

**Protein Profiling and *In Silico* Analysis of PPI Network in  
Meningitis CSF Samples**

*A Major Project Dissertation Submitted in Partial Fulfillment of the  
Requirement for the Degree of*

**Master of Technology  
In  
Biomedical Engineering**

*Submitted by*

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## CERTIFICATE

This is to certify that the M. Tech. dissertation entitled “*Protein Profiling and In Silico Analysis of PPI Network in Meningitis CSF Samples*”, submitted by Satya Prakash (DTU/13/MTECH/397) in partial fulfillment of the requirement for the major project dissertation during M.Tech, Delhi Technological University (Formerly Delhi College of Engineering, University of Delhi), is an authentic record of the candidate’s own work which is to be carry out by him under my guidance.

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## DECLARATION

I declare that my major project dissertation entitled “*Protein Profiling and In Silico Analysis of PPI Network in Meningitis CSF Samples*” submitted to Department of Biotechnology, Delhi Technological University as a result of the work carried out by me at “Molecular Neuroscience and Functional Genomic Laboratory”, Department of Biotechnology.

Place: Delhi

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## **ABBREVIATIONS**

Ab – Antibody

ADH – Antidiuretic Hormone

ATP – Adenosine triphosphate

BBB - Blood Brain Barrier

CD - Cell Adhesion

CDC - Centers for Disease Control and Prevention

CSF - Cerebrospinal Fluid

FDA – Food and Drug Administration

Hib - *Haemophilus influenzae* type b

HIV - Human Immunodeficiency Virus

HSP – Heat Shock Protein

IgA –Immunoglobulin A

IL – Interleukin

LPS – Lipopolysaccharide

PDB – Protein Data Bank

PPI- Protein Protein Interaction

PRP - Polyribosylribitol Phosphate

sHSP - Small Heat Shock Proteins

SIADH - Syndrome of Inappropriate Antidiuretic Hormone

TNF - Tumor Necrosis Factor



# **Title - Protein Profiling and *In Silico* Analysis of PPI Network in Meningitis CSF Samples**

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## **ABSTRACT**

Meningitis is a chronic neurodegenerative disorder in which inflammation of meninges occurs that results in leakage of CSF. Inflammation in meninges, which is the protective covering of the brain and spinal cord elicit the meningitis. Meningitis could be life threatening because of the inflammation of the meninges. Some common causes of meningitis include virus, fungi, bacteria, and parasites. In bacterial meningitis, inflammation of the meninges affecting the arachnoid, subarachnoid, and pia matter space that happens in response to bacterial products. Bacterial meningitis is also originated to be contagious. The mode of action of bacterial meningitis is direct contact with the respiratory secretion as well as throat and oral secretion of an infected person, such as coughing, sneezing etc. Most causative agents found to be *Haemophilus influenzae*, *Streptococcus pneumoniae*, and *Neisseria meningitidis*. Children under the age group of five years get affected by this disease mainly caused by *Haemophilus influenzae* type b. Etiopathology of bacterial meningitis have been altered by vaccination against following bacteria namely *Neisseria meningitidis*, *Streptococcus pneumoniae*, and *Haemophilus influenzae* type b. Vaccines have an essential role in prevention of bacterial meningitis. Vaccines against *Streptococcus pneumoniae*, *Neisseria meningitidis*, and *Haemophilus influenzae* are available at present, but each vaccine is specific for each bacterium and limited to some of the serotypes of each bacterium. For example, vaccines are currently available to inhibit *Haemophilus influenzae* infections due to serotype b but that could not be used for that infection which occurs due to other serotypes. HSPs are conserved proteins found in animals and others, acts as molecular chaperon that gets activated in stress condition and helps in correct folding of proteins. However in case of meningitis, inflammation in meninges ascertains the improper functioning of HSPs. Although in this project I have tried to find out the therapeutic role of two biomolecules i.e., Baicalin and Quercetin which could be used for the cure of meningitis. However, Meropenem is already approved by FDA in 1996 for treating bacterial meningitis. I have taken bexA, ctrA, HPD and SodC that are involved in meningitis and for curing this disease it was tried to retrieve the data required to validate the effectiveness of Quercetin and Baicalin as drug in treatment of meningitis.

# **INTRODUCTION**

## INTRODUCTION

During a survey performed in the small population of US in 1960-70s, it was found that pathogens like *Haemophilus influenzae*, *Neisseria meningitidis* and *Streptococcus pneumonia* are the main causing agent of meningitis. However, relatively small populations in these studies and therapeutic strategies were concentrating toward these microorganisms, provided the great chances of isolation of these specific pathogens [1-3]. Three identified pathogens including *Haemophilus influenzae*, *Neisseria meningitidis*, and *Streptococcus pneumonia* were contributing for more than 85% of cases of these pathological conditions. Another following laboratory based investigation study done over a population of almost 30 million from five states for all cases of bacterial meningitis in 1986. Investigation was performed for the five common etiological agents of bacterial meningitis and found that bacterial agents such as *Haemophilus influenzae*, *Streptococcus pneumonia* and *Neisseria meningitidis* comprises majority of cases of pathological condition. Bacterial meningitis is moreover a challenging issue in all over the world. Further it has been seen that in countries of African continent, rates of HIV infection is very high and the common cases of meningitis are occurred due to the activity of *Streptococcus pneumonia*, and this has been connected with high mortality rates [4-5]. Bacterial meningitis is predominantly found in young children. The most common pathogens during the neonatal period are Gram negative enteric Bacilli, *Streptococci*, and *Listeria monocytogenes*. In children of age group between 4 months to 15 years, the three major causative organisms namely *Streptococcus pneumoniae*, *Neisseria meningitidis* and *Haemophilus influenzae* type b accounts more than 90% of bacterial meningitis. The occurrence and relative frequencies of these bacteria mainly depends on genetic factors and the geographic area. Recently developed and introduction of effectual vaccines against Hib. Several risk factors associated with bacterial meningitis have been identified through Epidemiological studies. During studies it was found that, Boys get affected by bacterial meningitis more frequently than girls. Many studies have reported so far to show the presence of racial differences in the occurrence of bacterial meningitis. Socioeconomic determined factors are responsible for 3-4 times greater risk of bacterial meningitis in Black and Hispanic populations than Caucasians [6-9]. High frequency of bacterial meningitis has been found in native of North America. Every year out of one lakh, 200 get affected by bacterial meningitis in Canada [10].

# **REVIEW OF LITERATURE**

## **REVIEW OF LITERATURE**

### ***Haemophilus influenzae***

Results have shown a great decrease in the occurrence of *Haemophilus influenzae* type b meningitis with the use of Hib conjugate vaccines [11-13]. Each vaccine includes polyribosylribitol phosphate (PRP), or portion of the PRP covalently linked with carrier protein. Moreover, the outermost layer of the microorganism is mostly made up of complex polysaccharide; the process of conjugation converts the immunogenic processing of polysaccharide to a T-cell dependent antigen from a T-cell independent and greatly enhances immunogenicity. This vaccine is subjected to all the infants beginning at two months of age with a series of three inoculations, and further followed by booster dose at the age of 13-15 months. Up to 90% cases of Hib meningitis has been reduced during the vaccination in developed countries. In other countries for adequate uptake of vaccine has shown reduction up to 55-80%; this can be observed that conjugate vaccines is capable in minimizing the nasopharyngeal presence of the microorganism and subsequently, can drop the transmission process of microbial infections through herd immunity. A significant decline in *Haemophilus influenzae* type b disease due to the development of herd immunity was evidenced in children at the time period of less than one year of age before the vaccine was allowed for use in this age group [14].

Hib is a primary cause of meningitis in young infants, with maximum death rate around the world [15,16]. In 2007, it was found that only 42% of children had access to Hib vaccines, now almost 90% of the children are consuming the Hib vaccine. A wide analytical study for the use of Hib conjugate vaccines in developing countries is under supervision. Later studies have shown that in other developing countries, the overall vaccine effectiveness has reached up to 95% [17-20].

### ***Streptococcus pneumoniae***

*Streptococcus pneumoniae* is said to be most common cause of bacterial meningitis, which accounts for 58% of total cases in developed countries [21-23]. To lessen the occurrence of pneumococcal meningitis vaccination strategies has been employed. However the suggestion of Hib vaccine for certain high risk groups have shown less prolific results for the prevention of pneumococcal disease, even though 75-85% of the serotypes were restricted to significant valent pneumococcal polysaccharide vaccine isolated from CSF of pneumococcal meningitis patients. Pneumococcal conjugate vaccines were established which included carrier proteins from a nontoxic variant of tetanus toxoid, diphtheria toxin, and an outer membrane protein complex of meningococcal attached to capsular polysaccharides. Later developed heptavalent vaccine includes the seven common

pneumococcal serotypes [24]. With the use of pneumococcal serotypes in the vaccine for reticence of invasive pneumococcal disease, total effectiveness was found to be approximate 90% in fully vaccinated children. Introduction of the heptavalent pneumococcal conjugate vaccine shows a decrease in occurrence rate of the heptavalent pneumococcal conjugate vaccine up to 30% as it was the huge decrease in children less than five years of age (Survey of Nationwide Inpatient Service) [25]. In another study by CDC has proven the lesser chances of pneumococcal meningitis. However, number of meningitis cases caused by non-vaccine included serotypes was increased [26]. Later some of the unapproved studies also show decrease in the occurrence of pneumococcal meningitis where the serotypes have been replaced [27]. Although, various other studies have shown a rise of invasive pneumococcal disease caused due to serotypes which are not included in the heptavalent vaccine, so the study insist to develop a continued surveillance system for the advancement of vaccines with enhanced effectiveness against these other serotypes [28].

### ***Neisseria meningitidis***

It is found that approximate 90% of invasive meningococcal disease in the developed countries is sporadic. Occurrence of this disease was up to 30% due to serogroup B and C each and approx. 20% was due to serogroup Y which ultimately caused meningitis in 50% of cases in year 2008 in US [29]. However a contribution of each serogroup in development of meningococcal meningitis was not clearly specified. Many developing countries have shown major outbreaks of meningococcal meningitis initiated largely by serogroup A. Infection rates during these rises can approach less than 1% of the population [30-32]. A high frequency of serogroup X disease was recently notified for Black population, representing up to 50% of 1,140 cases of meningococcal meningitis in 2006 [33]. In the population with a higher risk of invasive meningococcal infection introduction of quadrivalent meningococcal polysaccharide vaccine against serogroups A, C, W135 and Y is supervised to eliminate the infection [34]. The vaccine was not supported for routine use in US since the overall reduced risk of infection, due to failure to protect against serogroup B disease, and the incapability to deliver long-lasting immunity to young children. On the basis of opposing effect of conjugate vaccine over invasive disease caused by Hib and *Streptococcus pneumonia*, conjugate vaccines against specific serogroups of *Neisseria meningitidis* were developed. These conjugated vaccines contain protein such as CRM197, tetanus toxoid, diphtheria toxoid conjugated to meningococcal polysaccharide and induces the development of immunological memory in young children [35]. After the introduction of effective vaccine in an analytical study program in which children and adult subjected with a single dose of the CRM197 meningococcal vaccine, the effectiveness for short term vaccination in children

and adults was up to 90% and 95% correspondingly [36]. In later studies for the first 18 months of the meningococcal C conjugate vaccine program in the United Kingdom, the extensive assumption was found to be 80% over the period 1998-2001 in serogroup C invasive cases, with some inconstancy based on age group [37]. In another case study of adolescents to identify vaccine effectiveness, the protective usefulness of the vaccine was 90% [38]. Presence of serogroup C among subjects age group 15-17 years was also reduced by 60% [39]. These decline in presence persisted for merely two years after vaccine introduction, with no sign of serogroup replacement [40]. In US a quadrivalent meningococcal conjugate vaccine consisting serogroups A, C, W135 and Y conjugated to diphtheria toxoid was approved and was largely proposed for routine immunization [41]. Later routine vaccination was proposed to the age group 10-18 years with single dose [42] and revaccination for the groups at a sustained and advanced risk of meningococcal disease [43]. It is to be believed that protective Ab in adults are likely to persist as long as, and maybe longer than, that after the introduction with meningococcal polysaccharide vaccine [44,45]. Further, the age group of pathogens is also important for their pathogenicity. At certain age they cause or create disease ambiances, and greatly affect the normal population. The major pathogens and their associated age group have been enlisted in following table below.

<b>Pathogens</b>	<b>Age Group</b>
<i>Escherichia coli</i> , <i>Listeria monocytogenes</i> <i>Streptococcus agalactiae</i> , <i>Streptococcus pneumoniae</i>	0-4 Weeks
<i>Haemophilus influenzae</i> , <i>Listeria monocytogenes</i> , <i>Neisseria meningitidis</i> , <i>Streptococcus pneumoniae</i>	1-3 Months
<i>Haemophilus influenzae</i> , <i>Neisseria meningitidis</i> , <i>Streptococcus pneumoniae</i>	3 Months-18 Years
<i>Neisseria meningitidis</i> , <i>Streptococcus pneumoniae</i>	18-50 Years
<i>Listeria monocytogenes</i> , <i>Streptococcus pneumoniae</i>	>50 Years

**Table No.-1: Pathogens that plays role at different age group**

## Heat Shock Protein

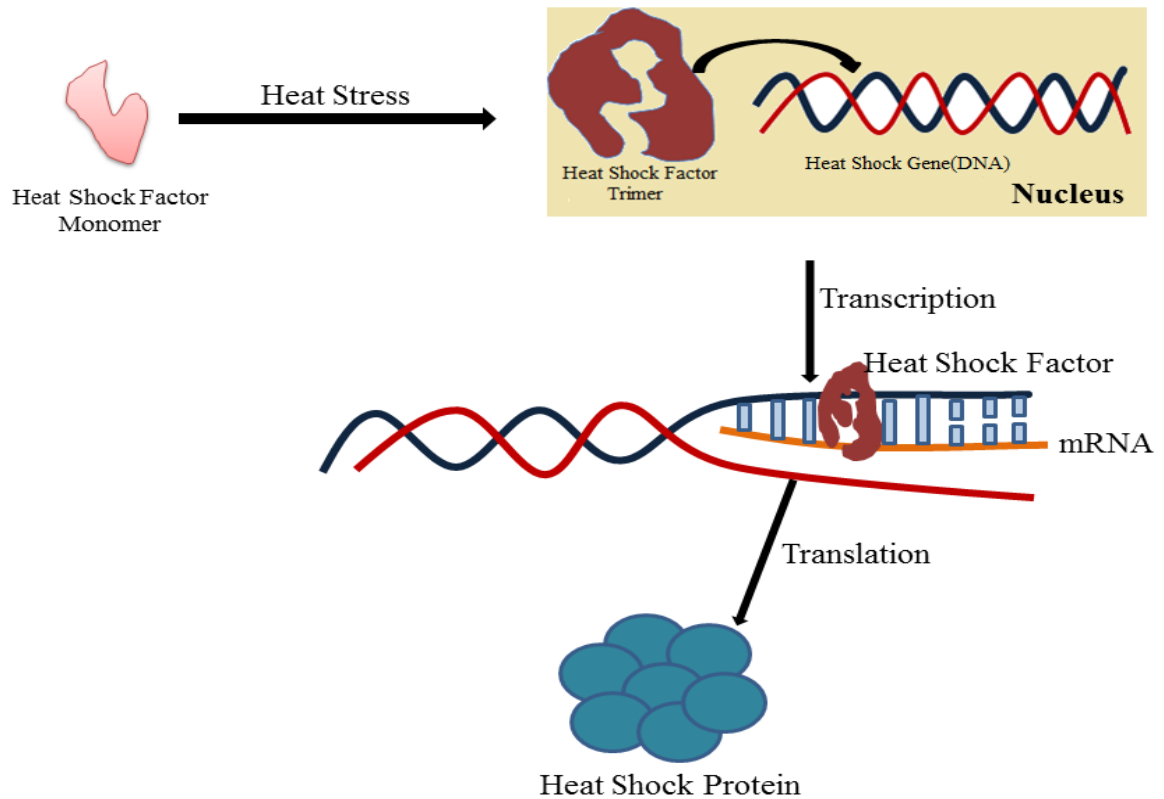
Most proteins do not fold spontaneously and are prone to aggregation during folding, protein folding efficiency in the cell would be too low to meet biological requirements without intervention [46]. Protein folding in vivo is facilitated by the presence of a large group of related proteins that interact with folding proteins throughout the folding process and beyond. These helper proteins have been termed "molecular chaperones". Molecular chaperones are a diverse group of structurally unrelated proteins that assist in the formation of correct protein structure without becoming a part of the final structure [47]. Protein folding with the aid of molecular chaperones can be referred to as "assisted self-assembly" [48]. Principle that requisite information for the achievement of the native structure is still upheld, as molecular chaperones do not guide folding or impart any information to facilitate folding. Rather, molecular chaperones prevent the association of partially-folded proteins by transiently interacting with regions of the folding intermediate and stabilizing its non-native structure [49]. The folding protein is thereby intercepted before it commits to alternative, unproductive pathways. Molecular chaperones do not act as catalysts in protein folding and their assistance does not increase the rate of folding. Instead, the chaperoning role increases the yield of correctly folded proteins by preventing interactions between molten globule intermediates [50]. Typically, more than 95% of nascent polypeptides fold into their native state under normal cellular conditions just because of the presence of molecular chaperones, or heat shock proteins (HSPs) [51].

The heat shock response was first noted in 1962 with the observation of chromosomal "puffs" corresponding to increased RNA synthesis under elevated temperatures in *Drosophila* [52]. Some 10 years later, it was shown that these puffs coincided with the expression of a group of proteins which were later termed heat shock proteins [53]. Although functionally related, molecular chaperones are a structurally diverse group of proteins. The five main families of HSPs defined by apparent molecular mass are HSP60, HSP70, HSP90, HSP100 and sHSP (Small Heat Shock Proteins). These HSPs are determined by SDS PAGE. Under physiological conditions, each of these HSP families performs roles that contribute to the functional form of "target" proteins. Some of the HSP groups also perform a range of diverse tasks. Interestingly different stress condition including biological, mechanical, nutritional, physical etc. plays a crucial role in various process like hormonal imbalance, shift from anaerobiosis to aerobiosis, starvation, and inflammation and so on. These processes are pivotal for normal protein biosynthesis, bioenergetics process, and other metabolic activity of body [54]. The table below showing the different stress type and their associated functions or descriptions and elucidate their role in different stress conditions.



Stress Type	Description
Alcohol	Ethanol, methanol, butanol, propanol, octanol
Antibiotics	Puromycin, tetracycline, nalidixic acid, doxorubicin
Biological	Infection, inflammation, fever
Mechanical	Compression, shearing, stretching
Nutritional	Starvation involving multiple or any one of following nutritional components (C,N,C <sub>6</sub> H <sub>12</sub> O <sub>6</sub> ,P and NO <sub>3</sub> <sup>-</sup> )
Oxygen	Reactive oxygen species, H <sub>2</sub> O <sub>2</sub> , reperfusion, ischemia
pH	Alkalosis, acidosis, pH shift
Physical	Heat , cold, irradiation, magnetic fields
Psychological	Emotions, emotion related conflicts, hormonal imbalance

**Table No.-2: Different nature that induce the stress condition**



**Figure-1: Mechanism showing the activation of heat shock protein**

## **HSP60**

The HSP60 (bacterial GroEL) family, also known as the chaperonin family, provides folding assistance for polypeptides that cannot achieve their native structure in the cellular environment, despite stabilisation by the HSP70 chaperones. It is estimated that approximately 15% of all bacterial proteins require interaction with HSP60 to fold correctly [55]. HSP60 is arranged in two heptameric discs with seven-fold rotational symmetry [56,57], forming a large, open cavity that can accommodate folding proteins of up to approximately 75 kDa [58,59]. Molten globule intermediates bind to hydrophobic binding sites on the inner apical surface of one of the HSP60 rings [60-62]. Binding of ATP allows the association of the co-chaperone HSP10 (bacterial GroES), a single heptameric ring of ~10 kDa subunits [63], which displaces the folding protein into the HSP60 cylinder and acts as a lid [75]. Protein folding therefore proceeds in isolation, negating the danger of aggregation due to hydrophobic interactions with other folding intermediates [64]. Co-operative hydrolysis of ATP causes conformational changes in the HSP60 subunits that lead to the interior becoming progressively more hydrophilic, thus encouraging the burial of hydrophobic regions of the target protein [65]. ATP hydrolysis in the opposite ring of GroEL triggers the bound HSP10 to dissociate and the target protein to be released into the bulk solution [66]. The polypeptide may fold to its native state within the cage or complete its folding after release from HSP60 [67]. Many proteins require several binding release cycles to attain their native structure. Upon release, these proteins still expose extensive hydrophobicity and are recaptured by HSP60 [68].

## **HSP70**

The HSP70 and HSP60 molecular chaperone families function as a co-operative team to facilitate the correct folding of cellular proteins. HSP70 (bacterial DnaK) is the first molecular chaperone encountered by the folding protein. This chaperone functions as a monomer and recognizes short, extended, hydrophobic-rich segments of the polypeptide chain, thus protecting unfolded polypeptides from interacting either with other regions on the extended chain or other non-native proteins in the cell [69-71]. The chaperone action of HSP70 is dependent on a co-chaperone of the HSP40 (bacterial DnaJ) family and ATP hydrolysis. HSP40 recognizes and binds to the polypeptide as it emerges from the ribosome, targeting ATP-bound HSP70 to the chain [72]. Because HSP70 is able to bind co-translationally to the translating polypeptide, one nascent chain may be stabilized by many HSP70 molecules [73]. Release of the polypeptide from HSP70 is dependent on cofactors and ATP [74]. Binding and release of HSP70 may undergo many cycles until a sufficient length of the chain has been

translated to allow the nascent chain to fold. The polypeptide may then proceed to fold independently or be passed to the HSP60 chaperone machinery for further stabilization [75,76].

## HSP90

The HSP90 family is important for the regulation of a wide range of functional proteins associated with cell signaling and is one of the most abundant molecular chaperones [77,78]. HSP90 functions as a dimer [79,80] and operates in association with various co-chaperones and ATP [81-83]. In eukaryotes, HSP90 has been shown to be important for the activation of steroid receptors, transcription factors, kinases and tumor suppressors [84,85] and can act cooperatively with HSP70 in the late stages of folding of steroid hormone receptors [86]. Once folded, the receptor is inactive and only attains its hormone-binding conformation after interaction with HSP90 [87,88]. Importantly, the locations and the molecular size of these heat shock proteins are an important signal for their normal functions. Due to stress environment, these proteins are constitutively expressed in organelle like cytosol and mitochondria, where it triggers their various activities. The table below enlisted these important HSPs and their associated action in different stress condition.

HSP	Molecular Size (kDa)	Location	Functions
HSP10	10	Mitochondria	Cofactor for HSP60
Low molecular weight HSPs	20-30	Cytosol/Nucleus	Regulation and migration of cellular cytoskeleton, regulate vascular tone and vessel wall remodeling.
HSP56	56	Cytosol	It stabilizes the steroid hormone receptor complex by binding with it
HSP60	60	Mitochondria	It is important for folding and assembly of newly imported proteins
HSP72	72	Cytosol/Nucleus	Highly stress inducible (tolerance)
HSP73	73	Cytosol/Nucleus	Constitutively expressed molecular chaperone

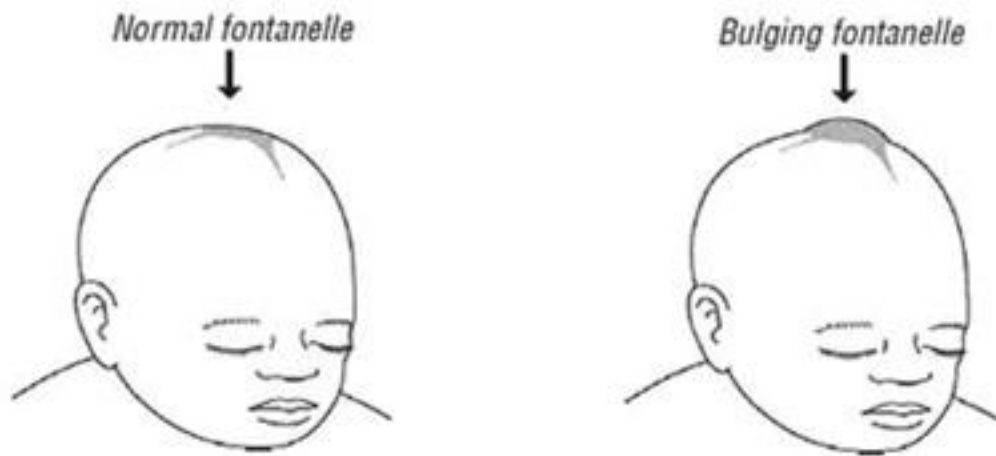
**Table-3: Short description of different heat shock proteins**

## **Pathogenesis of Infection**

Bacterial meningitis causing microorganisms presents different specific properties to promote adherence, colonization and invasion of the mucous membranes of the nasopharynx. Pilli and nonpolar adhesins are virulence factor which mediate the attachment of microorganism to mucous. Many host defense mechanisms evaded in course of attachment. For attachment and invasion, it is important to inactivate secretory IgA and escape from the ciliary clearance mechanisms of the nasopharyngeal mucosa. Bacteria cleaved the human IgA-1 by secreting protease. IgA-1 is the site of adherence and invasion by bacteria and it is dominant immunoglobulin class in the nasopharyngeal mucosa [89, 90]. Endocytotic process in *Neisseria meningitidis* leads to Invasion across the nasopharyngeal mucosa. Separations in the apical tight junctions of columnar epithelial cells in *Haemophilus influenzae* provide another route of invasion [91, 92]. Once the mucosal barrier is crossed, encapsulation is the most important virulence factor to invade the meninges and to overcome additional host defenses to survive in the bloodstream. The polysaccharide capsule helps in preventing classical complement pathway bactericidal activity by inhibiting neutrophil phagocytosis and thus enhances intravascular bacterial survival and replication.

## **Diagnosis of Bacterial Meningitis**

Nonspecific clinical findings such as abnormal temperature, lethargy, and poor feeding predominate in the neonate and in young infants. Characteristic sign in the age group of 3 months to 10 years are alteration of the mental status, nuchal rigidity, and the signs of Kernig and Brudzinski. Presence of a bulging fontanelle is a relatively a characteristic sign of bacterial meningitis but not present in early stage of the disease. A lumbar puncture also called spinal tap is performed to confirm the disease if the slightest evidence through characteristic sign suggests the presence of bacterial meningitis. However, quick diagnosis and commencement of therapy are the most important prognostic factors for positive outcome. Preliminary assessments are mainly based on the CSF characteristics (glucose, lactate, leukocytes, and protein). Structural and metabolic modification reflected by CSF parameters and Gram-staining, such as permeability amplification of BBB, which illustrate the inflammatory response.



**Figure-2: Bulging fontanelle, a characteristic sign of meningitis**

### **Leukocytes**

CSF leukocytosis is known to be a distinctive feature of bacterial meningitis. Before reaching the CSF, a crucial action of leukocytes for the adherence of vascular endothelium takes place which is followed by migration across the endothelial monolayer into the CSF compartment. This process mediates through adhesion promoting receptors and the endothelium and ligands located on leukocytes are activated by exposure to lipopolysaccharide (LPS) and cytokines: interleukin (IL)- $1\beta$ , tumor necrosis factor (TNF)- $\alpha$  and interferon- $\gamma$  [93-97]. Replication of Bacterial species or its lysis in the CSF compartment directs endothelial cells to generate IL-8. IL-8 is an effective chemo attracting agent [98]. Three lectin carbohydrate binding molecules called selectins, granule membrane protein-140 (CD62P), endothelial cell adhesion molecule-I (CD62E), and leukocyte adhesion molecule-1 (CD62L) facilitates the initial reversible adherence of leukocytes to endothelial cells. Each selectin molecule identifies precise carbohydrate sequences on either leukocytes or endothelial cells. Leukocytes are first observed to roll along endothelial cells adjacent to the extravascular site of inflammation. Studies indicate that selectins are involved in the leukocyte rolling. Strong adhesion mediates the binding of integrins to receptors that are available on endothelium. The integrin family of adhesion receptors is composed of heterodimeric glycoproteins having  $\alpha$  and  $\beta$  subunit. They may be categorized on the basis of their  $\beta$  subunit, e.g.  $\beta_2$  integrins (CD11a/CD18a and CD11b/CD18) and  $\beta_7$  integrins (CD49d/ $\beta_7$ ) [99]. By cleavage of the selectin from the cell surface or due to inhibition of its binding, the early selectin adhesion decreases with continued cytokine stimulation. At this instant  $\beta_2$  and  $\beta_7$  integrin facilitated neutrophils adherence to intercellular adhesion molecules (CD54 and CD102) and vascular cell adhesion molecules (CD106) on endothelial cells is directed. Successively, leukocytes navigate the cerebral capillary endothelium through diapedesis [100].

## **Glucose and lactate**

The fluctuation in the levels of glucose and lactate are not only influenced by living bacteria and leukocytes but the metabolism of anaerobic brain in bacterial meningitis is also added to the growth of elevated levels of CSF lactate concentration and hypoglycorrhachia [101]. It appears that local changes in the brain due to ischaemia or mediated by humoral factors, causes an increase in the lactate production. Experimental canine meningitis validated the additional explanation for the development of hypoglycorrhachia. In these animals, the inhibition of carrier mediated transport across the BBB is indicated by low level of CSF glucose. [102, 103]. The elevated usage of glucose in the brain and the abnormal glucose transport across the BBB may contribute to hypoglycorrhachia [104].

## **Protein**

The elevated concentration of protein in CSF during bacterial meningitis is caused by an increased permeability of the BBB. A uniform response consisting of an early and sustained increase in formation of pinocytotic vesicles and a progressive increase in the separation of tight junctions between endothelial cells is observed during the course of experimental meningitis [105]. The cytokine endothelium leukocyte interaction is probably responsible for the disruption of the barrier by opening intercellular junctions and thereby permitting the passage of serum proteins into the subarachnoidal space.

## **Therapy**

### **Antimicrobial therapy**

For many years, combination of chloramphenicol and ampicillin has been known as an effective practical therapy of bacterial meningitis. In many developed countries use of ampicillin has been limited due to the production of anti-ampicillin substance  $\beta$ -lactamase by *Haemophilus influenzae*. For all participating countries a collaborative data for such European study have shown a mean rate of resistance of 15% [106]. In preceding analysis, sporadic cases of chloramphenicol resistant *Haemophilus influenzae* have been recognized and collective resistances to  $\beta$ -lactams and chloramphenicol have been increased [107-112]. Resistance of *Neisseria meningitidis* to  $\beta$ -lactam antibiotics is also found progressively. Penicillin resistant *Neisseria meningitidis* is commonly found in Spain [113]. Infections caused by resistant pathogens are comparatively more dangerous than susceptible pathogens because resistant pathogen relatively results in higher rates of mortality. About the selection of primary empiric therapy of childhood meningitis is still missing due to lack of consent among experts. In children, 3rd generation cephalosporins have become vital antibiotics to cure

bacterial meningitis [114-117]. Ceftazidime, cefotaxime and ceftriaxone are most studied cephalosporins and these are highly potent against *Haemophilus influenzae*, *Neisseria meningitidis* and *Streptococcus pneumoniae* [118-120]. However, *Listeria monocytogenes*, *Streptococcus faecalis* and methicillin resistant staphylococci are resistant to cephalosporins. Ampicillin against *Listeria monocytogenes* and enterococci should be used to reduce the influence of bacterial meningitis in children up to the age group of 3 months. Identification and determination of the etiological agent and its susceptibility are the key factor to decide drug and its dose for the treatment of meningitis. Clinical response of the patients decides the duration of therapy, generally for *Haemophilus influenzae* and pneumococcal meningitis, 10 days are considered while 7 days for meningococcal infections [121].

### **Fluid restriction**

Adequate amount of CSF required to prevent SIADH lacks in children with bacterial meningitis [122,123]. However, in case of infants with bacterial meningitis shows the higher levels of ADH, which may also be described as a suitable response to intravascular volume reduction rather than dysfunction of hypothalamic pituitary axis [124]. Secretion of ADH to sustain sufficient cerebral blood flow compensates the loss of cerebrovascular autoregulation in bacterial meningitis. Cerebral perfusion pressures determined by the difference between the intracranial pressures and mean arterial blood pressure, which plays important role in determining the cerebral blood flow during bacterial meningitis. An increased anaerobic glycolysis of the brain, decrease in mean arterial blood pressure, and significantly decrease in cerebral blood flow have been found due to fluid restriction. However, brain edema is not influenced by fluid regimen [101,125]. Reduction in cerebral blood flow deteriorates the neurological outcome. Meningitic patient who fulfill the diagnostic criteria for SIADH have limited fluid restriction.

### **Vaccination**

Vaccines against *Haemophilus influenzae* type b are available in the market. These vaccines are effective and immunogenic in treatment of meningitis throughout span of the highest occurrence of meningitis caused by Hib, with low side effects [126-133]. Therefore, many countries have introduced childhood vaccination programs for Hib vaccination, resulting 90% reduction in *Haemophilus influenzae* meningitis [128,134]. In North, Latin America and European countries main cause of Meningococcal disease is *Neisseria meningitidis*; serogroup B along with other serogroups of *Streptococcus pneumoniae* which affects a significant number of children. In adults A, C, W135, and Y polysaccharide non-conjugate tetravalent meningococcal vaccine has found to

be immunogenic and safe, but shows opposite response in young infants which limits its use. Subsequently, the use of serogroup B polysaccharide vaccine is limited in humans as it is poorly immunogenic [135,136]. Later field trials also have confirmed only the partial protection against group B infection with the use of such vaccines [137,138]. Different antigenic proteins coupled with significant serotype vaccines for pneumococcal diseases are now open [139].



# **METHODOLOGY**

## **METHODOLOGY**

### **Retrieval and Visualization of 3D structure**

To visualize the 3D structure of the meningitis disease related proteins bexA, ctrA, HPD and SodC. Templates with PDB ID: 4K6I, 1CGI, 4J5R and 4OH2 were identified for meningitic related proteins bexA, ctrA, HPD and SodC respectively using Protein Data Bank (PDB). Once the PDB ID of proteins was identified, these were visualized using pymol.

RAMPAGE (<http://mordred.bioc.cam.ac.uk/~rapper/rampage.php>) was used for visualizing the Ramachandran Plot of proteins for the structural evaluation and stereochemical analysis of proteins.

### **Protein-Protein Interaction Network of HPD Proteins**

To visualize the protein-protein interaction of HPD protein, an online tool String database is used. Name of protein was uploaded in the search tool of this database and selecting particular organism as per required, it display the interaction of various proteins with that particular searched protein.

### **Lipinski Filter Analysis of Screened Drugs (Biomolecules)**

Another online tool Sanjeevini (<http://www.scfbio-iitd.res.in/sanjeevini/sanjeevini.jsp>) is used to get the information of drugs with the help of Lipinski Rule.

Lipinski rule (or Lipinski rule of five) helps to differentiate drug and nondrug like molecules. It is used to identify the possibility of success or failure due to drug likeness for molecules fulfilling with two or more of the following rules

- a) Molecular mass should be <500 Dalton.
- b) High lipophilicity (expressed as logP less than 5).
- c) Less than 5 hydrogen bond donors.
- d) Less than 10 hydrogen bond acceptors.
- e) Molar refractivity should be between 40 -130.

### **Active Site Prediction**

Dogsite Scorer ([www.dogsite.zbh.uni-hamburg.de/](http://www.dogsite.zbh.uni-hamburg.de/)) was used to predict the active sites of protein. This server calculates the possible headerpockets. PDB file of proteins was uploaded in the server and it showed the headerpockets with their binding site atoms present in proteins and involved in binding with ligands.

### **Ligand Optimization and Docking Study**

Sdf files of ligands along with their physical and chemical properties were retrieved from PubChem Compound Database (<http://www.ncbi.nlm.nih.gov/pccompound>). These sdf files converted into pdb format with the help OpenBabel tool. These ligand files and protein pdb files were imported to Hex 8.0 tool for docking. Hex tool was used to calculate the E. values of all the retrieved proteins bind to drug. Molecules with the lowest E. values have higher affinity towards particular protein.

# RESULTS

## RESULTS

### 3 D Structure of Proteins



Figure-3: BexA pdb id: 4K6I

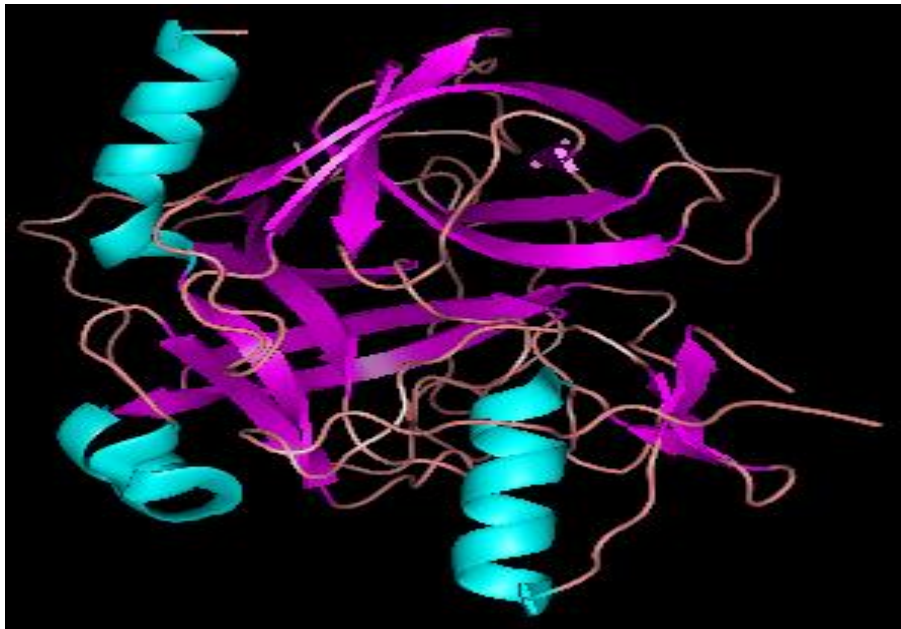
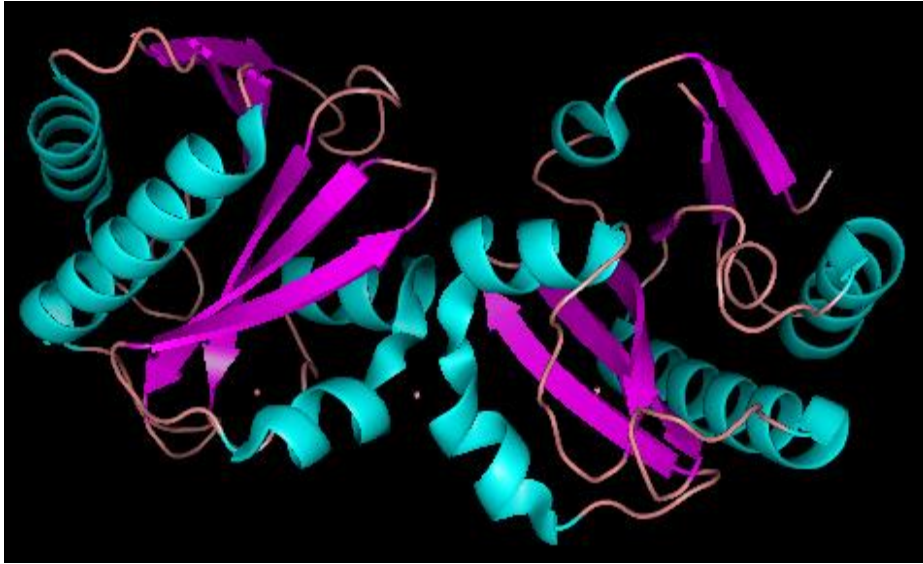
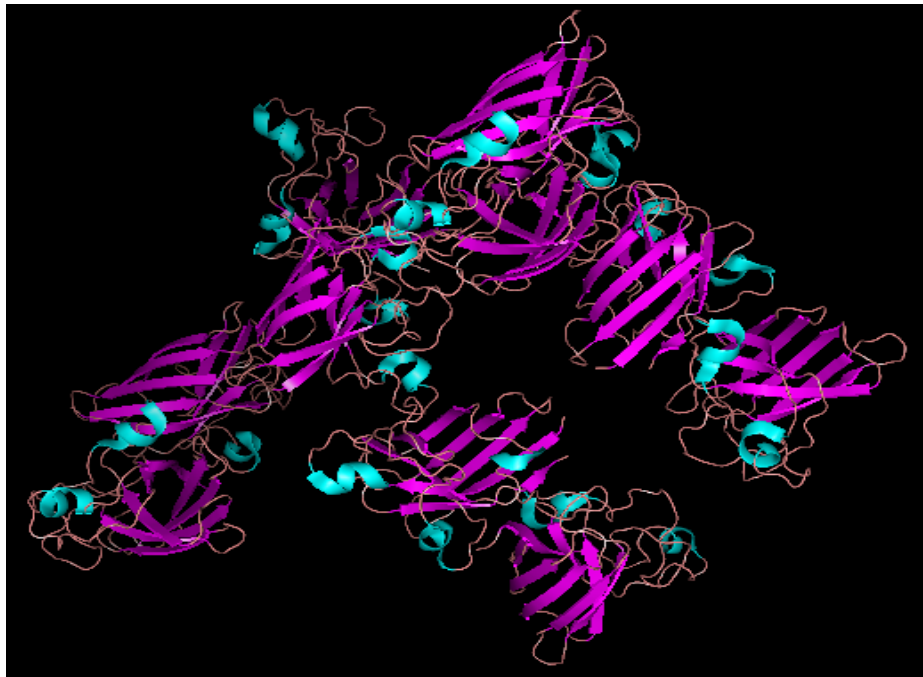


Figure-4: CtrA pdb id: 1CGI



**Figure-5: HPD pdb id: 4J5R**



**Figure-6: SODC pdb id: 4OH2**

3D structure of BexA, CtrA, HPD and SODC were generated using pymol in which alpha helix is shown in skyblue colour, beta sheets in magenta colour and loops in dirtyviolet colour.

## Ramachandran Plot of Proteins

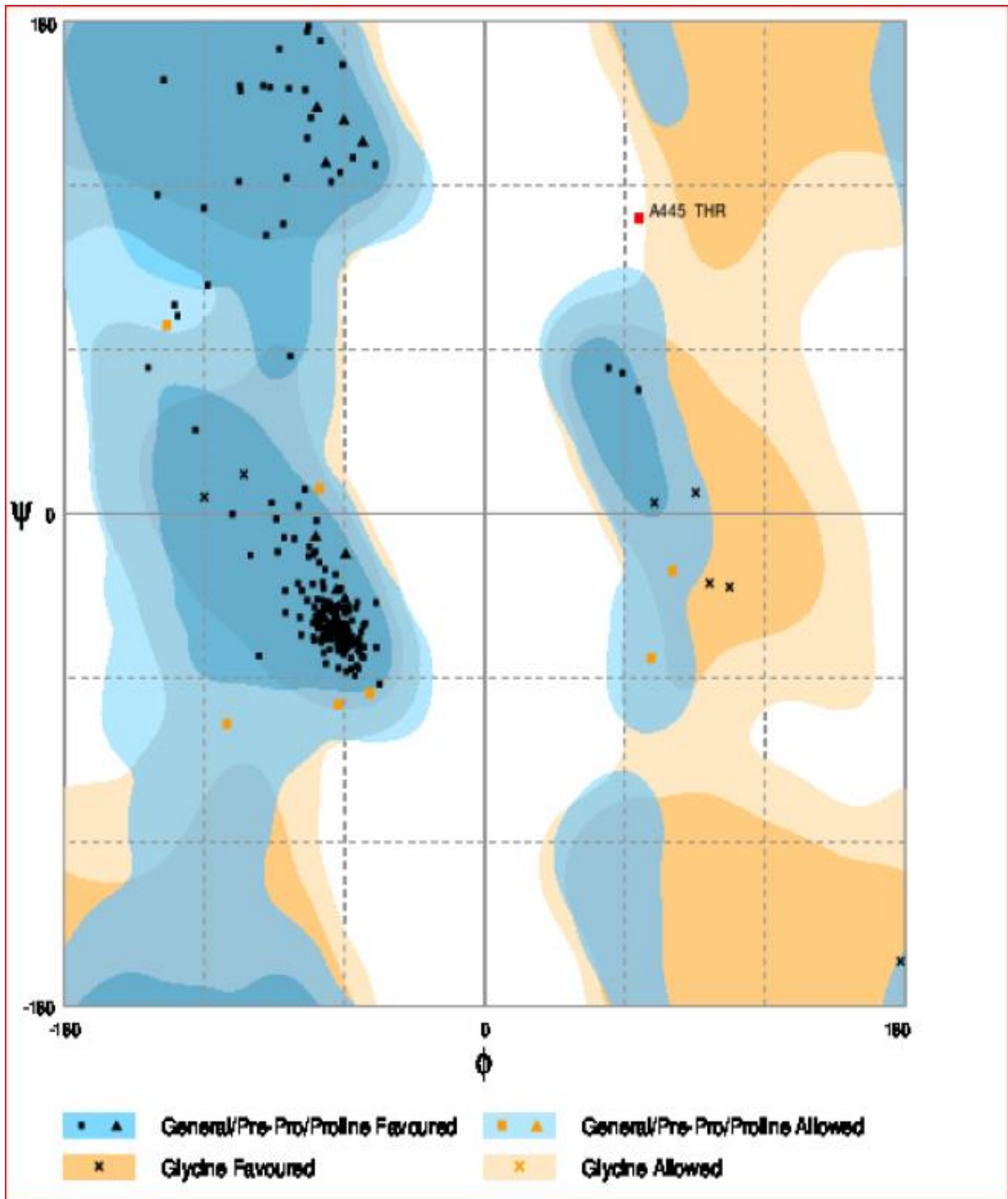


Figure-7: Ramachandra Plot of BexA pdb id: 4K6I

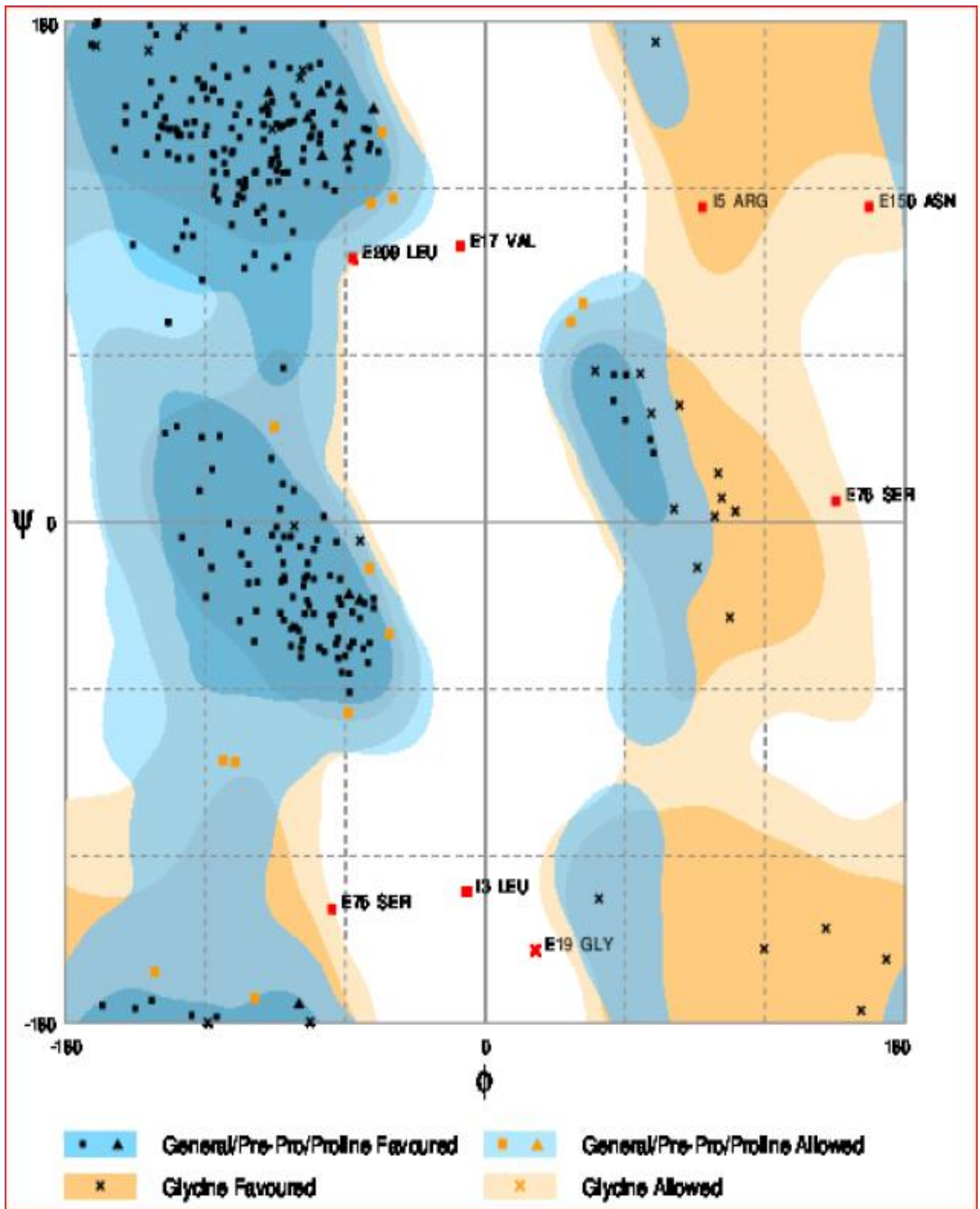


Figure-8: Ramachandra Plot of CtrA pdb id: 1CGI



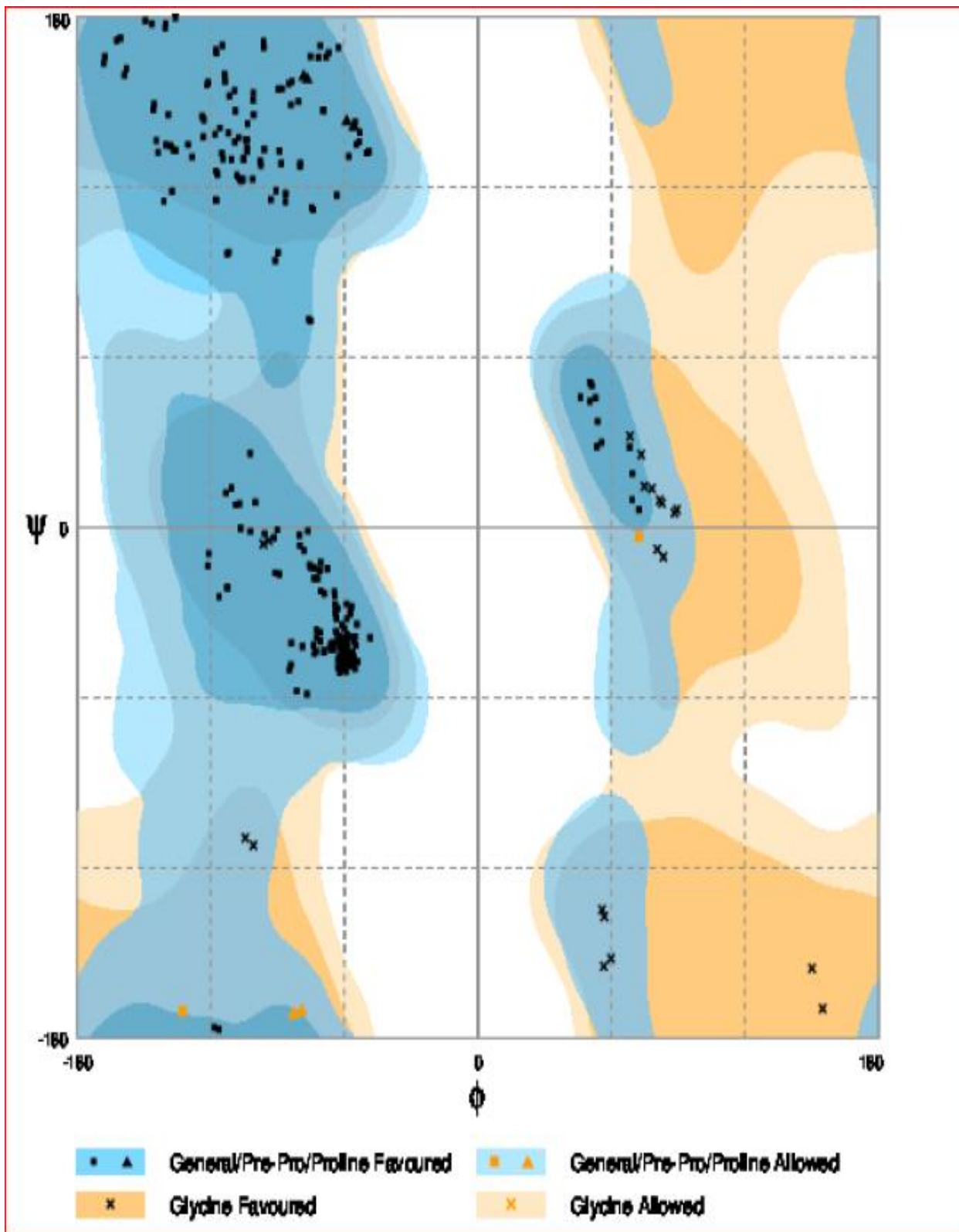
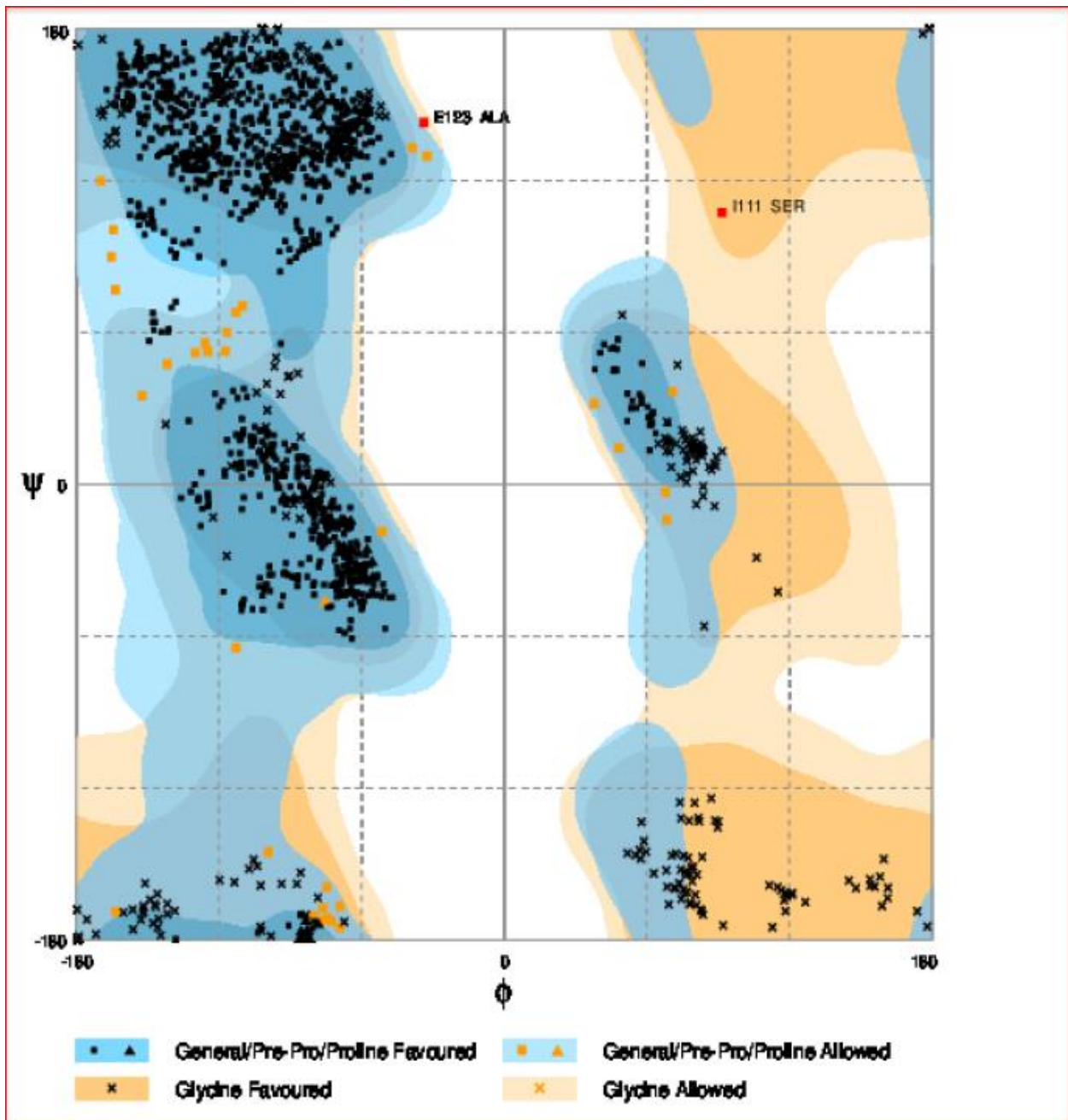


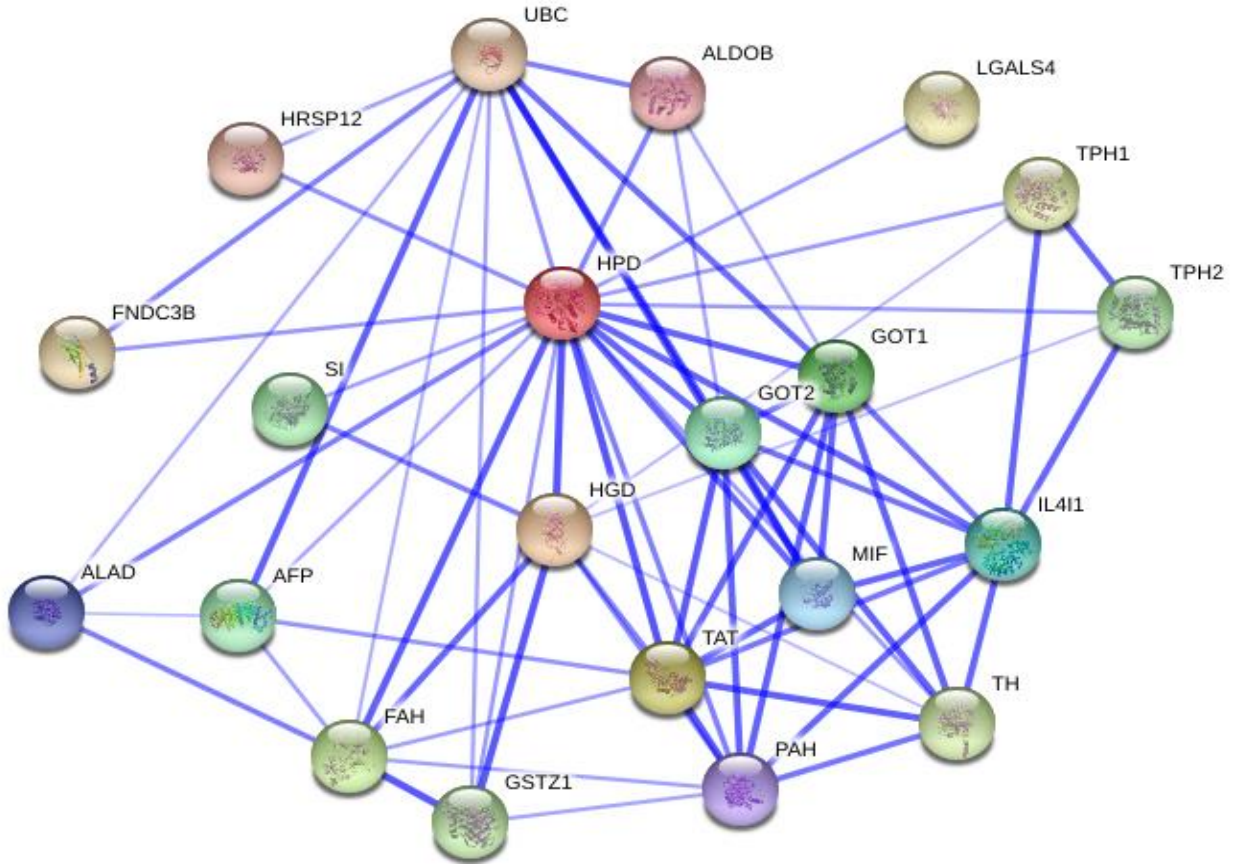
Figure-9: Ramachandra Plot of HPD pdb id: 4J5R



**Figure-10: Ramachandra Plot of SodC pdb id: 4OH2**

Ramachandran plots were obtained for BexA, CtrA, HPD and SodC for quality assessment. RAMPAGE displayed 96.8% of residues in the most favored regions, 3.1% residues in additionally allowed and 0.1% disallowed regions, for BexA, 95.9% of residues in the most favored regions, 3.5% residues in additionally allowed and 0.6% disallowed regions, for CtrA, 98.8% of residues in the most favored regions, 0.8% residues in additionally allowed and 0.4% disallowed regions for HPD and in case of SODC 96.7% of residues in the most favored regions, 3.3% residues in additionally allowed and no residues in disallowed regions.

## PPI Interaction of HPD Protein



**Figure-11: Interaction of HPD with other Proteins**

Protein–Protein interaction (PPI) network of human HPD protein was obtained. This interaction displayed that HPD had a functional interaction with HRSP12, UBC, TAT, GOT1, GOT2, MIF, IL4I1, HGD and FAH etc. HPD plays an important role in the degradation of tyrosine. UBC (Ubiquitin C) and HRSP12 (Heat Responsive Protein 12) are the important chaperons that may be involved in upregulate or downregulate of HPD.

### 3D Structure of Biomolecules

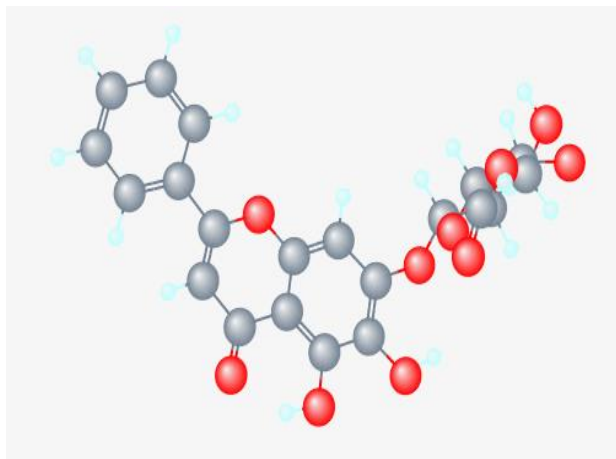


Figure-12: Baicalin

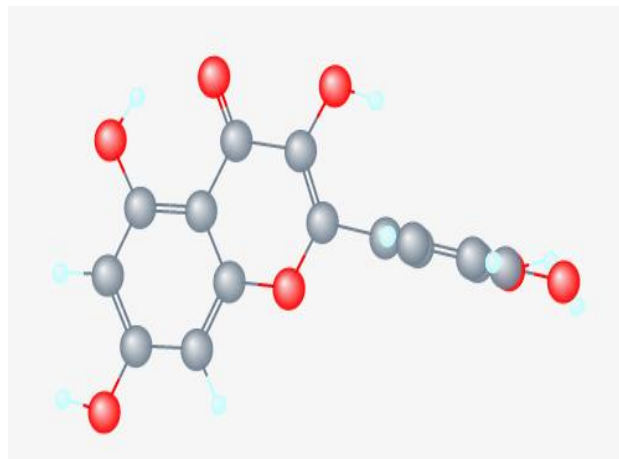


Figure-13: Quercetin

### Physical and Chemical Properties of Biomolecules

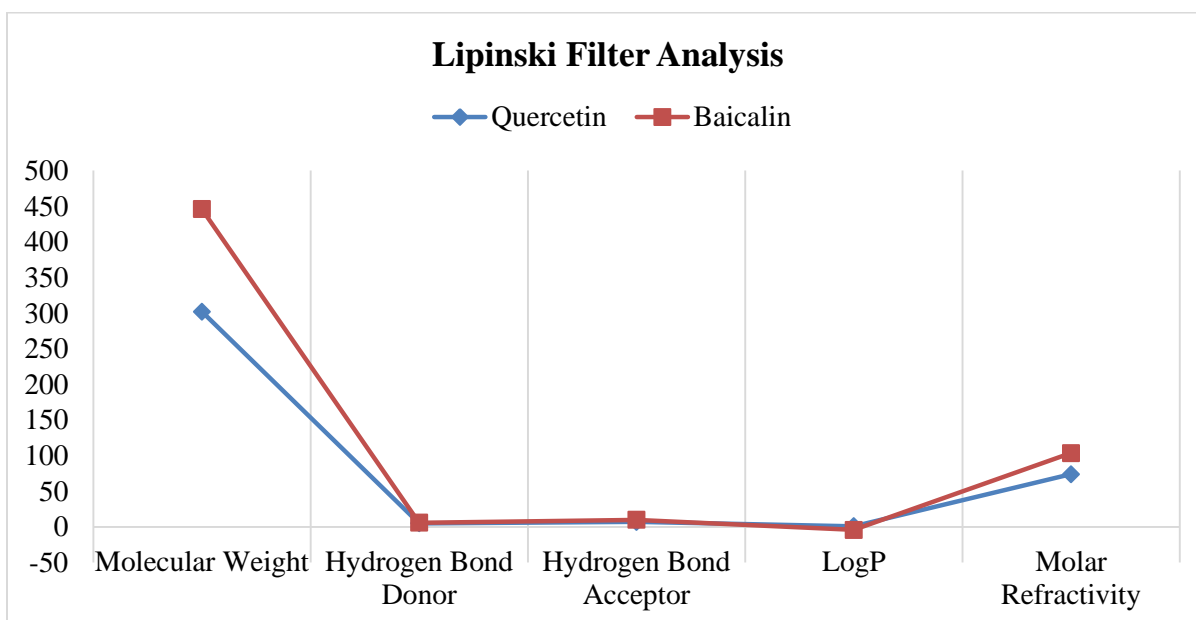
Properties	Baicalin	Quercetin
Molecular Weight	446.36102 g/mol	302.2357 g/mol
Molecular Formula	C <sub>21</sub> H <sub>18</sub> O <sub>11</sub>	C <sub>15</sub> H <sub>10</sub> O <sub>7</sub>
XLogP3	1.1	1.5
Hydrogen Bond Donor Count	6	5
Hydrogen Bond Acceptor Count	11	7
Rotatable Bond Count	4	1
Exact Mass	446.084911 g/mol	302.042653 g/mol
Monoisotopic Mass	446.084911 g/mol	302.042653 g/mol
Topological Polar Surface Area	183 Å <sup>2</sup>	127 Å <sup>2</sup>
Heavy Atom Count	32	22
Complexity	748	488
Defined Atom Stereocenter Count	5	0
Covalently-Bonded Unit Count	1	1

Table-4: Properties of Baicalin and Quercetin

### Lipinski filter analysis of screened drugs

Biomolecules	Molecular Weight	Hydrogen Bond Donor	Hydrogen Bond Acceptor	LogP	Molar Refractivity
Baicalin	446	6	10	-4.136	103.652
Quercetin	302	5	7	0.974	73.91

**Table-5: Differentiation of biomolecules on the basis of Lipinski Rule**



**Graph-1: Comparison between different drugs on the basis of Lipinski Rule**

Lipinski filter analysis was obtained which revealed that the two biomolecules act as drug on the basis of Lipinski rule of five. When it was analyzed that the two molecules had drug like property, these were then used for docking purposes to understand the interaction of Proteins and the analyzed drug molecule.

## Active site prediction

◇ Name	◇ Volume [Å <sup>3</sup> ]	◇ Surface [Å <sup>2</sup> ]	◇ Lipo surface [Å <sup>2</sup> ]	◇ Depth [Å]	◇ Drug Score
P0	1097.98	1138.43	872.08	26.32	0.82
P1	293.63	548.64	377.66	10.51	0.49
P2	287.04	532.48	323.83	12.64	0.56
P3	255.87	360.39	316.77	19.81	0.75

**Table-6: Calculation of headerpockets for BexA**

◇ Name	◇ Volume [Å <sup>3</sup> ]	◇ Surface [Å <sup>2</sup> ]	◇ Lipo surface [Å <sup>2</sup> ]	◇ Depth [Å]	◇ Drug Score
P0	587.26	701.73	418.75	22.94	0.85
P1	390.78	434.30	257.30	13.45	0.65
P2	224.64	327.47	176.34	13.53	0.55
P3	187.58	312.17	115.32	10.89	0.35
P4	166.53	292.84	119.38	11.24	0.40
P5	140.42	267.77	166.44	7.45	0.22
P6	134.21	279.19	124.35	7.90	0.16
P7	130.24	195.24	106.71	7.59	0.21
P8	114.75	325.08	159.83	7.95	0.22
P9	103.68	164.77	83.58	6.44	0.18

**Table-7: Calculation of headerpockets for CtrA**

◆ Name	◆ Volume [Å <sup>3</sup> ]	◆ Surface [Å <sup>2</sup> ]	◆ Lipo surface [Å <sup>2</sup> ]	◆ Depth [Å]	◆ Drug Score
P0	748.80	927.90	736.28	20.21	0.83
P1	522.11	655.04	469.97	12.74	0.67
P2	364.29	496.28	307.98	14.25	0.65
P3	327.62	524.06	346.37	14.18	0.58
P4	165.89	323.04	185.30	11.11	0.37
P5	151.49	335.58	240.74	7.59	0.22
P6	144.51	306.61	193.48	10.48	0.33
P7	138.50	240.51	61.56	7.86	0.18
P8	129.92	298.96	235.41	8.59	0.24
P9	119.68	224.65	111.33	7.12	0.15

**Table-8: Calculation of headerpockets for HPD**



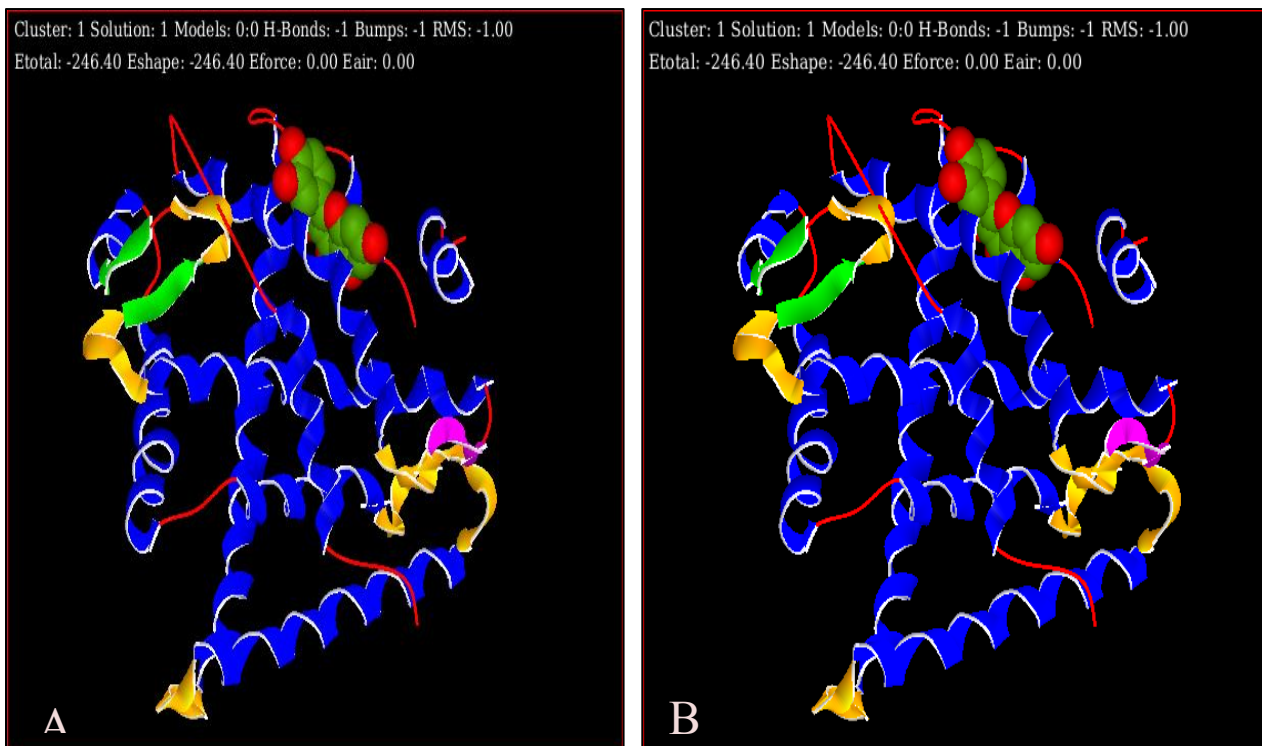
Name	Volume [Å <sup>3</sup> ]	Surface [Å <sup>2</sup> ]	Lipo surface [Å <sup>2</sup> ]	Depth [Å]	Drug Score
P0	1171.36	1316.71	859.55	24.46	0.81
P1	808.27	1138.28	703.19	15.58	0.74
P2	790.18	989.84	552.95	19.04	0.81
P3	755.75	952.98	490.88	19.36	0.81
P4	746.36	868.16	514.42	19.65	0.82
P5	695.93	657.61	435.32	19.83	0.81
P6	658.72	658.11	465.42	19.72	0.81
P7	634.02	919.09	576.43	21.97	0.83
P8	607.94	819.72	481.27	16.33	0.76
P9	576.99	880.58	543.04	15.82	0.74
P10	249.37	498.11	277.04	8.50	0.31
P11	245.89	222.89	115.82	11.70	0.47
P12	236.15	319.00	194.34	15.03	0.58
P13	233.72	381.37	257.34	14.08	0.53
P14	220.85	327.60	216.66	13.10	0.45
P15	216.67	387.69	300.04	12.76	0.50
P16	205.20	242.05	140.06	9.06	0.35
P17	198.94	181.19	102.30	7.34	0.26
P18	187.81	190.16	102.92	9.28	0.35
P19	186.76	275.55	157.67	14.03	0.50
P20	186.76	266.25	175.00	11.87	0.40

**Table-9: Calculation of headerpockets for SODC**

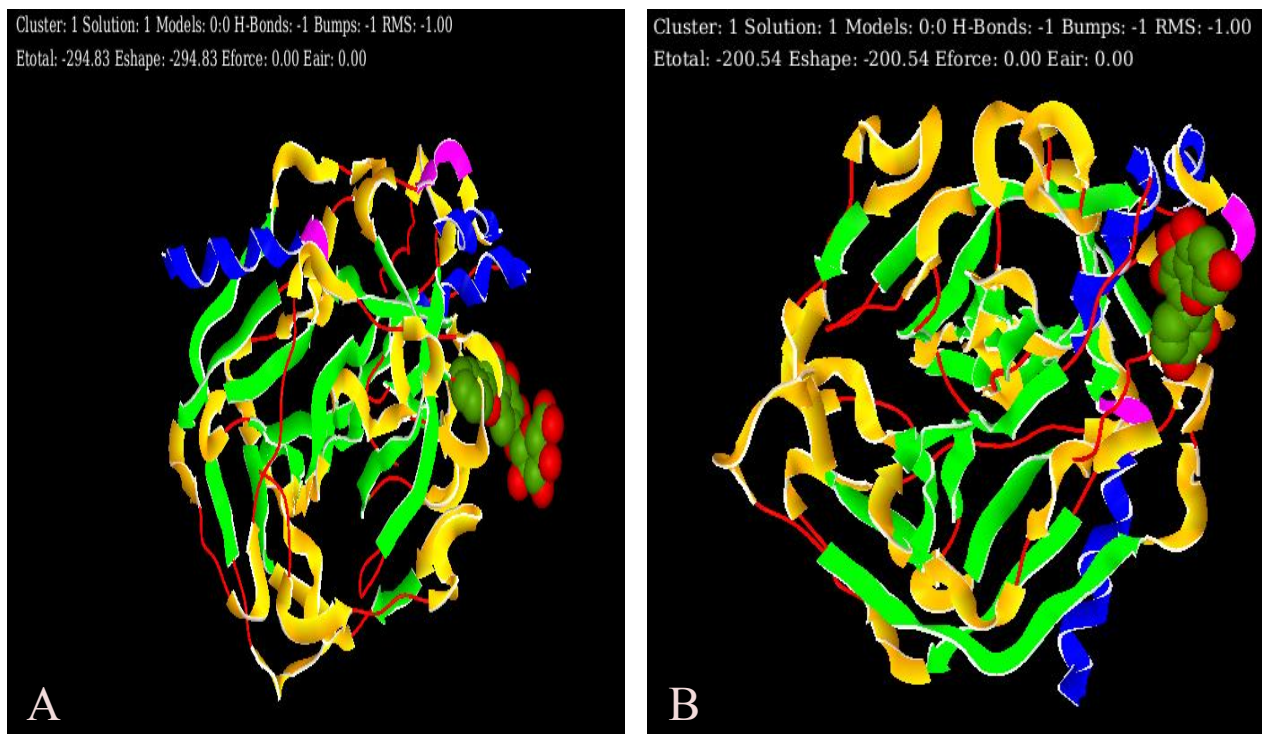
Dogsite-scorer server was used to detect the ligand binding sites in the form of pockets. This server determines the possible active sites from the 3D structure of the proteins. Active site prediction is useful to determine potential ligand binding sites for molecular docking. Site Volume, Surface Area, Liposurface Area, Depth and Drug Score for all the active sites for BexA, CtrA, HPD and SodC proteins were predicted. Pocket with maximum Drug Score is the most suitable site for the binding of biomolecules.



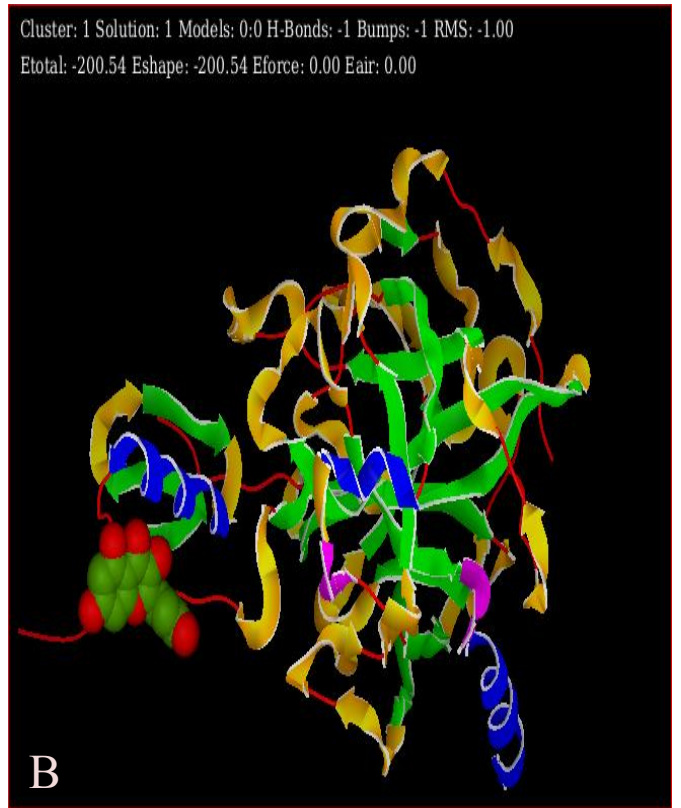
## Docking Result



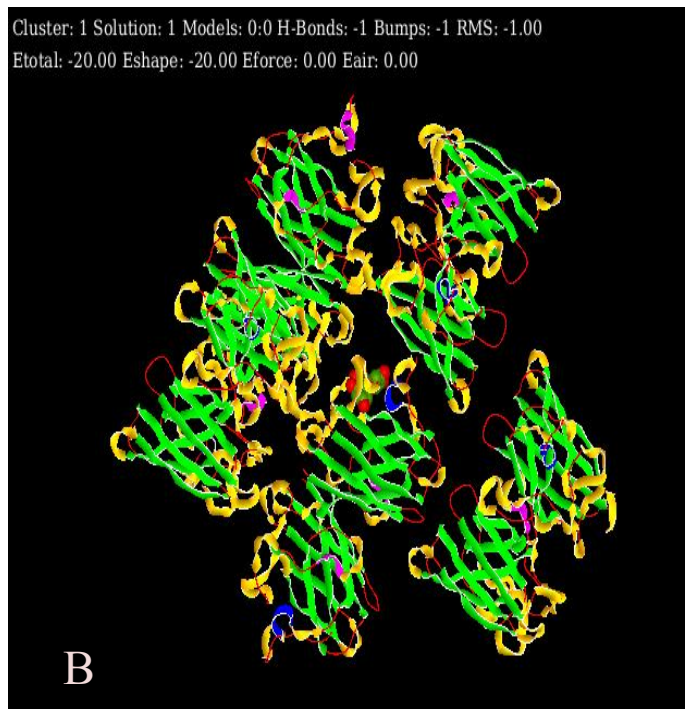
**Figure-14: Docking Result of BexA with (A) Baicalin and (B) Quercetin**



**Figure-15: Docking Result of CtrA with (A) Baicalin and (B) Quercetin**



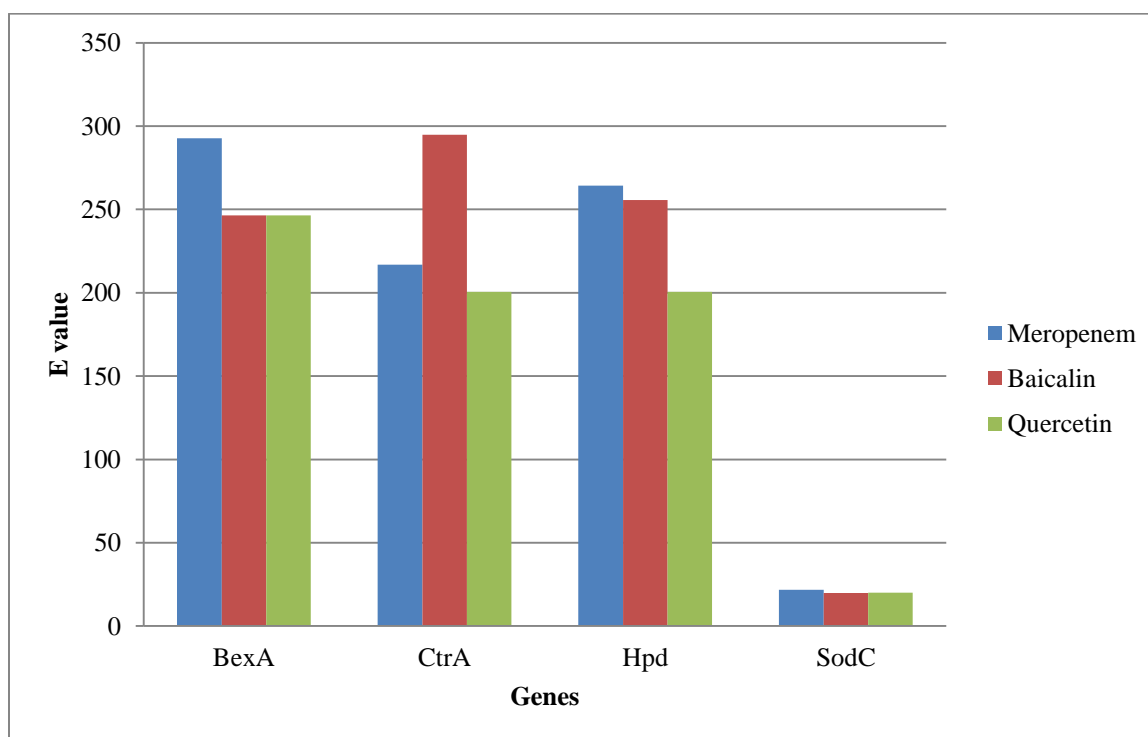
**Figure-16: Docking Result of HPD with (A) Baicalin and (B) Quercetin**



**Figure-17: Docking Result of SodC with (A) Baicalin and (B) Quercetin**

Protein	E. value of Meropenem	E. value of Baicalin	E. value of Quercetin
BexA	-292.78	-246.4	-246.4
CtrA	-216.82	-294.83	-200.54
HPD	-264.38	-255.67	-200.54
SodC	-21.73	-19.9	-20

**Table-10: E. values of Different Drugs**



**Graph-2: Plotted on the basis of E. values**

Hex tool was used for the analysis of the pockets and to identify the best site for the binding of ligand. This tool predicted the best possible site for ligand binding on the basis of E. values calculated from the 3D atomic coordinates of the protein and biomolecules. Docking result for Meropenem against BexA, CtrA, HPD and SodC -292.78, -216.82, -264.38, -21.73 respectively; for Baicalin against same proteins are found to be -246.4, -294.83, -255.67, and -19.9 respectively and for Quercetin against these proteins are found to be -246.4, -200.54, -200.54, and -20 in same sequence as mentioned above. From these data it is clear that Baicalin and Quercetin may work against bacterial meningitis like Meropenem.

# **DISCUSSION**

## DISCUSSION

Meningitis is a chronic neurodegenerative disorder in which inflammation of meninges occurs that results in leakage of CSF. CSF protects the brain from shock, so we termed it as a shock absorber of the brain. Meningitis could occur due to bacterial infection, viral infection or fungal infection. In bacterial meningitis *Neisseria meningitides*, *Streptococcus pneumoniae*, and *Haemophilus influenzae* type b plays an important role and on targeting *bexA*, *ctrA*, *HPD* and *SodC* of these bacteria, I tried to find out the crucial role of two biomolecules i.e., Baicalin and Quercetin with help of bioinformatics tools which could be used for curing this disease. It has been experimentally checked in wet lab that Baicalin can be used for delaying the influence of meningitis and Quercetine a well-known bioflavonoid used to provide protection to neuronal cell from oxidative stress. Although the drugs to delay the influence of meningitis are available in the market but still there is no permanent treatment of this disease. More than 90% of bacterial meningitis occurs in children. So, it is still a challenging task for the scientists and doctors to identify the permanent treatment of this disease. Ramachandran plot results for *BexA*, *CtrA*, *HPD* and *SODC* displayed 96.8% of residues in the most preferred regions, 3.1% residues in additionally permitted and 0.1% in hindered regions for *BexA*, 95.9% of residues in the most preferred regions, 3.5% residues in additionally permitted and 0.6% in hindered regions for *CtrA*, 98.8% of residues in the most preferred regions, 0.8% residues in additionally permitted and 0.4% in the hindered regions for *HPD* and in case of *SODC* 96.7% of residues in the most preferred regions, 3.3% in residues in additionally permitted and no residues in hindered regions. Baicalin and Quercetin are bioflavonoids may be used for the treatment of this disease. However, both biomolecules have qualified for the rules of Lipinski filter. Dogsite Scorer and Docking results states that Baicalin and Quercetin has more druggability like Meropenem. So, it may be effective in the treatment of meningitis.

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## REFERENCES

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