography (e.g., by magnetic fluids) can be employed for magnetic affinity adsorbents preparation [35]. For large scale purification processes usually cost-effective and robust synthetic affinity ligands including synthetic triazine dyes like CBD are predominantly used due to their particularly selective behavior for binding

with most proteins. Triazine dyes also show resistance to chemical and biological degradation.

Recently the production of recombinant proteins in a highly purified and well-characterized form has become an important task. The fusion proteins contain an appropriate affinity tag structure enabling single-step adsorption purification with a very little effect on the tertiary structure and biological activity and its smooth and distinct removal to help produce the native protein. Fusion tags with different sizes and biochemical properties have been constructed with respectable quantities; depending on their applications and biochemical properties, fusion tags are categorized into a number of groups (which may overlap with each other), including affinity fusion tags, fluorescence protein tags, enzyme tags, protein tags, peptide tags and epitope tags [36]. The most often used histidine-tagged (His-tag) proteins are usually magnetically separated with the particles having nitrilotriacetic acid or $N\alpha,N\alpha$ -Bis(carboxymethyl)-L-lysine hydrate ligands loaded with nickel or cobalt ions [25]. Typical examples of successful magnetic separation of recombinant enzymes are presented in Table 2.6.

In order to generate specific binding sites, one could use molecular imprinting as a way of achieving effectiveness. With this method, highly specified molecularly imprinted polymers (MIP) can be acquired. This type of process is highly advantageous to the natural process of generating receptors like antibodies. To date, different kinds of MIPs have been successfully developed for the separation of small molecules. On the other hand, MIP preparation for biomacromolecules, including enzymes, is not an easy task; entrapment of protein molecules in a polymer network and their subsequent removal is a problematic step [37]. Currently, mainly lysozyme is used as the enzyme template for the construction of magnetically responsive molecularly imprinted polymers; typical examples of lysozyme separation are presented in Table 2.7.

As shown in Tables 2.2 to 2.7, magnetic affinity separations of target enzymes have been successfully presented in many various papers. There is no simple strategy to isolate target enzymes; various approaches have been tested to obtain a purified enzyme. The data in the following tables can serve as an inspiration for

a broad scientific and technological community with the possibility to implement magnetic technologies into their experimental work in order to improve the conventional procedures.

Table 2.2. Examples of enzymes purified with magnetically responsive materials bearing natural or synthetic enzyme inhibitors.

Enzyme (Purified)	Main Source	Magnetic carrier	Inhibitor	Additional details	References
Aminopeptidase	<i>Arabidopsis</i>	Amine-terminated magnetic beads	N-1-Naphthylphthalamic acid	KCl gradient elution	[38]
Gastric aspartic protease	Rat gastric mucosa	Magnetic glyoxal 4% agarose beads	Synthetic heptapeptides containing D-amino acid residues	Elution with acetate and phosphate buffers containing 20% 2-propanol	[39]
Nattokinase	<i>Bacillus natto</i>	Magnetic poly(methyl methacrylate) beads	p-Aminobenzamide	Eluted by 0.1 M ammonium acetate buffer (pH 4.0)	[40]
Pepsin	Human gastric juice, rat gastric mucosa	Magnetic glyoxal agarose beads	Synthetic heptapeptide containing D-amino acid residues	Eluted by 20% acetonitrile in 0.1 M acetate buffer (pH 3.5)	[41]

Enzyme (Purified)	Main Source	Magnetic carrier	Inhibitor	Additional details	References
Protease (Savinase)	<i>Bacillus clausii</i>	Silanized magnetite nanoparticles	Bacitracin	High gradient magnetic separation used	[42]
Protease	<i>Bacillus licheniformis</i>	Silanized magnetite particles	Bacitracin	Semi-continuous <i>in situ</i> magnetic separation used	[43]
Protease	<i>Bacillus licheniformis</i>	Silanized magnetite particles	Bacitracin	High gradient fishing used	[44]
Subtilisin	Commercial preparation	Magnetic carrier bearing epoxy groups	Benzamidine	Elution at pH 6 (0.1 M of glycine-HCl buffer)	[45]
Trypsin	Porcine pancreatin	Silanized magnetic particles	Benzamidine	High gradient magnetic separation	[31]
Trypsin	Bovine pancreas	Magnetic poly(glycidyl methacrylate-co-methylmethacrylate) beads	p-Aminobenzamide	Separation in magnetically stabilized fluidized bed reactor	[23]

Enzyme (Purified)	Main Source	Magnetic carrier	Inhibitor	Additional details	References
Trypsin	Commercial preparation	Magnetite and magnetic chitosan particles	Soybean trypsin inhibitor	Batch stirred tank, and magnetically stabilized fluidized bed operations tested	[46]
Trypsin	Commercial preparation	Submicron ferrite particles	Soybean trypsin inhibitor	Trypsin recovered from casein solution after its hydrolysis	[47]
Trypsin	Commercial preparation	Magnetic chitosan particles	Aprotinin	Eluted by acetic acid including KCl solution	[48]
Urokinase	Crude preparation	Magnetic dextran microspheres	p-Aminobenzamide	Comparison with other affinity ligands	[49]
Urokinase	Crude preparation	Magnetic agarose microspheres	p-Aminobenzamide	Comparison with other affinity ligands	[50]

Table 2.3. Examples of enzymes purified with magnetically responsive materials bearing reactive dyes.

Enzyme (Purified)	Main Source	Magnetic carrier	Dye	Additional details	References
Alcohol dehydrogenase	Baker's yeast homogenate	Magnetic cross-linked polyvinyl alcohol	Cibacron blue F3GA	Eluted by phosphate buffer (pH 7.9) in 2 μ M 2-mercaptoethanol and 1.0 M NaCl	[51]
Alcohol dehydrogenase	<i>Saccharomyces cerevisiae</i>	Magnetic poly(HEMA) nanoparticles	Reactive Green 19	Eluted by 1 M NaCl	[52]
Cellulase	Cow's rumen fluid	Polymer grafted magnetic nanoparticles	Cibacron Blue F3GA	Eluted by 1 M NaCl	[53]
Lactate dehydrogenase	Porcine muscle	Magnetic agarose beads	Reactive Red 120	Eluted by NaCl, gradiently	[54]
Lysozyme	Commercial preparation	Magnetic cross-linked polyvinylalcohol	Cibacron blue 3GA	Eluted by 1 M NaCl	[51]
Lysozyme	Commercial preparation, chicken egg white	Magnetic poly(2-hydroxyethyl methacrylate) beads	Cibacron Blue F3GA	Eluted by 0.1 M Tris/HCl buffer in 0.5 M NaCl	[55]
Lysozyme	Commercial preparation, chicken egg white	Magnetic chitosan microspheres	Reactive Red 120	Eluted by phosphate buffer in 1M NaCl (pH 6.0)	[56]

Enzyme (Purified)	Main Source	Magnetic carrier	Dye	Additional details	References
Lysozyme	Commercial preparation	Magnetic poly(2-hydroxyethyl methacrylate) beads	Cibacron blue F3GA	Eluted by 1.0 M KSCN (pH 8.0)	[57]
Lysozyme	Commercial preparation	Magnetic agarose beads	Cibacron blue 3GA	Separation in a liquid magnetically stabilized fluidized bed	[58]
Lysozyme	Commercial preparation	Chitosan modified magnetic fluid	Cibacron Blue 3GA	Adsorption isotherm expressed by the Langmuir adsorption model	[59]
Phytase	Cow's rumen fluid	Polymer grafted magnetic nanoparticles	Cibacron blue F-3GA	Eluted by 1 M NaCl	[60]

Table 2.4. Examples of enzymes purified with magnetically responsive materials bearing specific affinity ligands.

Enzyme (Purified)	Main Source	Magnetic carrier	Affinity ligand	Additional details	References
Alkaline phosphatase	Hen's egg yolk	Six different types of magnetic nanocarriers with varying lengths of the linkers	Arsanilic acid	Eluted by 0.01M Tris/HCl buffer (pH 8.4) in 2.5 mM MgCl ₂ and 20 mM Na ₃ PO ₄ .12H ₂ O	[61]

Enzyme (Purified)	Main Source	Magnetic carrier	Affinity ligand	Additional details	References
Amylase	<i>Tilapia</i> intestine	Epichlorohydrin modified superparamagnetic particles	Soluble starch	Eluted by phosphate buffer (pH 7.0) in 1 M NaCl	[62]
Asparaginase	<i>E. coli</i> homogenate	Magnetic polyacrylamide gel particles	D-Asparagine	Eluted by D-asparagine solution	[63]
Cellulase	<i>Trichoderma viride</i>	Silica modified magnetite nanoparticles	Aminophenyl-boronic acid	Eluted under acidic conditions	[64]
Dehydrofolate reductase	HeLa cells cytoplasmic fraction	40 nm magnetite particles/ poly(styrene-co-glycidyl methacrylate (GMA))/ poly(GMA)	Methotrexate	Eluted by SDS-PAGE loading	[65]
Deoxycytidine kinase	THP-1 cells cytoplasmic fraction	40 nm magnetite particles/ poly(styrene-co-glycidyl methacrylate (GMA))/ poly(GMA)	Methotrexate	Eluted by SDS-PAGE loading	[65]
β -Galactosidase	<i>E. coli</i> homogenate	Silanized magnetite	p-Aminophenyl- β -D-thiogalactopyranoside	Eluted by borate buffer (pH 10)	[63]

Enzyme (Purified)	Main Source	Magnetic carrier	Affinity ligand	Additional details	References
Lysozyme	Chicken egg white	Silica coated magnetic particles	Anti-lysozyme affitin	Eluted by 100 mM glycine-HCl buffer, 0.15 M NaCl (pH 2.5)	[66]
Lysozyme	Chicken egg white	Magnetic poly(glycidyl methacrylate) [m-poly(GMA)] beads	L-tryptophan	Eluted by 0.1 M methylene glycol solution	[67]
Nattokinase	Natto powder	Carboxyl modified iron oxide nanoparticles	Arginine	Langmuir isotherm followed during the enzyme adsorption	[68]
Paraoxonase 1 (aryldialkylphosphatase)	Human serum	Magnetite nanoparticles with bound p-aminohippuric acid	Cholesterol	Eluted by sodium deoxycholate	[69]
Peroxidase	Horseradish	Silica coated magnetite particles	4-vinylphenyl-boronic acid	The particles have a high affinity for glycoenzyme	[70]
RNase B	Bovine	Carboxyl-functionalized magnetic beads	Concanavalin A	Elution performed under acidic conditions	[71]
RNase B	Bovine	Carboxyl-functionalized magnetic beads	Phenylboronic acid	Elution performed under acidic conditions	[71]

Enzyme (Purified)	Main Source	Magnetic carrier	Affinity ligand	Additional details	References
RNase B	Bovine	Carboxyl-functionalized magnetic beads	Aminophenyl-boronic acid	Bound enzyme used for (MALDI-TOF-MS).	[72]
Subtilisin	Commercial preparation	Magnetic carrier bearing epoxy groups	Phenylboronic acid	Eluted by 0.1 M ammonium acetate (pH 6) in 0.05 M MgCl ₂	[45]
Trypsin	Nile tilapia (<i>Oreochromis niloticus</i>)	Magnetic particles coated with polyaniline, activated with glutaraldehyde	Azocasein	Eluted by 3M NaCl	[73]

Table 2.5. Examples of enzymes purified by magnetically modified polysaccharides.

Enzyme (Purified)	Main Source	Magnetic affinity absorbent	Additional details	References
Amylase	<i>Bacillus megaterium</i>	Starch functionalized magnetic nanoparticles	12.5-fold purification obtained	[74]
α -Amylase	<i>Bacillus amyloliquefaciens</i>	Magnetic alginate microspheres	9-fold purification obtained	[75]
α -Amylase	Porcine pancreas	Magnetic alginate microspheres	12-fold purification obtained	[75]
α -Amylase	Wheat germ	Magnetic alginate beads	1 M maltose used for elution; 48-fold purification obtained	[34]

Enzyme (Purified)	Main Source	Magnetic affinity absorbent	Additional details	References
β -Amylase	Sweet potato	Magnetic alginate beads	1 M maltose used for elution; 37-fold purification obtained	[76]
Chitinase	<i>Euphorbia characias</i>	Chitin modified with microwave synthesized magnetic iron oxide particles	Complex enzyme characterization	[77]
Chitinase	<i>Euphorbia characias</i>	Chitin modified with microwave synthesized magnetic iron oxide particles	Tested as a novel and powerful plant-based pesticide against <i>Drosophila suzukii</i>	[78]
Cyclodextrin glucanotransferase	<i>Bacillus circulans</i>	Magnetic porous corn starch	CGTase recovery 60 – 70%; purification factor 19 – 25	[79]
Glucoamylase	<i>Aspergillus niger</i>	Magnetite alginate beads	1 M maltose used for elution; 31-fold purification obtained	[76]
Lysozyme	Hen egg white	Magnetically modified chitin	Comparison with magnetic agar and agarose	[80]
Lysozyme	Hen egg white	Magnetically modified chitin	The capacity was 2.5 mg of lysozyme per 1 mL of sorbent	[81]
Lysozyme	Hen egg white	Ferrofluid modified lignocellulose (spruce sawdust)	Eluted by 0.5 M NaCl	[82]
Lysozyme	<i>Ornithodoros moubata</i>	Magnetic chitin prepared from magnetic chitosan after acetic anhydride conversion	Lysozyme had a pI near 9.7 and pH optimum in the range between pH 5-7	[83]

Enzyme (Purified)	Main Source	Magnetic affinity absorbent	Additional details	References
Pectinase	<i>Aspergillus niger</i>	Alginate magnetite beads	Eluted by distilled water (pH 5.9) in 0.5 mM CaCl ₂	[84]
Pullulanase	<i>Bacillus acidopullulyticus</i>	Magnetite alginate beads	1 M maltose used for elution; 49-fold purification obtained	[76]

Table 2.6. Examples of recombinant enzymes purified with specifically designed magnetically responsive materials.

Recombinant Enzyme (Purified)	Main Source	Magnetic carrier	Affinity ligand	Additional details	References
Aldolase (histidine-tagged)	Pea (expressed in <i>E. coli</i>)	Magnetic kernel and nickel-silica composite matrix	Ni ²⁺	Eluted by imidazole including buffer	[85]
Arginine kinase (histidine-tagged)	Expressed in <i>E. coli</i>	Bifunctional Au-Fe ₃ O ₄ nanoparticles modified with nitrilotriacetic acid	Ni ²⁺	Eluted by imidazole solution	[86]
Carbonyl-reducing enzymes	Human (expressed in <i>E. coli</i>)	Commercial magnetic particles (SiMAG-NH ₂ , SiMAG-COOH, Perloza MG)	Oracin	Eluted by buffer 0.16% NH ₄ OH and 10% glycerol (pH 10)	[87]

Recombinant Enzyme (Purified)	Main Source	Magnetic carrier	Affinity ligand	Additional details	References
Cellulase (histidine-tagged)	<i>Clostridium cellulolyticum</i> (expressed in <i>E. coli</i>)	Fe ₃ O ₄ /(poly (N,N'-methylenebisacrylamide-co-glycidyl methacrylate)) microspheres bearing iminodiacetic acid	Ni ²⁺	Eluted by imidazole solution	[88]
CMP-Sialic acid synthetase (chitin binding domain-tagged)	Expressed in <i>E. coli</i>	Chitin modified magnetic nanoparticles	Water soluble chitin	Eluted by 80 mM 1,4-dithiothreitol	[89]
Endo-β-1,4-xylanases (histidine-tagged)	<i>Fusarium graminearum</i> (expressed in <i>E. coli</i>)	Ni-NTA magnetic agarose beads	Ni ²⁺	Study of enzyme inhibition	[90]
Esterase (histidine-tagged)	<i>Pseudomonas fluorescens</i> (expressed in <i>E. coli</i>)	MagneHis Ni particles	Ni ²⁺	Automated microscale purification	[91]
β-Glucuronidases	<i>Penicillium purpurogenum</i> Li-3 (expressed in <i>E. coli</i> BL21)	Carboxyl modified magnetic beads	Aptamers	Eluted by NaCl (>330 mM)	[92]
Helper component-proteinase (maltose-binding protein-tagged)	<i>Zucchini yellow mosaic virus</i> (expressed in <i>E. coli</i>)	Amylose magnetic beads	Amylose	Eluted by MPB-buffer in 10 mM maltose	[93]

Recombinant Enzyme (Purified)	Main Source	Magnetic carrier	Affinity ligand	Additional details	References
Heparinase I (maltose-binding protein-tagged)	<i>Flavobacterium heparinum</i> (expressed in <i>E. coli</i>)	Fe ₃ O ₄ @SiO ₂ -poly(ethylene oxide)-maltose nanoparticles	Maltose	Adsorbed enzyme used during production of low molecular weight heparins	[94]
Urikase (histidine-tagged)	<i>Bacillus</i> (expressed in <i>E. coli</i>)	Ni ion-chelating magnetic beads	Ni ²⁺	Eluted by cleavage with proteinase K	[95]

Table 2.7. Purified enzymes using molecularly imprinted polymers

Enzyme (Purified)	Main Source	Magnetic affinity absorbent	Additional details	References
Bromelain	Commercial preparation	Magnetic pericarpium granati-derived carbon modified with polydopamine layer in the presence of bromelain in a weak alkaline aqueous solution	Eluted by 2% acetic acid and SDS	[96]
Lysozyme	Egg white	Superparamagnetic lysozyme surface-imprinted polymer synthesized by atom transfer radical polymerization procedure	Eluted by PEG/sulphate aqueous two-phase system	[97]

Enzyme (Purified)	Main Source	Magnetic affinity absorbent	Additional details	References
Lysozyme	Commercial (egg white)	Silica coated Fe ₃ O ₄ nanoparticles coated with MIP film formed from acrylamide and methacrylic acid as co-monomers	Eluted by 0.5 M NaCl	[98]
Lysozyme	Real egg white samples	Magnetic nanoparticles coated with thermoresponsive MIP layer using (N-methacryloyl-L-alanine methyl ester) as the functional monomer and N,N'-methylenebis(acrylamide) as the crosslinker	Eluted by altering the temperature of aqueous solution.	[20]
Lysozyme	Commercial preparation	The imprinted polymers were coated on the surface of silica-coated magnetite nanoparticles by the surface graft copolymerization.	Eluted by 0.5 M NaCl	[99]
Lysozyme	Commercial preparation	Core-shell magnetic chitosan submicrospheres functionalized with maleic acid and then coated with imprinted polymer layers	Eluted by 0.5 M NaCl	[100]
Lysozyme	Egg white	Fe ₃ O ₄ nanoparticles modified with 3-(methacryloyloxy)propyltrimethoxysilane and coated with a polymer film formed by the copolymerization of functional monomer acrylamide, cross-linking agent N,N'-methylenebisacrylamide, the initiator azodiisobutyronitrile, and lysozyme	Elution by 3% (v/v) acetic acid/ 10% (w/v) SDS	[101]
Lysozyme	Human urine	Fe ₃ O ₄ nanoparticles coated with a thin film obtained using lysozyme as a template, methacrylic acid and acrylamide as functional co-monomers, and N,N'-methylenebisacrylamide as a crosslinker	Eluted by 0.5 mM NaCl (pH 13)	[102]

2.4.Computational Approach to Affinity Interactions in Chromatography

The techniques for the separation and purification of macromolecules, such as proteins and enzymes, are improving day by day. It has been an essential requirement for many of the developments made in bioscience and biotechnology over the last decades. Innovations in materials and computerized devices, with the increased use of *in vivo* tagging, have made macromolecules separation processes more predictable and controllable. Therefore, usage of such advanced techniques positively causes a time gain for researchers because they provide an adequate way to purify an enzyme or hormone from a cell extract even before the experimentation.

The fundamental basis of a variety of applications is the understanding of protein-ligand interactions. These kinds of applications cover biopharmaceutical products, innovative studies, medicinal development initiatives, biotechnology goods, molecular target verification, and large scale data analyses like high-throughput screening. In general, ligands interact with specific binding sites of macromolecular targets.

2.4.1.Molecular Modeling and Molecular Docking

Molecular modeling currently is a promising field. It covers a vast amount of possibilities such as building and visualizing molecules in 3D as well as performing complex computer simulations on macromolecules of several proteins. Many software packages make it possible to do molecular modeling. Via those software packages, molecular models can be visualized, rotated, manipulated in 3D, and optimized with several algorithms. Of course, simple calculations can be performed in a few seconds while more advanced and complicated calculations possibly can take weeks or months to complete, even if a supercomputer is involved.

Computational approaches to functional site discovery, comparative modeling, characterization of ligand binding sites in protein-protein or protein-ligand docking arrangements, and molecular dynamics have become more and more significant. Even some results surpass experimental possibilities and provide guidance for

some.

Molecular docking investigates the interaction of two or more molecules, preferably protein-ligand or protein-protein, to provide a stable adduct. It is possible to calculate the 3D structure of any complex based on the interaction properties of proteins and ligands in question with the usage of different algorithms with different approaches. The behavior of this relationship can be illustrated by molecular docking (Figure 2.2).

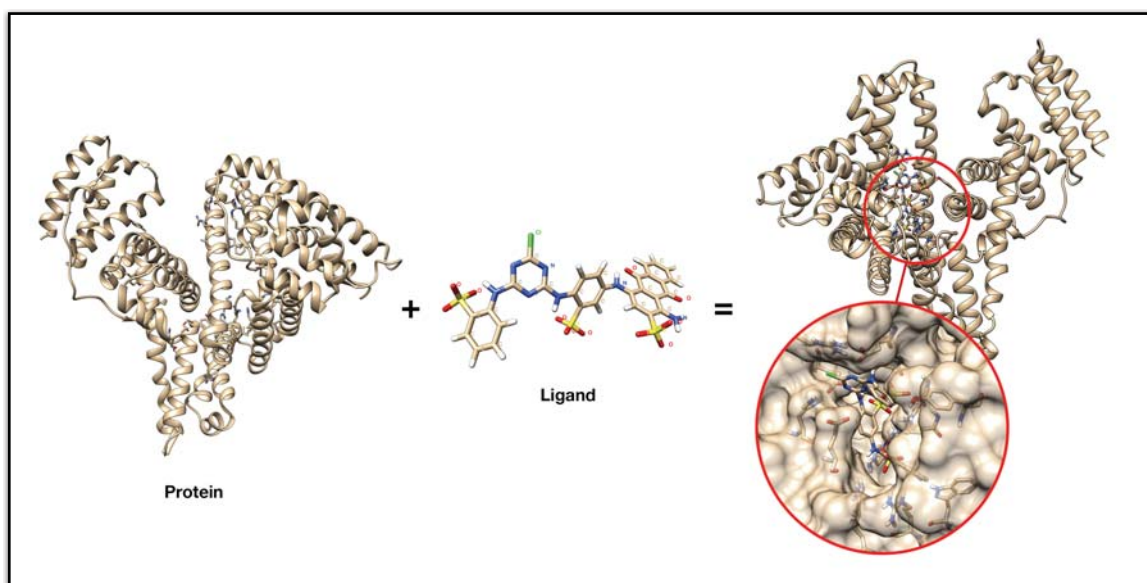


Figure 2.2. Elements in molecular docking. In this example; protein is HSA and ligand is CBD.

There are many possibilities after a molecular docking process completed, but the results are determined and ranked via many parameters using a scoring function in the software package. It is the total energy of the system with differentiating correct binding mode, gives the optimized result of the docked conformation. There are several potential paths; however, tautomerism and ionization based ligand chemistry, the single conformation of the rigid receptor calculation based on receptor flexibility, and scoring function remained the limitations.

Molecular docking is an exciting and continuously developing field which revolves around the potential activity and specificity of ligands and proteins to achieve a stable complex by determining favored binding sites of the protein for which the ligand to bind with [103,104].

The primary goal of molecular docking method is to achieve a ligand-protein adduct with optimum conformation. The net predicted ΔG_{bind} , the binding free energy, is unveiled in terms of several parameters such as hydrogen bond ($\Delta G_{\text{H-bond}}$), torsional free energy (ΔG_{tor}), electrostatic (ΔG_{elec}), desolvation (ΔG_{desolv}), dispersion and repulsion (ΔG_{vdw}), total internal energy (ΔG_{total}) and unbound system's energy (ΔG_{unb}) [105].

2.4.2.Importance of Using Computational Simulation

Molecular docking is primarily a computer simulation between a receptor and a ligand in order to predict interaction based on calculable variables and molecular properties.

A molecule's interaction orientation behaviors and conformational properties are essential when predicting its natural biological activity with a potentially active site. Specific attractiveness and repulsiveness are the basis of molecular recognition in biological practices. The primary purpose of computational simulation is to determine interactions between proteins and ligand via their 3D structural properties. Therefore molecular geometries and affinity properties of molecules are essential for interaction calculation. Also, it is crucial to be aware of the fact that molecular interactions function in an extremely non-additive way.

Fundamental biological processes like cell regulation, antibody-antigen identification, and enzyme inhibition, or signal transduction, transport, gene expression control, and multi-domain protein assembly incorporate important molecular interactions.

Experimental methods often costly and arduous when it comes to ascertaining stable protein-protein or protein-ligand complexes compared to computational molecular interaction calculation. Consequently, computational simulations are admittedly a fruitful solution for gaining knowledge about certain interactions [106-108].

Protein Data Bank (PDB) and the Worldwide Protein Data Bank (wwPDB) have almost a million protein structures. Such structures uploaded by many researchers

around the world created the opportunity for other researchers to tinker with those proteins to pave the way to other important investigations. Such as there are now binary complex structures databases available; in PDDBIND [109], PLD [110], AffinDB [111] and BindDB [112]. As time went by, because of the multiplying studies on proteins from before-mentioned resources, improvements are happening one after another [113].

2.4.3.Applications of Molecular Docking

Molecular docking can be used as a tool for determination the feasibility of an experiment before doing the actual experiment. Hence there are some revolution-like findings where molecular docking is essential. In particular, ligand-protein interaction could possibly foretell the activation or inhibition of an enzyme. Rational drug designing could benefit from such results.

Protein purification is another field where molecular modeling could be of assistance. Determining the interaction among a target macromolecule and separation media provide ample information for efficient purification for the separation systems.

2.5.Software

2.5.1.AutoDock and AutoGrid

AutoDock is a molecular modeling simulation software primarily used for protein-ligand docking procedures for its effectiveness. The latest stable release is v.4.2.6, which was also the version used in this study. It is obtainable via download from its website. AutoDock is developed under GNU General Public License, and by the Scripps Research Institute [114].

AutoDockTools, or ADT for short, is the GUI component of AutoDock which makes it humanly possible to visualize the docking process as well as setting up rotatable bonds in the ligands and easing docking results analysis process.

AutoGrid is a grid calculation module for AutoDock. In the study, v4.2.6 was used

alongside AutoDock with AutoDockTools.

AutoDock helps researchers who study

- X-ray crystallography,
- structure-based drug design,
- lead optimization,
- virtual screening (HTS),
- combinatorial library design,
- protein-protein or protein-ligand docking,
- chemical mechanism research.

2.5.2.UCSF Chimera

UCSF Chimera (or Chimera for short) is a highly extensible library-packed software package, which developed by the UCSF Resource for Biocomputing, Visualization, and Informatics, offers users to visualize interactive solutions and possibility to analyze data of molecular structures and other complementary information, such as density maps, supramolecular assemblies, sequence alignments, docking calculations, trajectories, and conformational ensembles to name a few [115, 116].

The latest stable release is v1.13.1, which was also the version used in this study.

2.5.3.Amber

Amber is a software package that consists of a collection of countless sub-programs that work with each other to arrange, carry out, and examine molecular dynamics simulations. Amber helps the user with input files preparation. It also analyzes the gathered results in a comprehensive way. Amber named after molecular mechanics force fields, primarily modeled for the simulation of biomolecules [117].

2.5.4. Antechamber

Antechamber has a variety of additional modules for molecular mechanic (MM) studies. Antechamber is committed to solving the following problems while doing molecular mechanic calculations: (1) atom type identification; (2) bond type recognition; (2) evaluating the atomic equivalence; (3) residue topology file generation; (4) determining missing force field parameters and providing reasonable and similar substitutes. AmberTools has the Antechamber package as an accessory in its tools' gamut. With AmberTools, Antechamber can produce input automatically for most organic molecules in a database. Said algorithms doing these manipulations are possibly useful for other programs as well as Amber family of programs [118].

2.5.5. MMTK

MMTK which is an abbreviation of The Molecular Modeling Toolkit is an Open Source library. MMTK is used for molecular simulation applications whilst providing standard algorithms based turnkey implementations. While dealing with standard and non-standard issues in molecular simulations, MMTK can serve as a library for helping such situations, and it can be extended and modified [119].

2.6. Molecules

2.6.1. Human Serum Albumin (HSA)

HSA is a vital healing proxy with high demand for the market. Proteins and drugs can be bound to HSA. Consequently, HSA is being monitored for an extensive selection of 64 triazine-based ligands at physiological conditions, being an inspirational figure, its binding and elution from human plasma conditions were neatly optimized [120].

Human plasma contains 30-50 g/l of HSA, which makes it the most available protein in it. HSA also has approximately 20 days of serum half-life [121] as well as osmotic pressure stabilization in veins whilst having a vital delivery job for fatty acids and hormones. Additionally, HSA can increase the circulation time of drug

pharmacokinetics, which is a drug carrier behavior. Meanwhile; hypovolemia, shock, trauma, and surgical blood loss used to be treated by HSA as a healing agent. HSA got its biopharmaceutical potential from being able to be found in different conditions such as a sole compound or a complex with other proteins [122]. The global plasma protein market has its 15% share in HSA, which is well over 20\$ Billion as of 2019 [123].

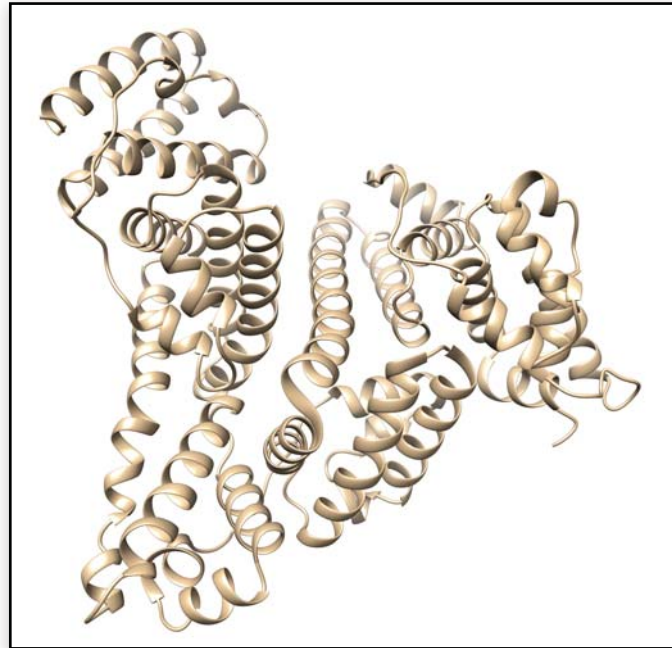


Figure 2.3. HSA ribbon structure

Presently, purification of HSA needs multiple unit operation acts, such as precipitation, heat-shock fractionation [124]. These processes also include ion-exchange chromatography and hydrophobic interaction chromatography as chromatographic methods [125,126].

Affinity chromatography still being used for protein purification regardless it has roots from the 1940s when Cohn first generate a blood surrogate for patients suffering from blood loss [127]. Therefore many affinity-based products are commercially available for the process now.

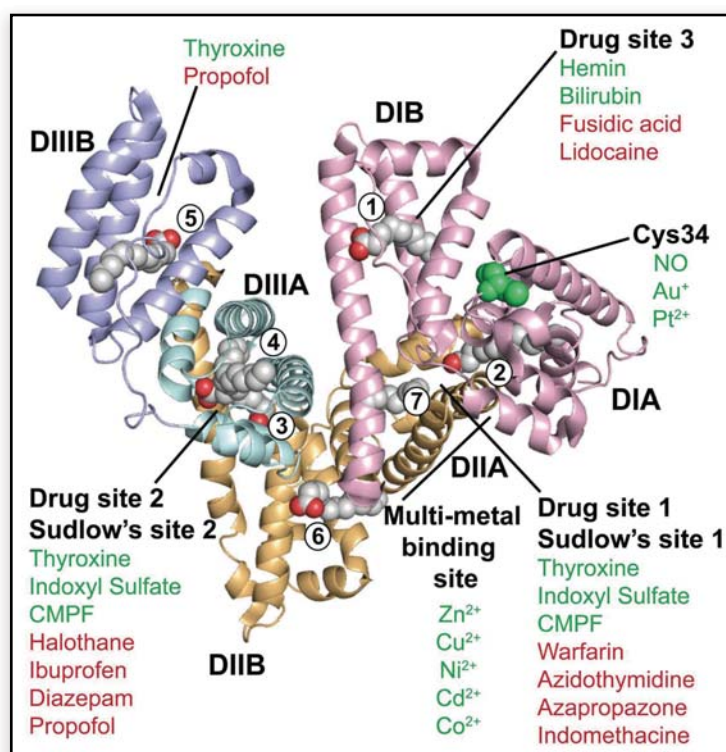


Figure 2.4. The crystal structure of HSA showing drug binding sites.

The clear structure of HSA solved in the saturated palmitic acid can be seen in Figure 2.4. The three domains (DI, DII, and DIII) consisted of α -helical structures. Each domain and consecutively the structures are divided into subdomains (A and B) as indicated in the figure. The fatty acid binding site 1, the free cysteine (C34), and drug binding site 3 constitute the pink-colored domain of Domain I (DI). The other items in the figure colored green and red show endogenous and exogenous ligand binding sites, respectively [128].

2.6.2. Cibacron Blue (CBD)

Cibacron Blue F3GA is a relatively more obtainable substance for HSA purification, which was a sulfonated triazine dye-based adsorbent [129], in which low purity can be yielded by heterogeneous samples [130,131]. The use of triazine structuring drew attention at the end of the 1980s. It offers an advantageous strategy to develop low-priced, stable, and customized novel adsorbents for specific targets [132,133]. In particular, dissimilar ligands with triazine scaffold have been produced for a long time for immunoglobulins [134,135], insulin [136], and viral particles [137].

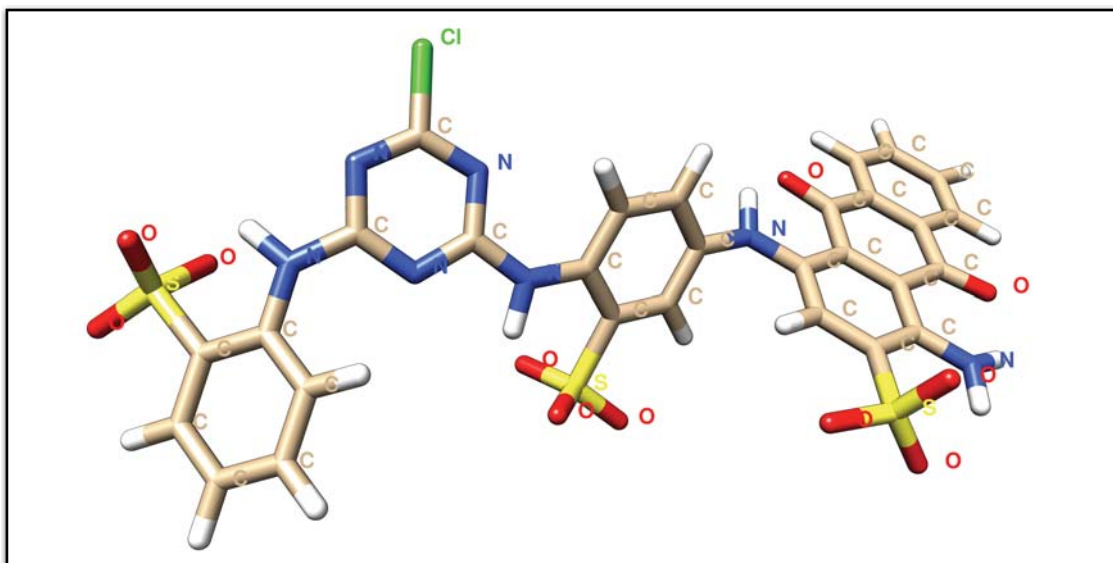


Figure 2.5. Cibacron Blue structure showing elements.

3.EXPERIMENT

3.1.Hardware and Operating Systems

The study was conveyed on an Apple iMac (Retina 5K, 27-inch, Late 2015, model identifier iMac17,1) with 4 GHz Intel Core i7 processor with 64-bit Skylake architecture which has Hyper-Threading enabled 4 cores with 8 threads, 32 GB 1867 MHz DDR3 RAM, 512GB SSD hard drive, and as GPU it has AMD Radeon R9 M395 with 2 GB VRAM. Operating system for the iMac is macOS Mojave (v10.14) which used as the primary system for biocomputing software UCSF Chimera, but for molecular modeling simulation software, AutoDock by the Scripps Research Institute was used on a virtual Microsoft Windows environment via hypervisor software VMWare Fusion v10 with a clean installation of Microsoft Windows 10 x64 (v1809) with 3 processing cores and 6144MB memory setting.

3.2.Softwares

UCSF Chimera is a biocomputing software developed by the UCSF Resource for Biocomputing, Visualization, and Informatics (RBVI). In the study, v1.13.1 (build 41965) was used under macOS Mojave.

AutoDock is a molecular modeling simulation software developed by the Scripps Research Institute. In the study, v4.2.6 was used with the AutoDockTools GUI (Graphical User Interface) component v1.5.6.

AutoGrid is a grid calculation module for AutoDock developed by the Scripps Research Institute. In the study, v4.2.6 was used alongside AutoDock with AutoDockTools.

Amber is a software package that consists of a collection of numerous programs that work as a whole to arrange, carry out, and examine molecular dynamic simulations. Amber libraries were included in Chimera.

Antechamber has a variety of additional modules for molecular mechanic (MM)

studies. Antechamber algorithms were included in Chimera as well.

MMTK is an Open Source library for molecular simulation applications which provided minimization routines for UCSF Chimera.

3.3.Preparation of Macromolecules

In the study;

- UCSF Chimera was used for minimization and dock preparation of ligand and protein structures.
- AutoGrid was used for pre-calculation of grids for the protein-ligand interaction.
- AutoDock was used for performing the docking process of the ligand to the grid of the target protein, in which grid was calculated by AutoGrid.
- AutoDockTools provided the GUI in order to ease the processing with AutoGrid and AutoDock.
- MMTK, the Molecular Modeling Toolkit, was used by Chimera for minimization routines.
- Amber and Amber's Antechamber module used for minimization processes.

3.3.1.Structures from the PDB

3.3.1.1.Cibacron Blue (CBD)

Structure of 1QRD, Cibacron Blue complexed with quinone reductase, FAD, and druoquinone, from the PDB was used as ligand structure source.

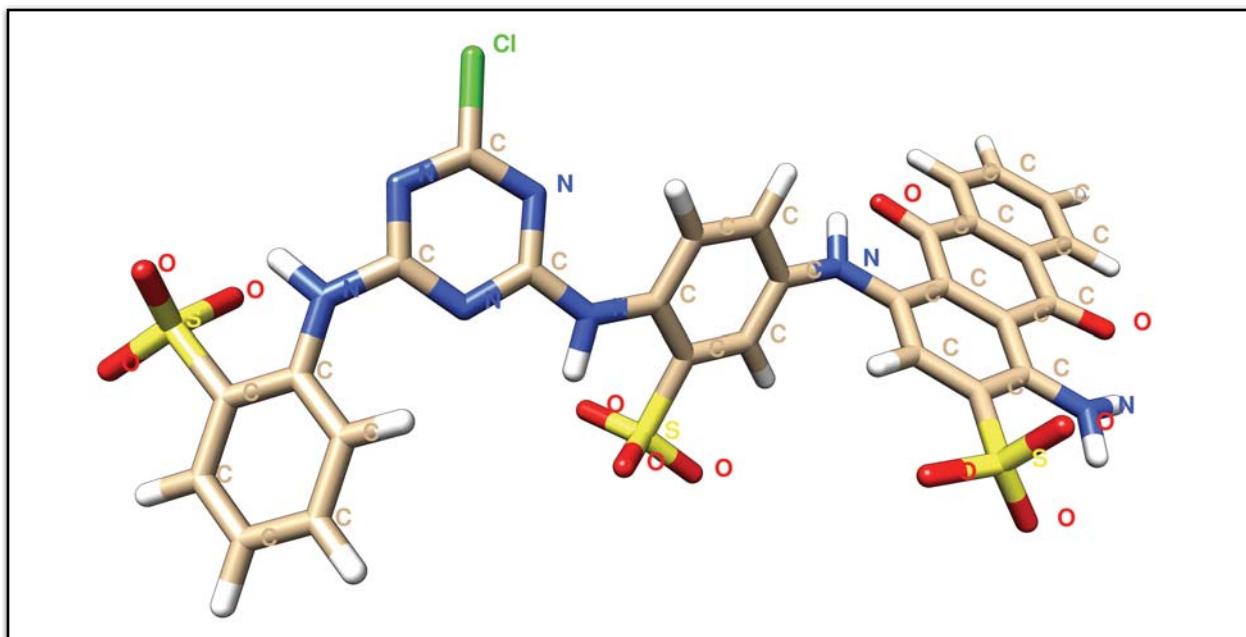


Figure 3.1. Cibacron Blue structure, minimized and prepared for docking.

Figure 3.1 shows the CBD structure generated from 1QRD, consequently minimized and prepared for docking [138].

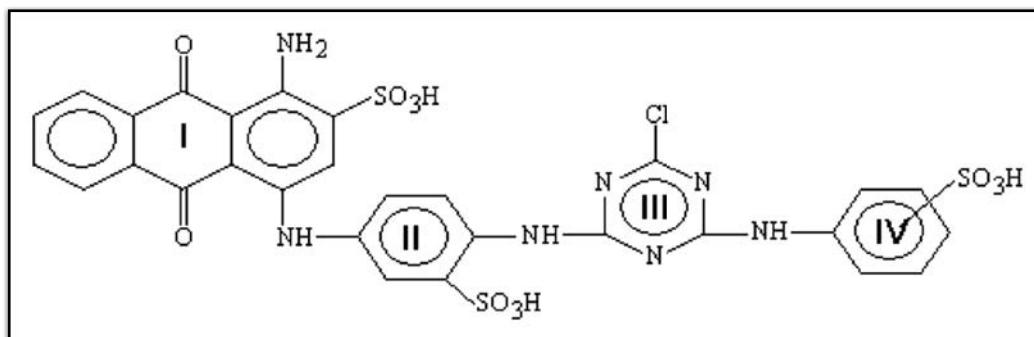


Figure 3.2. Cibacron Blue structure showing active regions [139].

In Figure 3.2, active regions shown as (I) anthraquinone and three (II, III, IV) diazine regions.

3.3.1.2. Human Serum Albumin (HSA)

The main structure for the HSA downloaded as a .pdb file inside UCSF Chimera from the Protein Data Bank (PDB) via entry of 2BXQ, which is human serum albumin complex containing myristate, phenylbutazone and indomethacin was

used as protein structure source.

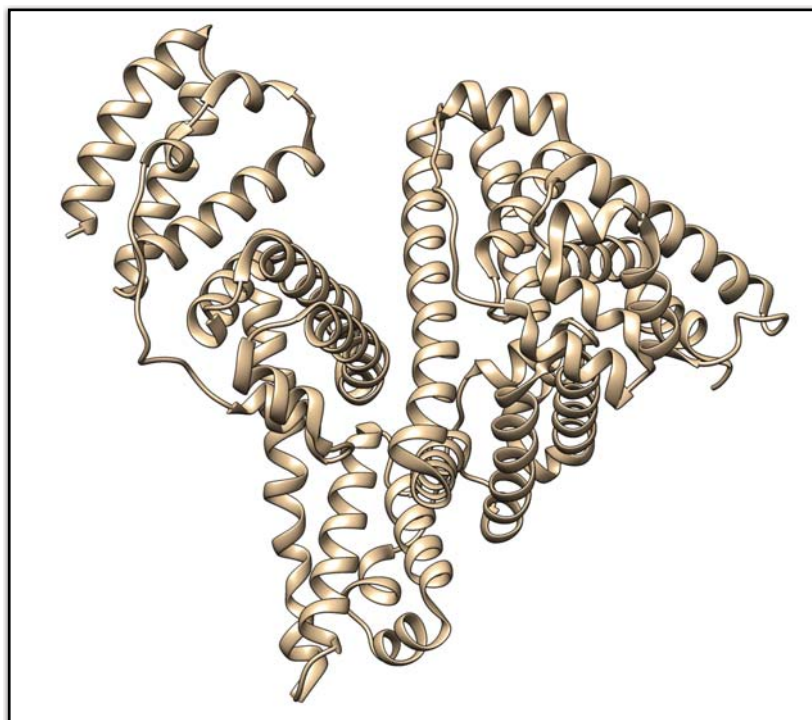


Figure 3.3. HSA structure, minimized, and prepared for docking.

Figure 3.3 shows the HSA structure generated from 2BXQ consequently minimized and prepared for docking [140].

3.4.Minimization and Dock Preparation

UCSF Chimera software was used for minimization of structures then preparation for docking. Minimization command minimizes the energy of molecular models. In some cases minimization command optionally holds some atoms fixed. Minimization procedures are based on MMTK (Molecular Modeling Toolkit) algorithms, which is in UCSF Chimera's repository. For standard residues, Amber parameters and libraries were used. On the other hand, non-standard residues, Antechamber module provided parameters [141].

Prior to performing energy calculations, structural irregularities must be corrected. There is AddH command for adding hydrogens, and AddCharge command for assigning charges. Minimize command calls said commands before executing the Dock Prep command. As a result, prepared structures became available for

processing. While AddH and AddCharge commands are need-to-run basis, they were in fact ran in this study.

For the source of the protein structure, ProteinDataBank (PDB) was used via UCSF Chimera which means that UCSF Chimera downloaded the .pdb files itself hence there were no alterations possible on the file front. The downloaded file was started a new session in the software automatically. After removing the non-standard residues from the main structure, the minimization process was done with default parameters. H-bonds were also considered while adding hydrogens for Dock Prep. For incomplete side chains, Dunbrack 2010 rotamer library was used [142]. Then AMBER ff14SB was used for standard residue charge calculation. For other residues, Gasteiger from Amber's Antechamber module was used [143]. Gasteiger method is based on iterative partial equalization of orbital electronegativity also it is faster and more approximate than its counterpart.

3.4.1.Targeting Binding Sites

The target protein was preserved rigid throughout the docking process, while drug molecules were allowed flexibility. The search area was defined to cover two distinct HSA drug-binding sites. Binding Site 1 (BS1) was covered within a region with coordinates at the center along the X, Y and Z axis as -4.326, -4.756 and 9.449 respectively, and dimensions (Å) along the X, Y and Z axis were set to 10 Å. In Binding Site 2, the search area region was centered at the coordinates (X, Y, Z) 9.187, 3.021, -14.306 respectively while the dimensions along these axes were also set to 10 Å [144].

For conformations 1 to 4, a cubical lattice of $126 \times 126 \times 126$ points was used in which the values show each point count through x, y, and z coordinates with a spacing of 0.375 Å. Docking simulations were conducted with 150 as population size and 1.0×10^7 number of evaluations [145] using Lamarckian Genetic Algorithm v4.2.

For conformations 5 and 6, a cubical lattice of $60 \times 60 \times 60$ points was used in which the values show each point count through x, y, and z coordinates with a spacing of 0.375 Å. Docking simulations were conducted with 150 as population

size and 2.5×10^6 number of evaluations using Lamarckian Genetic Algorithm v4.2.

All conformations had a 10 run of GA with 150 as population size and a 27000 maximum number of generations. Other values were left as is.

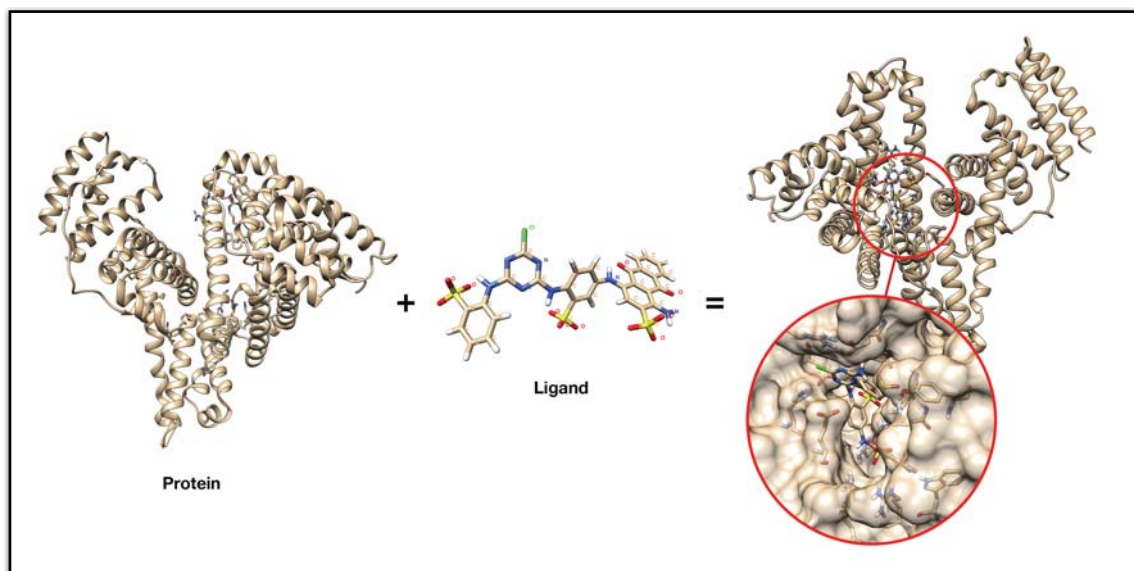


Figure 3.4. Docking of CBD on HSA.

Figure 3.4 shows visual representation of docking of CBD to HSA.

4.RESULT AND DISCUSSION

AutoDock v4.2.6 was used for docking CBD to identify active locations for specific targeting of binding sites on HSA. For trials, Lamarckian Genetic Algorithm (LGA) was used with several different configurations such as evaluation counts of 2.5×10^6 and 1.0×10^7 . Grid box sizes differ as $60 \times 60 \times 60$ and $126 \times 126 \times 126$ for different conformation simulations as well as target coordinates change from default to BS1 to BS2 which all will be explicitly mentioned for each conformation.

4.1.Results

4.1.1.Conformation 1

For conformation 1, a grid box of $126 \times 126 \times 126$ was used with 1.0×10^7 evaluations, and Binding Site 1 was targeted.

4.1.1.1.Cluster Analysis for Conformation 1

Conformation 1 was the lowest energy ranked of 10 conformations in this analysis. The RMSD cluster analyses were performed using 56 of 56 total atoms and using ligand atoms only.

Structurally similar clusters were shown in Table 4.1 sorted by increasing energy.

Distinct conformational clusters count in total of 10 runs was 10 while using an RMSD tolerance of 2.0 Å. Moreover, docking analyses were performed at 298.15 K temperature.

4.1.1.1.1.Clustering Histogram Data for Conformation 1

Data was collected while performing docking one molecule of CBD to HSA on BS1.

Table 4.1. Clustering Histogram data for Conformation 1

Clustering Rank	LBE (Kcal/mol)	Run Count	MBE (Kcal/mol)
1	-9.23	1	-9.23
2	-8.89	3	-8.89
3	-8.52	7	-8.52
4	-8.14	9	-8.14
5	-7.94	2	-7.94
6	-7.37	10	-7.37
7	-7.19	5	-7.19
8	-6.65	4	-6.65
9	-6.55	8	-6.55
10	-5.94	6	-5.94

All ranks had a Number in Cluster value of 1.

4.1.1.1.2.RMSD Table for Conformation 1

Table 4.2. RMSD Values and Binding Energies of each run on Conformation 1.

Rank	Run Order	Binding Energy(Kcal/mol)	Reference RMSD
1	1	-9.23	36.44
2	3	-8.89	34.70
3	7	-8.52	32.79
4	9	-8.14	26.82
5	2	-7.94	27.08
6	10	-7.37	37.68
7	5	-7.19	32.59
8	4	-6.65	35.94
9	8	-6.55	32.84
10	6	-5.94	29.11

All ranks had a Sub-Rank value of 1 and Cluster RMSD value of 0.00.

4.1.1.2. Information Entropy for Cluster 1 of Conformation 1

Information entropy for cluster rank 1 of conformation 1 is 1.00 with a root mean square tolerance for reclustering of 2.00 Å.

4.1.1.3. Thermodynamic Analysis for Conformation 1

Partition function for Conf 1, $Q = 10.13$
Free energy for Conf 1, $G \sim -1371.88$ (kcal/mol)
Internal energy for Conf 1, $U = -7.64$ (kcal/mol)

All results were for 298.15 K temperature and entropy (S) was 4.58 kcal/mol/K.

4.1.1.4. Lowest Ranked Docking of Conformation 1

Table 4.3. Data for Lowest Energy Docking of Conformation 1

Run order	1
Rank of cluster	1
Conformation count in this cluster	1
Reference structure RMSD value	36.445 Å
Evaluated Binding Free Energy	-9.23 kcal/mol
Evaluated Inhibition Constant, K_i	172.03 nM (nanomolar)
Final Intermolecular Energy	-12.21 kcal/mol
vdW + Hbond + desolv Energy	-7.59 kcal/mol
Electrostatic Energy	-4.62 kcal/mol
Final Total Internal Energy	-5.87 kcal/mol

Torsional free energy is +2.98 kcal/mol and unbound system's energy is the same as the final total internal energy.

4.1.2. Conformation 2

For conformation 2, a grid box of $126 \times 126 \times 126$ was used with 1.0×10^7 evaluations, and Binding Site 2 was targeted.

4.1.2.1. Cluster Analysis for Conformation 2

Conformation 2 was the lowest energy ranked of 10 conformations in this analysis. The RMSD cluster analyses were performed using 56 of 56 total atoms and using ligand atoms only.

Structurally similar clusters were shown in Table 4.4 sorted by increasing energy.

Distinct conformational clusters count in a total of 10 runs was 10 while using an RMSD tolerance of 2.0 Å. Moreover, docking analyses were performed at 298.15 K temperature.

4.1.2.1.1. Clustering Histogram Data for Conformation 2

Data was collected while performing docking one molecule of CBD to HSA.

Table 4.4. Clustering Histogram data for Conformation 2

Clustering Rank	LBE (Kcal/mol)	Run Count	MBE (Kcal/mol)
1	-6.08	5	-6.08
2	-5.89	4	-5.89
3	-5.72	8	-5.72
4	-5.60	2	-5.60
5	-5.55	9	-5.55
6	-5.33	3	-5.33
7	-5.09	1	-5.09
8	-5.06	7	-5.06
9	-4.83	6	-4.83
10	-3.54	10	-3.54

All ranks had a Number in Cluster value of 1.

4.1.2.1.2.RMSD Table for Conformation 2

Table 4.5. RMSD Values and Binding Energies of each run on Conformation 2.

Rank	Run Order	Binding Energy(Kcal/mol)	Reference RMSD
1	5	-6.08	41.12
2	4	-5.89	43.91
3	8	-5.72	38.27
4	2	-5.60	46.31
5	9	-5.55	27.17
6	3	-5.33	41.65
7	1	-5.09	41.18
8	7	-5.06	22.26
9	6	-4.83	30.39
10	10	-3.54	43.47

All ranks had a Sub-Rank value of 1 and Cluster RMSD value of 0.00.

4.1.2.2. Information Entropy for Cluster 1 of Conformation 2

Information entropy for cluster 1 of conformation 2 is 1.00 with a root mean square tolerance for reclustering of 2.00 Å.

4.1.2.3. Thermodynamic Analysis for Conformation 2

Partition function for Conf 2, $Q = 10.09$

Free energy for Conf 2, $G \sim -1369.51$ (kcal/mol)

Internal energy for Conf 2, $U = -5.27$ (kcal/mol)

All results were for 298.15 K temperature and entropy (S) was 4.58 kcal/mol/K.

4.1.2.4.Lowest Ranked Docking of Conformation 2

Table 4.6. Data for Lowest Energy Docking of Conformation 2

Run order	5
Rank of cluster	1
Conformation count in this cluster	1
Reference structure RMSD value	41.116 Å
Evaluated Binding Free Energy	-6.08 kcal/mol
Estimated Inhibition Constant, Ki	34.67 µM (micromolar)
Final Intermolecular Energy	-9.07 kcal/mol
vdW + Hbond + desolv Energy	-8.05 kcal/mol
Electrostatic Energy	-1.01 kcal/mol
Final Total Internal Energy	-5.62 kcal/mol

Torsional free energy is +2.98 kcal/mol and unbound system's energy is the same as the final total internal energy.

4.1.3.Conformation 3

For conformation 3, a grid box of 126 × 126 × 126 was used with 1.0×10^7 evaluations, and Binding Site 1 was targeted.

4.1.3.1.Cluster Analysis for Conformation 3

Conformation 3 was the lowest energy ranked of 10 conformations in this analysis. The RMSD cluster analyses were performed using 56 of 56 total atoms and using ligand atoms only.

Structurally similar clusters were shown in Table 4.7 sorted by increasing energy.

Distinct conformational clusters count in a total of 10 runs was 10 while using an RMSD tolerance of 2.0 Å. Moreover, docking analyses were performed at 298.15 K temperature.

4.1.3.1.1. Clustering Histogram Data for Conformation 3

Data was collected while performing docking one molecule of CBD to HSA.

Table 4.7. Clustering Histogram data for Conformation 3

Clustering Rank	LBE (Kcal/mol)	Run Count	MBE (Kcal/mol)
1	-12.64	7	-12.64
2	-12.31	10	-12.31
3	-11.41	5	-11.41
4	-11.39	9	-11.39
5	-10.98	2	-10.98
6	-10.74	8	-10.74
7	-10.04	6	-10.04
8	-9.91	4	-9.91
9	-9.86	1	-9.86
10	-8.71	3	-8.71

All ranks had a Number in Cluster value of 1.

4.1.3.1.2. RMSD Table for Conformation 3

Table 4.8. RMSD Values and Binding Energies of each run on Conformation 3.

Rank	Run Order	Binding Energy(Kcal/mol)	Reference RMSD
1	7	-12.64	11.67
2	10	-12.31	11.75
3	5	-11.41	12.52
4	9	-11.39	12.46
5	2	-10.98	12.53
6	8	-10.74	10.66
7	6	-10.04	12.81
8	4	-9.91	11.89
9	1	-9.86	12.69
10	3	-8.71	10.39

All ranks had a Sub-Rank value of 1 and Cluster RMSD value of 0.00.

4.1.3.2. Information Entropy for Cluster 1 of Conformation 3

Information entropy for cluster 1 of conformation 3 is 1.00 with a root mean square tolerance for reclustering of 2.00 Å.

4.1.3.3. Thermodynamic Analysis for Conformation 3

Partition function for Conf 3, $Q = 10.18$
Free energy for Conf 3, $G \sim -1375.04$ kcal/mol
Internal energy for Conf 3, $U = -10.80$ kcal/mol

All results were for 298.15 K temperature and entropy (S) was 4.58 kcal/mol/K.

4.1.3.4. Lowest Ranked Docking of Conformation 3

Table 4.9. Data for Lowest Energy Docking of Conformation 3

Run order	7
Rank of cluster	1
Conformation count in this cluster	1
Reference structure RMSD value	11.672 Å
Evaluated Binding Free Energy	-12.64 kcal/mol
Evaluated Inhibition Constant, K_i	544.23 pM (picomolar)
Final Intermolecular Energy	-15.62 kcal/mol
vdW + Hbond + desolv Energy	-14.38 kcal/mol
Electrostatic Energy	-1.24 kcal/mol
Final Total Internal Energy	-6.44 kcal/mol

Torsional free energy is +2.98 kcal/mol and unbound system's energy is the same as the final total internal energy.

4.1.4. Conformation 4

For conformation 4, a grid box of $126 \times 126 \times 126$ was used with 1.0×10^7 evaluations, and Binding Site 2 was targeted.

4.1.4.1. Cluster Analysis for Conformation 4

Conformation 4 was the lowest energy ranked of 10 conformations in this analysis. The RMSD cluster analyses were performed using 56 of 56 total atoms and using ligand atoms only.

Structurally similar clusters were shown in Table 4.10 sorted by increasing energy.

Distinct conformational clusters count in a total of 10 runs was 10 while using an RMSD tolerance of 2.0 Å. Moreover, docking analyses were performed at 298.15 K temperature.

4.1.4.1.1. Clustering Histogram Data for Conformation 4

Data was collected while performing docking one molecule of CBD to HSA.

Table 4.10. Clustering Histogram data for Conformation 4.

Clustering Rank	LBE (Kcal/mol)	Run Count	MBE (Kcal/mol)
1	-13.75	5	-13.75
2	-12.46	9	-12.46
3	-11.63	4	-11.63
4	-11.37	6	-11.37
5	-10.89	8	-10.89
6	-10.32	3	-10.32
7	-9.82	2	-9.82
8	-9.66	7	-9.66
9	-9.18	10	-9.18
10	-8.79	1	-8.79

All ranks had a Number in Cluster value of 1.

4.1.4.1.2.RMSD Table for Conformation 4

Table 4.11. RMSD Values and Binding Energies of each run on Conformation 4.

Rank	Run Order	Binding Energy(Kcal/mol)	Reference RMSD
1	5	-13.75	13.20
2	9	-12.46	12.00
3	4	-11.63	11.50
4	6	-11.37	6.96
5	8	-10.89	11.33
6	3	-10.32	11.17
7	2	-9.82	11.25
8	7	-9.66	11.76
9	10	-9.18	10.82
10	1	-8.79	12.74

All ranks had a Sub-Rank value of 1 and Cluster RMSD value of 0.00.

4.1.4.2. Information Entropy for Cluster 1 of Conformation 4

Information entropy for cluster 1 of conformation 4 is 1.00 with a root mean square tolerance for reclustering of 2.00 Å.

4.1.4.3. Thermodynamic Analysis for Conformation 4

Partition function for Conf 4, $Q = 10.18$

Free energy for Conf 4, $G \sim -1375.03$ (kcal/mol)

Internal energy for Conf 4, $U = -10.79$ (kcal/mol)

All results were for 298.15 K temperature and entropy (S) was 4.58 kcal/mol/K.

4.1.4.4.Lowest Ranked Docking of Conformation 4

Table 4.12. Data for Lowest Energy Docking of Conformation 4

Run order	5
Rank of cluster	1
Conformation count in this cluster	1
Reference structure RMSD value	13.202 Å
Evaluated Binding Free Energy	-13.75 kcal/mol
Evaluated Inhibition Constant, Ki	84.08 pM (picomolar)
Final Intermolecular Energy	-16.73 kcal/mol
vdW + Hbond + desolv Energy	-15.21 kcal/mol
Electrostatic Energy	-1.51 kcal/mol
Final Total Internal Energy	-6.51 kcal/mol

Torsional free energy is +2.98 kcal/mol and unbound system's energy is the same as the final total internal energy.

4.1.5.Conformation 5

For conformation 5, a grid box of 60 × 60 × 60 was used with 2.5 × 10⁶ evaluations and default grid coordinates were used, hence no binding site was specifically targeted.

4.1.5.1.Cluster Analysis for Conformation 5

Conformation 5 was the lowest energy ranked of 10 conformations in this analysis. The RMSD cluster analyses were performed using 56 of 56 total atoms and using ligand atoms only.

Structurally similar clusters were shown in Table 4.13 sorted by increasing energy.

Distinct conformational clusters count in a total of 10 runs was 10 while using an RMSD tolerance of 2.0 Å. Moreover, docking analyses were performed at 298.15 K temperature.

4.1.5.1.1.Clustering Histogram Data for Conformation 5

Data was collected while performing docking one molecule of CBD to HSA

Table 4.13. Clustering Histogram data for Conformation 5.

Clustering Rank	LBE (Kcal/mol)	Run Count	MBE (Kcal/mol)
1	-13.69	1	-13.69
2	-12.40	3	-12.40
3	-9.94	4	-9.94
4	-9.28	2	-9.28
5	-8.71	6	-8.71
6	-8.49	10	-8.49
7	-8.36	7	-8.36
8	-8.18	8	-8.18
9	-7.53	5	-7.53
10	-6.57	9	-6.57

All ranks had a Number in Cluster value of 1.

4.1.5.1.2.RMSD Table for Conformation 5

Table 4.14. RMSD Values and Binding Energies of each run on Conformation 5.

Rank	Run Order	Binding Energy(Kcal/mol)	Reference RMSD
1	1	-13.69	10.88
2	3	-12.40	11.30
3	4	-9.94	10.83
4	2	-9.28	10.53
5	6	-8.71	9.43
6	10	-8.49	11.63
7	7	-8.36	9.92
8	8	-8.18	10.28
9	5	-7.53	8.97
10	9	-6.57	8.70

All ranks had a Sub-Rank value of 1 and Cluster RMSD value of 0.00.

4.1.5.2. Information Entropy for Cluster 1 of Conformation 5

Information entropy for cluster 1 of conformation 5 is 1.00 with a root mean square tolerance for reclustering of 2.00 Å.

4.1.5.3. Thermodynamic Analysis for Conformation 5

Partition function for Conf 5, $Q = 10.16$
Free energy for Conf 5, $G \sim -1373.56$ (kcal/mol)
Internal energy for Conf 5, $U = -9.32$ (kcal/mol)

All results were for 298.15 K temperature and entropy (S) was 4.58 kcal/mol/K.

4.1.5.4. Lowest Ranked Docking of Conformation 5

Table 4.15. Data for Lowest Energy Docking of Conformation 5

Run order	1
Rank of cluster	1
Conformation count in this cluster	1
Reference structure RMSD value	10.884 Å
Evaluated Binding Free Energy (kcal/mol)	-13.69
Evaluated Inhibition Constant, K_i	91.58 pM (picomolar)
Final Intermolecular Energy (kcal/mol)	-16.68
vdW + Hbond + desolv Energy (kcal/mol)	-11.91
Electrostatic Energy (kcal/mol)	-4.77
Final Total Internal Energy (kcal/mol)	-5.92

Torsional free energy is +2.98 kcal/mol and unbound system's energy is the same as the final total internal energy.

4.1.6. Conformation 6

For conformation 6, a grid box of $60 \times 60 \times 60$ was used with 2.5×10^6 evaluations

and default grid coordinates were used, hence no binding site was specifically targeted.

4.1.6.1.Cluster Analysis for Conformation 6

Conformation 6 was the lowest energy ranked of 10 conformations in this analysis. The RMSD cluster analyses were performed using 56 of 56 total atoms and using ligand atoms only.

Structurally similar clusters were shown in Table 4.16 sorted by increasing energy.

Distinct conformational clusters count in a total of 10 runs was 8 while using an RMSD tolerance of 2.0 Å. Moreover, docking analyses were performed at 298.15 K temperature.

4.1.6.1.1.Clustering Histogram Data for Conformation 6

Data was collected while performing docking one molecule of CBD to HSA.

Table 4.16. Clustering Histogram data for Conformation 6.

Clustering Rank	LBE (Kcal/mol)	Run Count	MBE (Kcal/mol)	Number in Cluster
1	-10.73	4	-10.73	1
2	-10.71	7	-9.65	3
3	-10.38	2	-10.38	1
4	-9.78	10	-9.78	1
5	-9.69	1	-9.69	1
6	-8.08	5	-8.08	1
7	-7.79	3	-7.79	1
8	-7.18	8	-7.18	1

4.1.6.1.2.RMSD Table for Conformation 6

Table 4.17. RMSD Values and Binding Energies of each run on Conformation 6.

Rank	Sub-Rank	Run Order	Binding Energy(Kcal/mol)	Cluster RMSD	Reference RMSD
1	1	4	-10.73	0.00	8.65
2	1	7	-10.71	0.00	8.41
2	2	9	-10.09	1.70	9.24
2	3	6	-8.14	1.48	8.66
3	1	2	-10.38	0.00	9.02
4	1	10	-9.78	0.00	11.22
5	1	1	-9.69	0.00	9.71
6	1	5	-8.08	0.00	9.46
7	1	3	-7.79	0.00	7.86
8	1	8	-7.18	0.00	7.91

4.1.6.2.Information Entropy for Cluster 1 of Conformation 6

Information entropy for cluster 1 of conformation 6 is 0.86 with a root mean square tolerance for reclustering of 2.00 Å.

4.1.6.3. Thermodynamic Analysis for Conformation 6

Partition function for Conf 6, $Q = 10.16$

Free energy for Conf 6, $G \sim -1373.50$ (kcal/mol)

Internal energy for Conf 6, $U = -9.26$ (kcal/mol)

All results were for 298.15 K temperature and entropy (S) was 4.58 kcal/mol/K.

4.1.6.4.Lowest Ranked Docking of Conformation 6

Table 4.18. Data for Lowest Energy Docking of Conformation 6

Run order	4
Rank of cluster	1
Conformation count in this cluster	1
Reference structure RMSD value	8.653 A
Evaluated Binding Free Energy (kcal/mol)	-10.73
Evaluated Inhibition Constant, Ki	13.74 nM (nanomolar)
Final Intermolecular Energy (kcal/mol)	-13.71
vdW + Hbond + desolv Energy (kcal/mol)	-9.13
Electrostatic Energy (kcal/mol)	-4.58
Final Total Internal Energy (kcal/mol)	-4.75

Torsional free energy is +2.98 kcal/mol and unbound system's energy is the same as the final total internal energy.

4.2.DISCUSSION

4.2.1.Binding Affinity of CBD to Human Serum Albumin (HSA)

Six conformations of CBD were implemented in AutoDock v6.2 software for predicting the binding preference of CBD to HSA. Conformation, grid and grid box features, and binding site, free energy and possibility of CBD interaction with HSA were listed in Table 4.19.

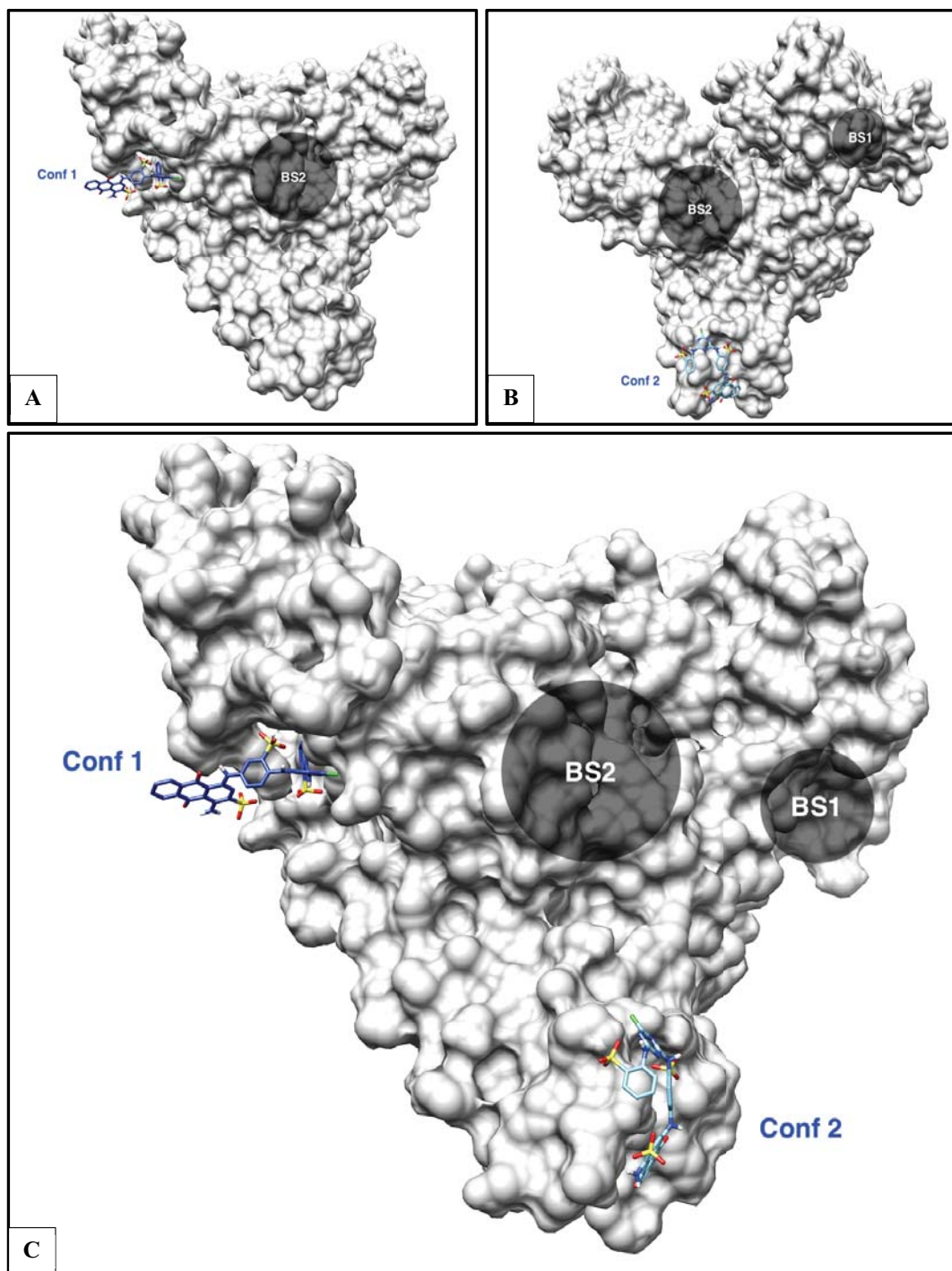
Table 4.19. Conformation features and binding free energies of CBD bound to HSA.

Conformation #	Grid box	Grid	Evaluation	Binding Site	Binding Energy (kcal/mol)	Binding Possibility
1	126/126/126	BS1	1.0x10 ⁷	Default	-9.12	No Binding
2	126/126/126	BS2	1.0x10 ⁷	Default	-6.08	No Binding
3	126/126/126	BS1	1.0x10 ⁷	BS3	-12.64	Favorable
4	126/126/126	BS2	1.0x10 ⁷	BS1	-13.75	No Binding
5	60/60/60	Default	2.5x10⁶	BS2	-13.69	Favorable
6	60/60/60	Default	2.5x10 ⁶	BS1	-10.74	Favorable

In the process, only DockPrep command was used for dock preparation for Conf #3, 4, and 5. Although for Conf #1, 2, and 4 Min command was used alongside DockPrep as well. Also, all conformations were implemented by Gasteiger Method in the AutoDock software.

According to Table 4.19; Although the binding free energy of Conf # 1, 2 and 4 are favorable as -9.12, -6.08 and -12.64, respectively, they indicate no binding possibility since CBD is located out of binding sites. The reason why is explained in sections 4.2.2 and 4.2.3 in detail. Conf # 3, 5, and 6 have favorable binding energy. Among these, Conf # 5 (in bold) has the most favorable binding free

energy as -13.69 kcal/mol, which is located to binding site 2 of HSA.



4.2.2. Binding Properties of CBD docked to HSA for Conf #1 and Conf #2

Figure 4.1. A) Conformation 1, B) Conformation 2, C) Conformation 1 and 2 of CBD interaction with HSA (solid grey surface).

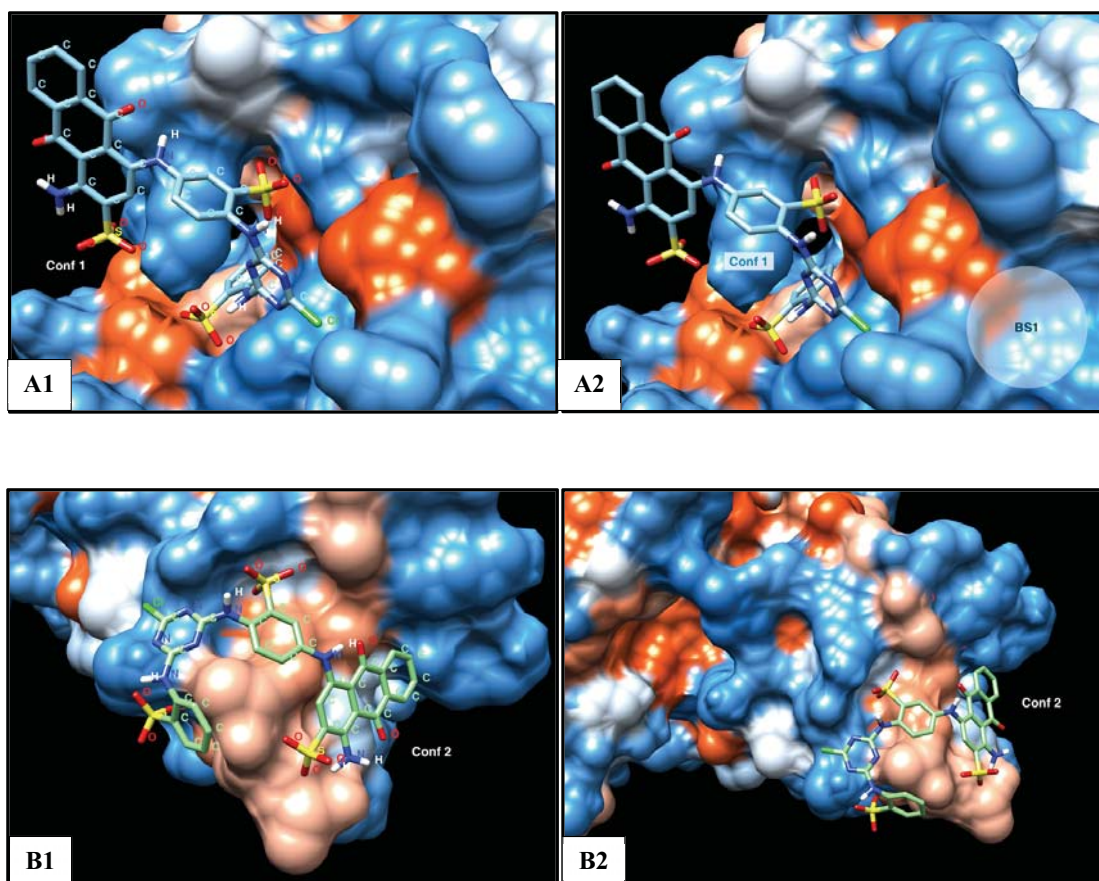


Figure 4.2. A) Conformation 1 and B) Conformation 2 of CBD interaction with HSA interactive hydrophobicity solid surface. (Dodger blue denotes more hydrophilic surface and orange denotes more hydrophobic surface.)

As seen in Figure 4.2, Conf #1 and #2 of CBD interacts with HSA. Note that; the surface of HSA is interactive hydrophobicity solid surface. This view has the coloring of "hydrophobicity surface" preset in which color scales for most hydrophilic areas as dodger blue, and the most hydrophobic areas as orange-red with white in between. The CBD-binding pocket is blue and orange, pointing out its both hydrophilic and hydrophobic character. However, Conformations #1 and #2 of CBD (Figure 4.2 A and B) are located out of binding sites despite the binding free energies are negative (-). There is no binding interaction was observed in this case.

4.2.3. Binding Properties of CBD docked to HSA for Conf #3, #4, #5 and #6

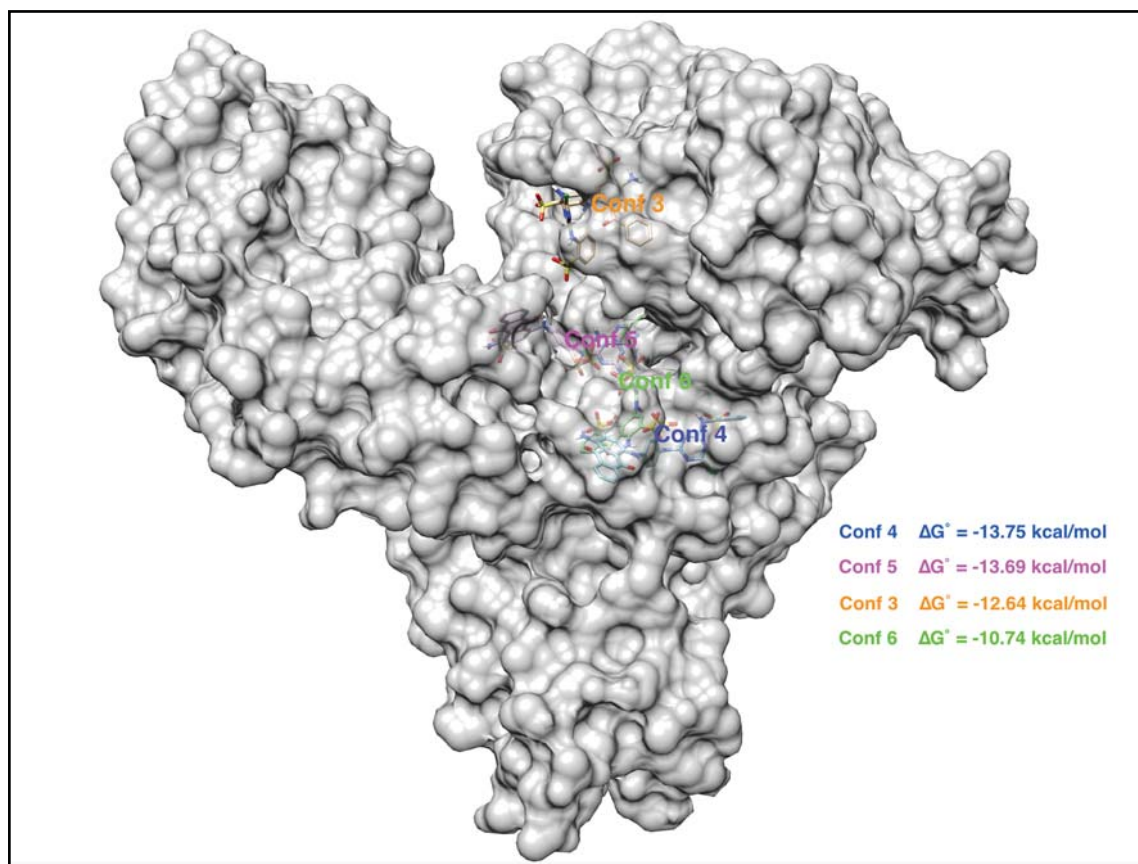
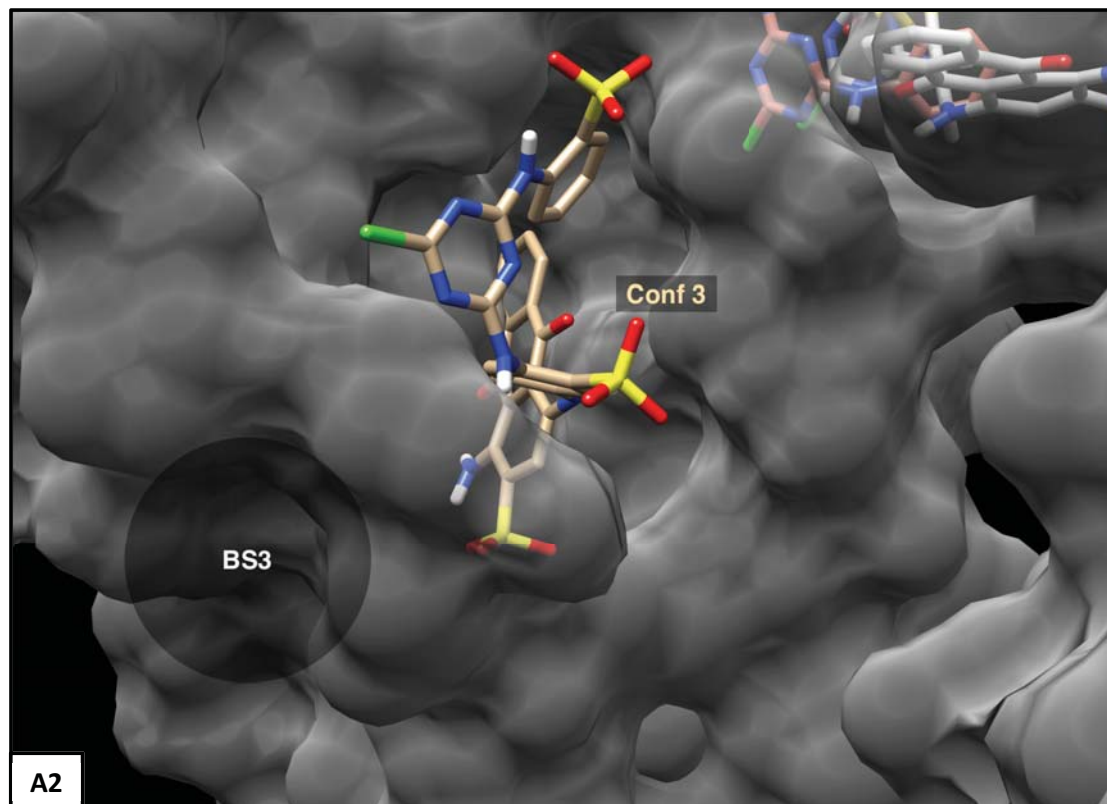
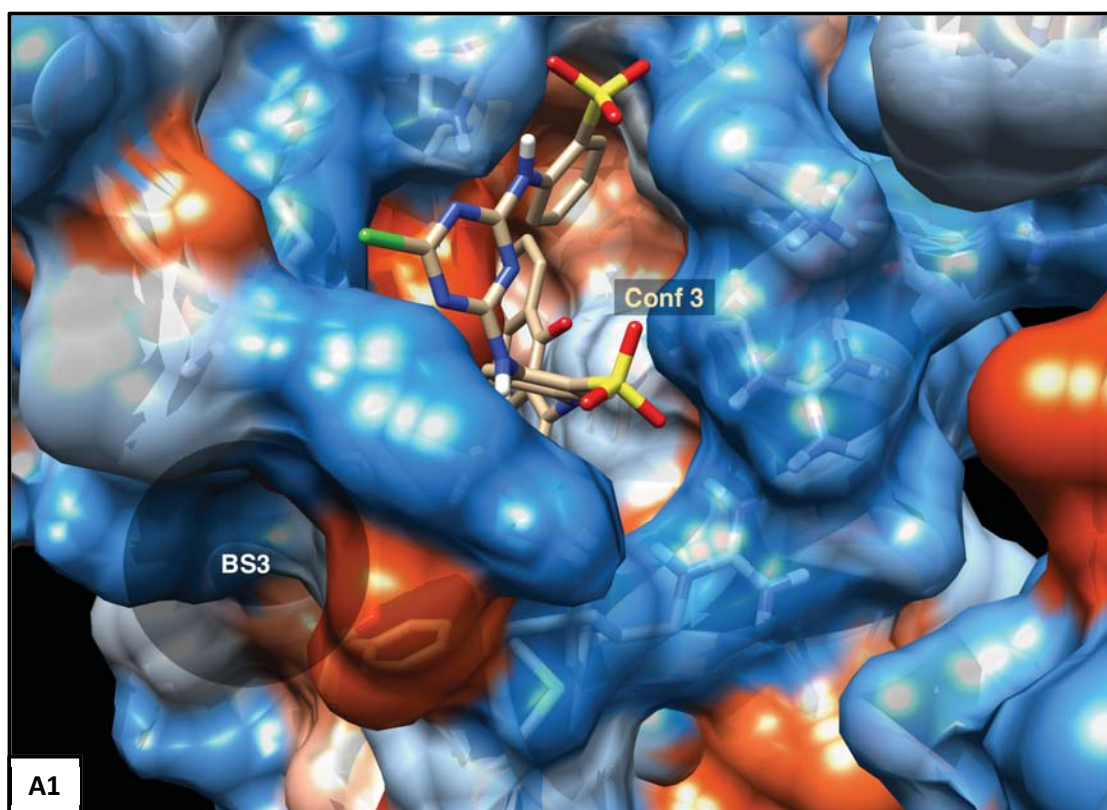


Figure 4.3. Conf 3, 4, 5, and 6 of CBD interaction with HSA (solid grey surface).

Four conformations of CBD (3,4,5 and 6) are seen in Figure 4.3 with their binding free energies. They are located in different binding sites of HSA. In Figure 4.3; Conf #4 and #6 are located at binding site 1 (BS1) of HSA, Conf #5 located at binding site 2 (BS2), namely Sudlow's site (Figure 2.3) and Conf #3 located at binding site 3 (BS3). All four conformations are energetically favorable.

4.2.3.1. Binding Properties of Conf #3 and #4



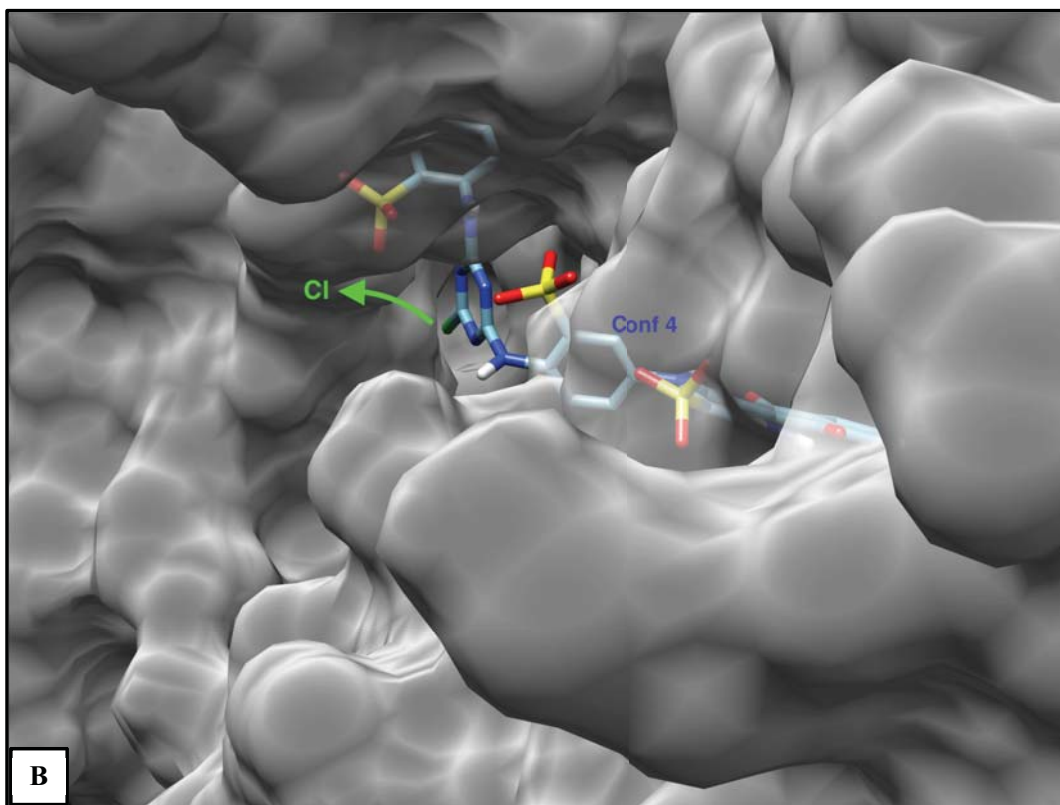


Figure 4.4. **A1)** Conformation 3 of CBD interaction with HSA (interactive hydrophobicity of solid surface). **A2)** Conformation 3 of CBD interaction with HSA (dark grey solid surface). **B)** Conformation 4 of CBD interaction with HSA (dark grey solid surface).

Figure 4.4 represents the Conf #3 and #4 of CBD molecule in complex with HSA. As seen in Figure 4 A1 and A2, Conf #3 of CBD located around BS3 of HSA, where the molecules such as hemin, bilirubin, fusicid acid, and lidocaine can also bind in this site (Figure 2.3). Figure 4 A1 particularly shows the interaction profile of Conf #3 of CBD with HSA seems both from hydrophilic and hydrophobic sites of protein through sulfonic acid and anthraquinone moiety of CBD, respectively.

Furthermore, the chloride atom (Cl) colored as the bright green oriented outer side of HSA, which means that Conf #3 of CBD is well fitted to HSA since CBD ligand should be covalently immobilized to magnetic polymers through Cl atom by a substitution reaction. In terms of thermodynamic parameters such as binding free energy, Conf #3 of CBD docking to HSA is energetically favorable with a binding free energy of -12.64 kcal/mol.

On the other hand, Figure 4B represents Conf #4 of CBD in complex with HSA, which is illustrated in dark grey solid surface. Conf #4 of CBD is located around BS1 of HSA, where different drugs can also bind this site such as thyroxine, warfarin, and indomethacin. Although the binding mode of Conf #4 of CBD is energetically most favorable among the other conformations (-13.75 kcal/mol), the Cl atom is aligned to the inner face of the protein which means that binding mode of Conf #4 of CBD to HSA is impossible due to the steric hindrance of magnetic polymer. So, it can be concluded from this result; there is no binding to HSA in Conf #4.

4.2.3.2. Binding Properties of Conf #5 and #6

Figure 4.5 illustrates Conf #5 and #6 of CBD molecule in complex with HSA. Figure 4.5A and 4.5B correspond to Conf #5 and #6 of CBD that interacts with HSA in interactive hydrophobic solid surface and dark grey solid surface, respectively. As seen in Figure 4.5, Conf #5 of CBD located around BS2, while Conf #6 of CBD located around BS1 of HSA. BS2 is the binding site 2 of HSA, where the drugs such as thyroxine, ibuprofen, and diazepam can also bind in this site (Figure 2.3). These two conformations are well fitted to HSA, and their binding modes are energetically favorable. Moreover, both Cl atoms of Conf #5 and Conf #6 are aligned to the outer face of the protein, which means that binding modes of these conformations are possible (Figure 4.5B). Among Conf #5 and Conf #6, the most favorable binding energy confirms with Conf #5 (-13.69 kcal/mol), where it oriented around BS2 to HSA (See Table 4.19). From this point, the hydrogen bonding and hydrophobic interactions are considered for Conf #5 of CBD in complex with HSA.

Conf #5 of CBD, which is the most favorable one and located around BS2, contributes both hydrophobic and hydrophilic interactions with HSA. In Figure 4.5A, sulfonic acid groups of Conf #5 of CBD interact with HSA through the most hydrophilic sites of the protein, which is denoted as orange color. In addition to, anthraquinone domain of CBD docked to HSA through the most hydrophobic sites of the protein, which is denoted as dodger blue color.

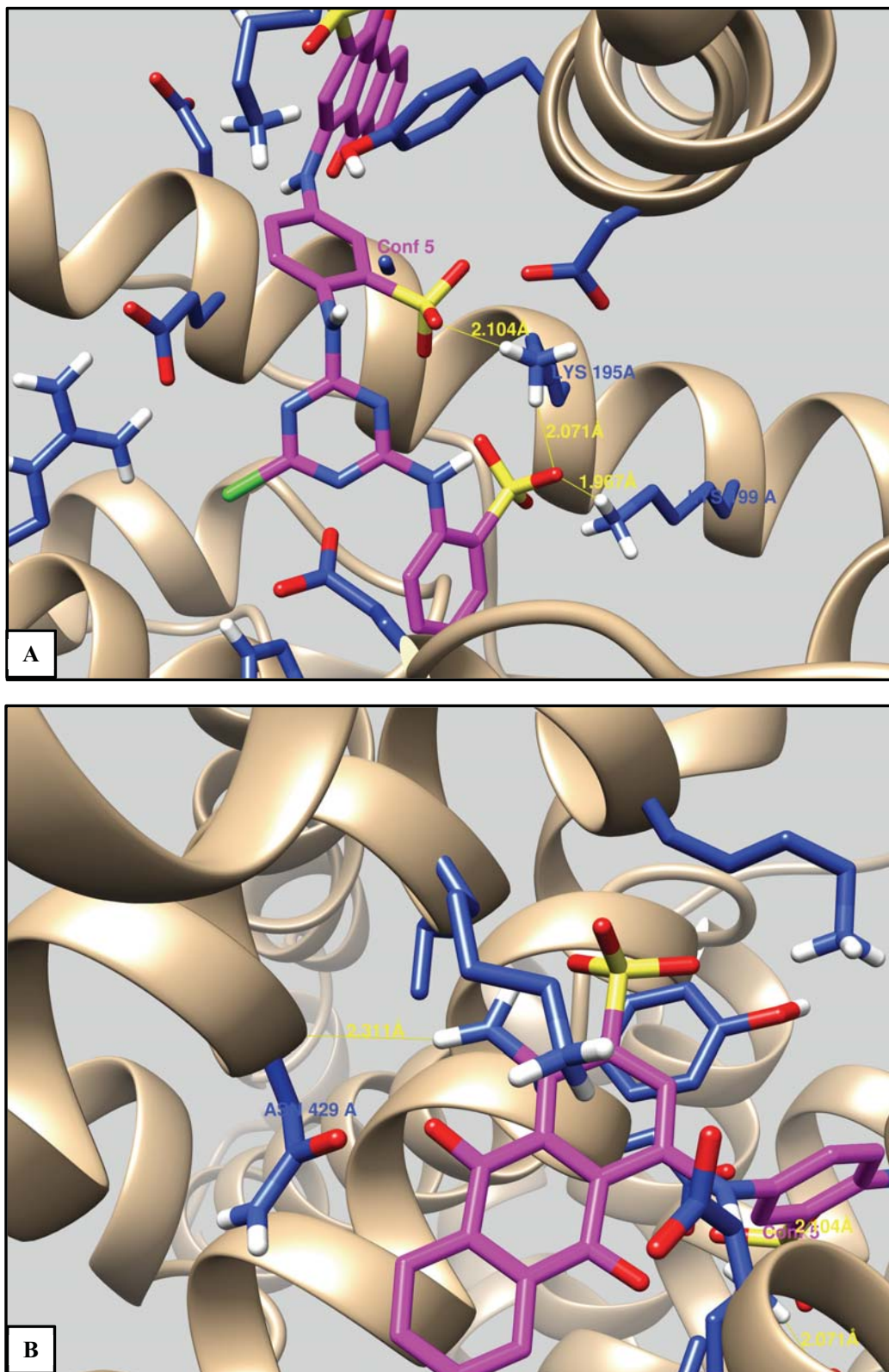


Figure 4.5. **A)** Conformation 5 and 6 of CBD interaction with HSA (interactive hydrophobicity of surface). **B)** Conformation 5 and 6 of CBD interaction with HSA (dark grey solid surface).

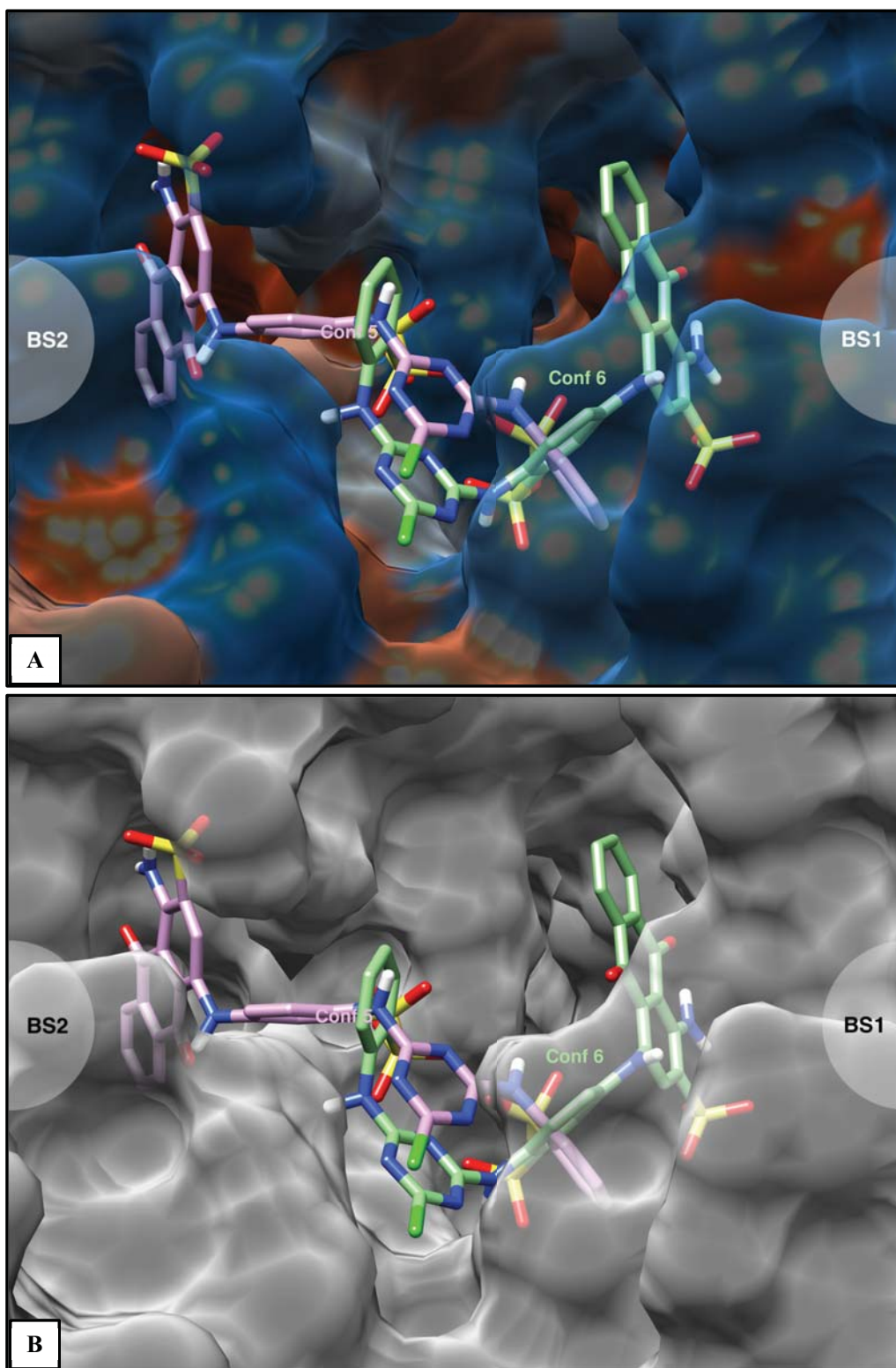


Figure 4.6. A and B) H-bonding of Conf #5 of CBD interacts with HSA (ribbon structure) in different views.

Figure 4.6 represents H-bonding interactions of Conf #5 with neighboring residues

of HSA. It is clearly seen that the sulfonic acid groups of CBD have H-bonding with LYS 195 and 199 in Domain IIIA of HSA (Figure 4.6A). In addition to, it seems an H-bonding between NH₂ group of CBD in anthraquinone domain and ASN 429 amino acid backbone in Domain IIIA of HSA (Figure 4.6B).

The AutoDock also analyses the specific ligand CBD interactions in a different display with neighboring amino acid residues of HSA. In Figure 4.7, the ligand is shown with a solvent-excluded molecular surface view. Atoms in the receptor which are hydrogen-bonded or in close-contact to atoms in CBD are visible as spheres. Furthermore, some pieces of the receptor are displayed for sequences of 3 or more residues in HSA which have interaction towards CBD. In this circumstance, Conf #5 is well fitted with amino acid residues of HSA.

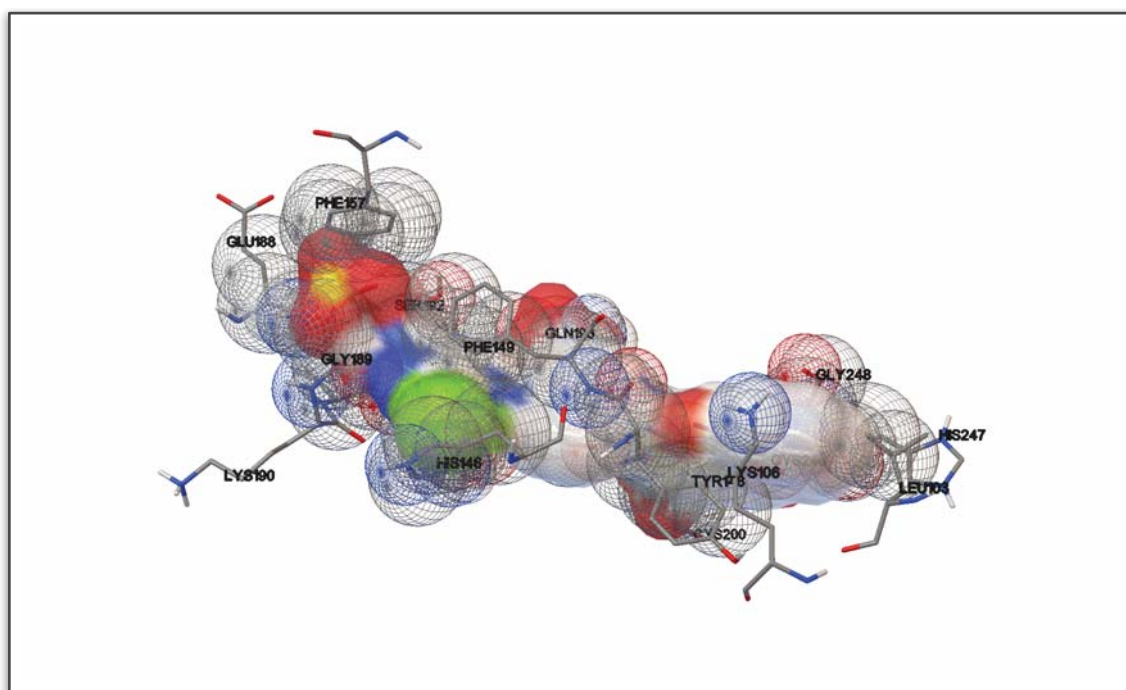


Figure 4.7. Interaction of Conf #5 of CBD with neighboring amino acid residues of HSA.

5.CONCLUSION

In this thesis, six different conformations of CBD in complex with HSA was evaluated by molecular docking software AutoDock v6.2 in order to investigate appreciate the molecular binding mode of CBD to HSA. Table 4.20 summarizes the binding possibilities of six conformers of CBD. Among all the conformations, Conf #5 is the most favorable one.

Table 4.20. Summary of binding features of CBD to HSA.

Conformation #	Binding Site	Binding Energy (kcal/mol)	Binding Possibility
1	--	-9.12	No Binding
2	--	-6.08	No Binding
3	BS3	-12.64	Favorable
4	BS1	-13.75	No Binding
5	BS2	-13.69	Most Favorable
6	BS1	-10.74	Favorable

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APPENDIX

APPENDIX 1 - Originality Report



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GRADUATE SCHOOL OF SCIENCE AND ENGINEERING
MASTER THESIS ORIGINALITY REPORT

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