

Exploring the Molecular Interactions and Inhibitor Binding of Japanese Encephalitis Virus Proteins through Molecular Docking and Simulation Studies

Abstract

This investigation delves into an intricate analysis utilizing molecular docking techniques for the Japanese encephalitis virus (JEV). As a virus transmitted through mosquito vectors, JEV holds the capacity to inflict severe neurological implications by primarily targeting the central nervous system. The ramifications can be dire, ranging from debilitating neurological impairments to fatality. While vaccination serves as a potent preventive strategy, the persistent threat of JEV necessitates a comprehensive exploration of additional therapeutic avenues. In this pursuit, this study focuses on computational docking and simulation methods with an aim to uncover potential pharmaceutical agents that could present fresh solutions for Japanese encephalitis. The research's broader objective is to contribute to a more robust arsenal of strategies against this menacing virus, thereby safeguarding susceptible populations from its profound neurological afflictions.

KEY WORDS

Japanese encephalitis virus (JEV), Computational docking, Simulation method, Neurological afflictions.

Introduction

Japanese encephalitis is a significant health concern caused by the Japanese encephalitis virus (JEV), which belongs to the Flavivirus group. This virus primarily induces inflammation in the central nervous system and is primarily transmitted through mosquito vectors, particularly during warmer months. While its impact is most strongly felt in specific regions of Asia, it has managed to expand its geographical reach, posing global health concerns. The genetic makeup of JEV is characterized by a single-stranded positive-sense RNA genome, spanning approximately 11 kilobases in length. This RNA serves as the blueprint for the synthesis of a polyprotein, a precursor molecule that undergoes subsequent processing by both viral and host enzymes to generate essential structural and non-structural proteins¹. Among the various proteins produced during this process, the envelope proteins hold particular significance. They play a crucial role in enabling the virus to interact with host cells and gain entry into them. The envelope protein, specifically the E protein, is of particular interest due to its multifaceted functions and structural complexity.

The E protein consists of three distinct parts or domains, each contributing to its essential roles in the virus life cycle. One of its primary functions is to facilitate the fusion of the viral membrane with the host cell membrane, a crucial step that allows the virus to enter the host cell. This fusion process is critical for the virus's ability to infect and replicate within the host organism. Additionally, the E protein is involved in other vital functions during the virus life cycle. It plays a key role in viral attachment to host cell receptors, which is the initial step in the infection process. This protein also participates in the assembly and maturation of the virus particles, contributing to the production of infectious virions. Understanding the structural and functional intricacies of the E protein within the envelope proteins of JEV is essential for developing strategies to combat Japanese encephalitis. Research efforts aimed at targeting this protein may lead to the development of vaccines or antiviral drugs that can mitigate the impact of this disease, especially in regions where it poses a significant public health threat².

Japanese encephalitis (JEV) manifests as a diverse range of symptoms in individuals who become infected with the virus³. In severe cases, patients often experience a constellation of symptoms, including high fever, severe headaches, and a host of neurological issues, such as seizures. These neurological complications can escalate to life-threatening levels, underscoring the gravity of the disease. Indeed, JE has the potential to result in fatal outcomes, particularly in cases where timely intervention and treatment are lacking. While vaccines against JE do exist, it's important to note that these vaccines primarily offer protection against specific strains of the Japanese encephalitis virus (JEV). This presents a notable limitation in the overall effort to safeguard populations from this viral threat. The variability of JEV strains in different regions has led to gaps in the effectiveness of existing vaccines, as they may not provide comprehensive coverage against all circulating strains.

In response to these limitations, researchers have embarked on a quest to explore innovative and alternative strategies to combat the virus effectively. The urgency of addressing Japanese encephalitis and the need for broader protection has spurred a growing interest in developing novel approaches to prevent and treat the disease. These endeavours encompass a wide range of research, from exploring new vaccine candidates to investigating antiviral drugs and therapeutic interventions that can mitigate the severity of the disease. The multifaceted nature of Japanese encephalitis, with its spectrum of symptoms and potential for severe neurological complications, underscores the importance of continued research and innovation in the field. Scientists and healthcare professionals are committed to finding ways to enhance our defenses against JE,

ensuring that individuals in affected regions receive the most effective protection and treatment possible. Ultimately, these efforts are critical in reducing the impact of JE and preventing the loss of lives due to this formidable viral disease⁴

This research study is primarily centred around the application of computational methods, specifically molecular docking and molecular dynamics simulations, as powerful tools for the identification of potentially beneficial small molecules derived from plants. The primary focus of these methods is to disrupt the entry process of the Japanese encephalitis virus (JEV) into host cells. The overarching goal of this study is to pinpoint plant-derived compounds that exhibit a high potential for binding to JEV's envelope protein, a critical step that could potentially lead to the development of effective antiviral drugs⁵. The central objective of this research is to leverage computational techniques to screen a wide range of plant-derived compounds and identify those with the strongest affinity for JEV's envelope protein. These compounds are of particular interest because they have the potential to interfere with the virus's ability to enter and infect host cells. This strategy represents a promising new avenue for the development of antiviral drugs targeting JEV, which is increasingly becoming a global health concern due to encephalitis-related illnesses⁶.

Given the rising global concerns associated with JEV and the illnesses it causes, this research seeks to contribute significantly to our understanding of the virus and to explore innovative strategies to combat it. The integration of advanced computational tools with biomedical knowledge is a key feature of this study. By doing so, researchers aim to elucidate the intricate interactions between JEV and the potential drug candidates derived from plant sources. The goal of this research is to identify compounds that can effectively disrupt the virus's entry into host cells, thus mitigating its pathogenicity. By harnessing the power of computational methods and merging them with a deep understanding of JEV biology, this study endeavours to shed light on critical aspects of the virus-host interaction. This knowledge, in turn, has the potential to pave the way for the development of novel antiviral therapeutics, which could be instrumental in countering the global threat posed by JEV.

2. MATERIALS AND METHODS

2.1 Target protein retrieval

Six potent proteins were selected mentioned in (Table 1), and their interaction with the drugs was assessed through docking. These proteins belonged to different functional classes and play important roles in various cellular

processes. The docking procedure involves computationally predicting the binding strength between a ligand and a protein target. PDB IDs of these proteins were obtained from the Protein Data Bank (PDB), and their respective PDB format files were downloaded ⁷. Using the BIOVIA Discovery Studio Visualizer (<https://discover.3ds.com/discovery-studio-visualiser-download>), a 3D molecular visualization software, the team eliminated pre-bound ligand groups, heteroatoms, water molecules, and any unwanted components from the protein structures, ensuring they were refined and free from duplications.

Table 1: List of protein targets for docking analysis.

PDB ID	Protein description	Protein description	Resolution (Å°)
4K6M	Crystal Structure of the full-length Japanese encephalitis virus NS5	The full-length crystal structure of the Japanese encephalitis virus NS5 has been determined using X-ray crystallography. NS5 is a viral protein that plays a crucial role in viral replication, including the synthesis of RNA and viral proteins ¹²	2.60
5WSN	Structure of Japanese encephalitis virus Protein function Protein	The structure of Japanese encephalitis virus (JEV) consists of a lipid envelope containing E and M glycoproteins, surrounding a nucleocapsid core with the viral RNA genome encoding structural and non-structural proteins. The E protein facilitates viral entry and fusion, while M and prM proteins are involved in assembly. Non-structural proteins play critical roles in replication and immune evasion, with NS5 containing important domains for viral RNA synthesis. Understanding the structure and function of JEV is crucial for developing antiviral drugs and vaccines ¹² .	4.30
5MV1	Crystal structure of the E protein of the Japanese encephalitis virulent virus	Crystal structure of the E protein of the Japanese encephalitis virulent virus Protein function Protein - The crystal structure of the E protein of the Japanese encephalitis virus (JEV) provides insights into its function in viral entry and fusion. The E protein is a type II viral fusion protein consisting of three domains: domain I, II, and III. The fusion loop in domain I inserts into the host cell membrane during viral fusion. The dimerization of the E protein is mediated by interactions between domain II of each monomer. The receptor binding site in	2.25

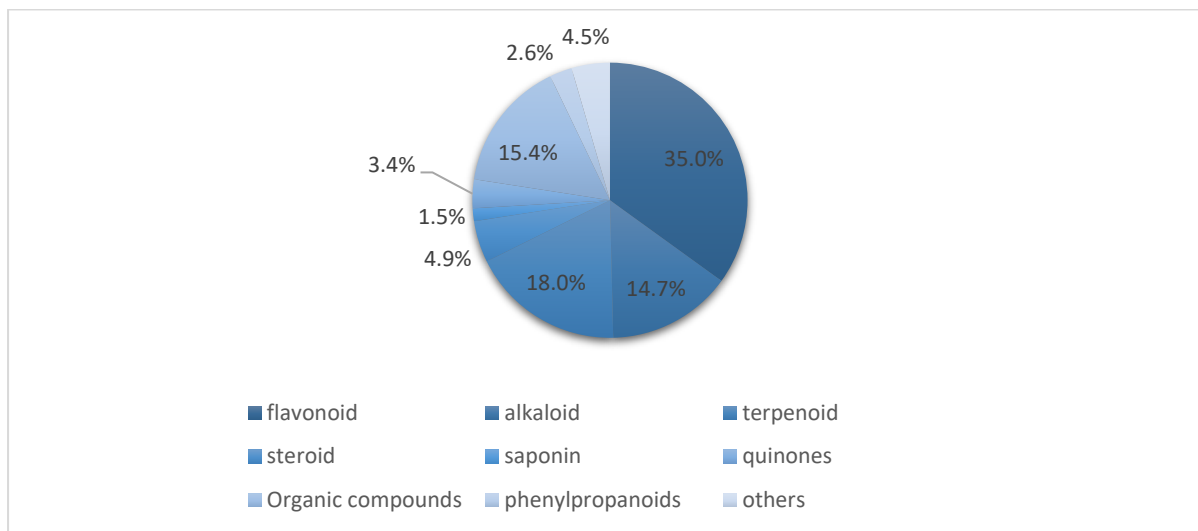
		domain III interacts with host receptors during viral entry, leading to conformational changes that expose the fusion loop and facilitate fusion. Understanding the function of the JEV E protein is important for developing antiviral drugs and vaccines ¹²	
3P54	Crystal Structure of the Japanese Encephalitis Virus Envelope Protein, strain SA-14-14-2.	The crystal structure of the Japanese encephalitis virus (JEV) envelope protein, strain SA-14-14-2, provides insights into its function in viral entry and fusion. The envelope protein is a type I viral fusion protein consisting of three domains: domain I, II, and III and the crystal structure also reveals potential antigenic sites that can be targeted for vaccine development. Understanding the function of the JEV envelope protein is crucial for developing antiviral drugs and vaccines against this virus ¹²	2.10
5YWO	Structure of JEV-2F2 Fab complex	- The crystal structure of the JEV-2F2 Fab complex provides insights into the molecular interactions between the viral envelope protein and a potent neutralizing antibody. The study shows that the 2F2 antibody binds to a conserved epitope on the E protein of the virus, which is essential for virus entry into host cells. The binding of the antibody induces conformational changes in the E protein that prevent the virus from undergoing the necessary conformational changes required for membrane fusion and entry into host cells. This understanding of the molecular mechanisms of neutralization could aid in the development of antiviral therapeutics and vaccines against Japanese encephalitis virus ¹²	4.70
4HDH	Crystal Structure of viral RdRp in complex with ATP	The binding of ATP to the RdRp can induce conformational changes in the enzyme, which are important for its function. For example, the binding of ATP can trigger the closure of the active site, allowing the enzyme to catalyze the formation of phosphodiester bonds between the nucleotides and act as catalysis of RNA synthesis, energy source of RNA synthesis and Regulation of RdRp activity ¹²	2.28

2.2 Drug preparation

In this study, Dr Duke's Phytochemical and Ethnobotanical Databases was used to retrieve a total of 287 potential phytochemical drugs that might exhibit anticancer activity against Japanese Encephalitis Virus (JEV). The database consists of phytochemical which constituents of GRAS (Generally Recognized as Safe) herbs and other economic plants. Further, the phytochemicals were categorized based on their class, with most being flavonoids, alkaloids, terpenoids, and organic compounds, and only a few linked to Steroids, Saponins, Quinones, Phenylpropanoids, and others. (Figure 1). PubChem database was used to obtain the 2D structure SDF (Structured

Data File) format for each drug <https://www.ncbi.nlm.nih.gov>. The obtained 2D structure SDF files were then used in the molecular docking process to determine the binding affinity of each drug with the selected protein targets ²

Figure 1: Phytochemicals classes



2.3. Energy Minimization of Docking Entities

The proteins were then subjected to energy minimization using the UCSF Chimera software⁸ with the help of DockPrep, a surface/binding analysis tool and the hydrogen bonds and charges obtained from Dunbrack Library were added at the appropriate locations. The ligands were procured from PubChem in SDF format and then converted to pdbqt format using the Open Babel Tab provided in Pyrx virtual screening tool software.

2.4. Docking Methodology

In the molecular docking process, it is extremely important to remove any superfluous interactions between the drug and receptor molecules with other molecules that are already present in order to help drug binding at competitive position on the receptor. A standard docking protocol of energy-minimizing each target protein and was using it as a macromolecule was followed. Even ligands were appropriately energy minimized to initiate the docking procedure using the PyRx Virtual Screening Tool Software's Vina Wizard Control, with the Vina Search Space set to maximum and the Vina Run exhaustiveness set to eight. Binding affinity (kcal/mol) and Root Mean Square Deviation (RMSD) lower and upper bound values were recorded for each run, up to the set run value ⁹

2.5. Visualization and Analysis of Docking Results

Only the top scores were selected out of all the RMSD values. Further the ten ligands with the greatest binding affinity ratings for each protein were chosen. The drug-ligand complexes in their 2D form were visualised with the help of BIOVIA Discovery Studio Visualizer. The structure of the ligand and its corresponding target-protein complex showed various types of interactions such as Van der Waals, conventional H-bond, π -anion, π -cation, amide π -stacked, alkyl and π -alkyl, π -sigma, π - π T shaped, Carbon H-bond, π -Sulfur, π - π Stacked, Unfavourable Donor-Donor, and Unfavourable Acceptor-Acceptor interactions ⁶.

2.6. Bioavailability Radar and Pharmacokinetic (SWISS ADME) Profile analysis

The bioavailability radar is a tool that helps to assess the drug-likeness of a molecule based on six physicochemical properties. The pharmacokinetic analysis report obtained from the SWISS ADME web tool (<http://www.swissadme.ch/>), evaluates the drug-likeness of a compound based on its bioavailability. The tool is part of the web tools group provided by the Swiss Drug Design platform, which is supported by the Swiss Institute of Bioinformatics. The report provides an assessment of the compound's pharmacokinetic properties, including its ability to be absorbed, distributed, metabolized, and excreted in the body. A compound with high drug-similarity is more likely to be developed into a successful drug, as it has properties that are desirable for pharmacological activity and can be easily absorbed and distributed in the body¹⁰.

2.7. Computational Toxicity Prediction

The ligands that met Lipinski's rule of five were analyzed to predict their potential toxicity using web-based tool, Protox II. It is a virtual laboratory that uses in silico methods to predict the toxicity of small molecules. The canonical smiles of each ligand were used to analyze their toxicity profiles¹¹. These tools can help to identify potential toxicity issues with drug candidates, allowing to make informed decisions about which compounds to prioritize for further testing.

2.8 MOLECULAR DYNAMICS SIMULATIONS:

After performing docking on the 6 viral proteins, the top ligand showing the best binding affinity was selected for performing a 100ns (nano seconds) long simulation. The software used for these simulations was GROMACS 2023. ¹³on HP-Z4-G4-LLEBSEN workstation with 8 Intel Xeon W-2245(16 threads) and NVIDIA RTX A4000 GPU. The Simulations were performed under AMBER99SB-ILDN force field which are extremely compatible for proteins and their side chains and the ligand was prepared using acpype 2023 ¹⁴ which were solvated in SCP216

(single point charge) water molecules and TIP3P (transferable intermolecular potential with 3 points) water model in a dodecahedron cell of 1 nm dimensions from the complex.

2.9 ENERGY MINIMIZATION:

After solvation of the complexes, Na⁺ Cl⁻ counter ions were introduced to neutralize the charges and later energy minimization was performed. The first energy minimization included a steepest decent method which was followed by a second energy minimization in conjugate gradient method to ensure that the complex is relaxed and has flexible interactions with the solvent molecules. Each energy minimization process had about 50000 steps (each step of 2 fs) until it reached maximum force of 10 kJ/mol, which allowed us to eliminate any bad contacts present in the complex. Later, these complexes were equilibrated with NVT and NPT simulation process at 300 K temperature and 1 bar of pressure for 100 ps. We used V-rescale, a modified Berendsen thermostat and Berendsen barostat along with Partial Mesh Ewald (PME) algorithm for long-range electrostatics and Verlet cut-off for VDW interactions for the equilibrium phases. For the equilibration the VDW (r_{vdW}) cut-off distance was fixed at 1.2 nm as well as coulomb cut-off (r_{coulomb}) and neighbourlist (rlist) were fixed to 1.2. Finally, we performed MD production for all the top ranked ligand complexes with the viral proteins for a time period of 100 ns which included steps of about 50000000 steps (each step were 2 fs). All the trajectories were analysed for their Root Mean Square Deviations (RMSDs), Root Mean Square Fluctuations RMSFs (RMSFs), R_g (Radius of Gyration), Solvent accessible surface areas (SASAs) and the hydrogen bond between protein-ligand complexes.

2.10 MD-Based Binding Energy Calculations

Molecular Dynamics based Binding energy involves studying the interactions energies between protein and ligand. MM-GBSA (Molecular Mechanics- Generalized Born Surface Area) energy methods calculate the end state free energy of the complex. This method calculates the energy difference between the bound and unbound state of the protein-ligand complex or difference between two different solvation states of the same complex. Thus, it analyses the rate of change in the Gibbs Free Energy (ΔG) of the complex. In this study, we performed MM-GBSA calculations to determine the end-state binding free energy of the protein-ligand complexes. In general terms, the binding free energy of the protein with ligand in the solvent can be expressed as:

$$\Delta G_{\text{binding}} = G_{\text{complex}} - (G_{\text{protein}} + G_{\text{ligand}})$$

where, $\Delta G_{\text{binding}}$ represents the binding free energy, G_{complex} represents the free energy of the protein-ligand complex and G_{protein} and G_{ligand} are the independent free energies for the protein and ligand in their isolated

solvated state. These calculations are calculated in implicit solvation model, which involve polar and nonpolar solvation energies. For determining the values of the protein complexes, we used the package gmx_MMPBSA, which allowed us to use gromacs trajectories on AMBER MMPBSA method along with providing visualizations on the energies obtained throughout the simulation. This method allows us to predict the binding energies from an ensemble average of the protein-ligand complex trajectories. Solvent Accessible Surface (SASA) model was used to estimate the non-polar solvation energy [15, 16, 17] term and Coulomb and Lennard-Jones (LJ) potentials were used to extrapolate the (non-bonded) include both electrostatic (Eelec) and VDW (Evdw) interactions. Meanwhile, hydrogen bonds also play crucial role in stable binding between the protein-ligands¹⁸. Further to identify which residues are responsible for the binding and stabilization of the complex we performed decomposition analysis. This allowed us to map the exact residues responsible for the energetics of complex formation.

3.RESULTS AND DISCUSSION

Japanese encephalitis is a viral disease transmitted by mosquitoes in rural Asian areas. It leads to brain inflammation and symptoms like fever, headache, and paralysis. While some people don't show symptoms, it can be severe or fatal. Vaccination is crucial for prevention in affected areas. A study focused on how natural chemicals bind to proteins linked to the virus. They used computer models to predict these interactions. They picked 287 chemicals with antiviral properties from plant databases. These compounds, ranging from fats to amino acids, have potential health benefits like reducing inflammation and fighting viruses. The computer predictions revealed which chemicals strongly attach to the virus-related proteins. This offers insight into potential treatments. The study lays groundwork for exploring natural compounds as therapeutic options against Japanese encephalitis, aiding the development of new drugs for this dangerous viral disease¹⁹

3.1. Molecular docking

Molecular docking is a computational technique used to study the interaction between proteins and ligands. The goal of this technique is to identify potential drug candidates by predicting how a ligand will bind to a protein's binding pocket. The binding pocket is a region of the protein where the ligand can fit in and interact with the protein to either improve or inhibit its activity. In this study, molecular docking was done with the selected six proteins and 287 bioavailable ligands. They then filtered the best protein-ligand pairs based on their binding scores to identify the most potent drug candidate. The binding scores are a measure of the strength of the interaction

between the protein and ligand, with higher scores indicating a better fit between the two. The identified 287 ligands that showed the highest binding affinity with the protein targets, based on the top ten ligands of each protein ranked on the basis of their binding energy values (Table 2). Binding affinity refers to the strength of the interaction between the ligand and the protein, and is influenced by factors such as hydrogen bonding and electrostatic interactions. The higher binding affinity scores were typically associated with ligands that fit perfectly into the protein cavity and formed hydrogen bonds with the protein. The presence of π -cation and π -sigma bonds also played a role in the intercalation of the ligand in the protein's binding sites. Overall, molecular docking is a powerful technique that can help identify potential drug candidates by predicting the interaction between proteins and ligands. In this study, the researchers used this technique to identify the most promising ligands for inhibiting the proteins associated with Japanese encephalitis virus.

Table 2: Top ten ligands showcasing highest binding affinity scores against each protein candidate.

Protein	Ligand Chemical Name	Binding affinity (-kcal/mol)	Grid box parameters
4K6M	WITHAFERIN-A	-9.7	Centre: X:19.35 Y: -46.07 Z:44.45 Dimensions (A°): X:132.69 Y:90.32 Z:94.18
	CASTELANONE	-9.6	
	SILYMARIN	-9.4	
	ATALAPHILLININE	-9.2	
	HAINANOLIDE	-9.1	
	ISOLICOFLAVONOL	-9.1	
	CHAPARRINONE	-9.0	
	SANGUINARINE	-8.9	
	SCILLARENIN	-8.9	
	GLABRANIN	-8.8	
5WSN	SANGUINARINE	-9.2	Centre: X:301.09 Y:223.231 Z:415.37 Dimensions (A°): X: 95.96 Y:72.83 Z:167.92
	WITHAFERIN-A	-9.1	
	SILYMARIN	-8.9	
	HAINANOLIDE	-8.8	
	CHELERYTHRINE	-8.8	
	SCILLARENIN	-8.4	
	GLAUCARUBOLONE	-8.4	
	CHAPARRINONE	-8.2	
	GLABRANIN	-8.2	
	GLYCYCOUMARIN	-8.2	
3P54	WITHAFERIN-A	-9.0	Centre: X: 12.54 Y: -16.93 Z: -23.90 Dimensions (A°): X: 44.62 Y:50.16 Z:129.9359

5MV1	SANGUINARINE	-7.9	Centre: X:17.81 Y:-5.11 Z:22.18 Dimensions (A°): X:112.43 Y:39.65 Z:81.66
	SCILLARENIN	-7.8	
	ATALAPHILLININE	-7.7	
	ISOLICOFLAVONOL	-7.7	
	SILYMARIN	-7.6	
	4',7-DIHYDROXY-3-METHOXY- 5,6-DIMETHYLFLAVONE	-7.6	
	GLAUCARUBOLONE	-7.5	
	EMETINE	-7.5	
	CHELERYTHRINE	-7.4	
	DIHYDROFISSETIN	-7.5	
	PERIVINE	-7.5	
	HAINANOLIDE	-7.4	
	PELARGONIDIN	-7.3	
	NARINGENIN	-7.2	
	PELARGONIDIN	-7.2	
	GLAUCARUBOLONE	-7.2	
CHRY SIN	-7.2		
SCUTELLAREIN	-6.9		
GLYCYCOUMARIN	-6.9		
4HDH	WITHAFERIN-A	-10.5	Centre: X:37.54 Y:9.65 Z:28.21 Dimensions (A°): X:76.50 Y:94.75 Z:93.61
	SANGUINARINE	-9.9	
	KAEMPFEROL	-9.5	
	SILYMARIN	-9.4	
	PELARGONIDIN	-9.3	
	FISSETIN	-9.1	
	MORIN	-9.1	
	CRYPTOPLEURINE	-9.1	
	DEOXYPODOPHYLLOTOXIN	-9.0	
	CAMPTOTHECIN	-9.0	
5YWO	GLAUCARUBOLONE	-7.1	Centre: X:517.76 Y:321.92 Z:604.38 Dimensions (A°): X: 181.60 Y:84.40 Z:72.61
	HAINANOLIDE	-6.7	
	TERNATIN	-6.3	
	QUERCETIN	-6.2	
	5,4'-DIHYDROXY-3,7,3'- TRIMETHOXYFLAVONE	-6.2	
	QUERCETIN-3,3'- DIMETHYLETHER	-6.2	
	CODEINE	-6.1	
	GLYCYCOUMARIN	-6.1	
	PENDULETIN	-6.1	
	ARCTIGENIN	-6.0	

3.2. Evaluation of Pharmacokinetic and Pharmacological Properties

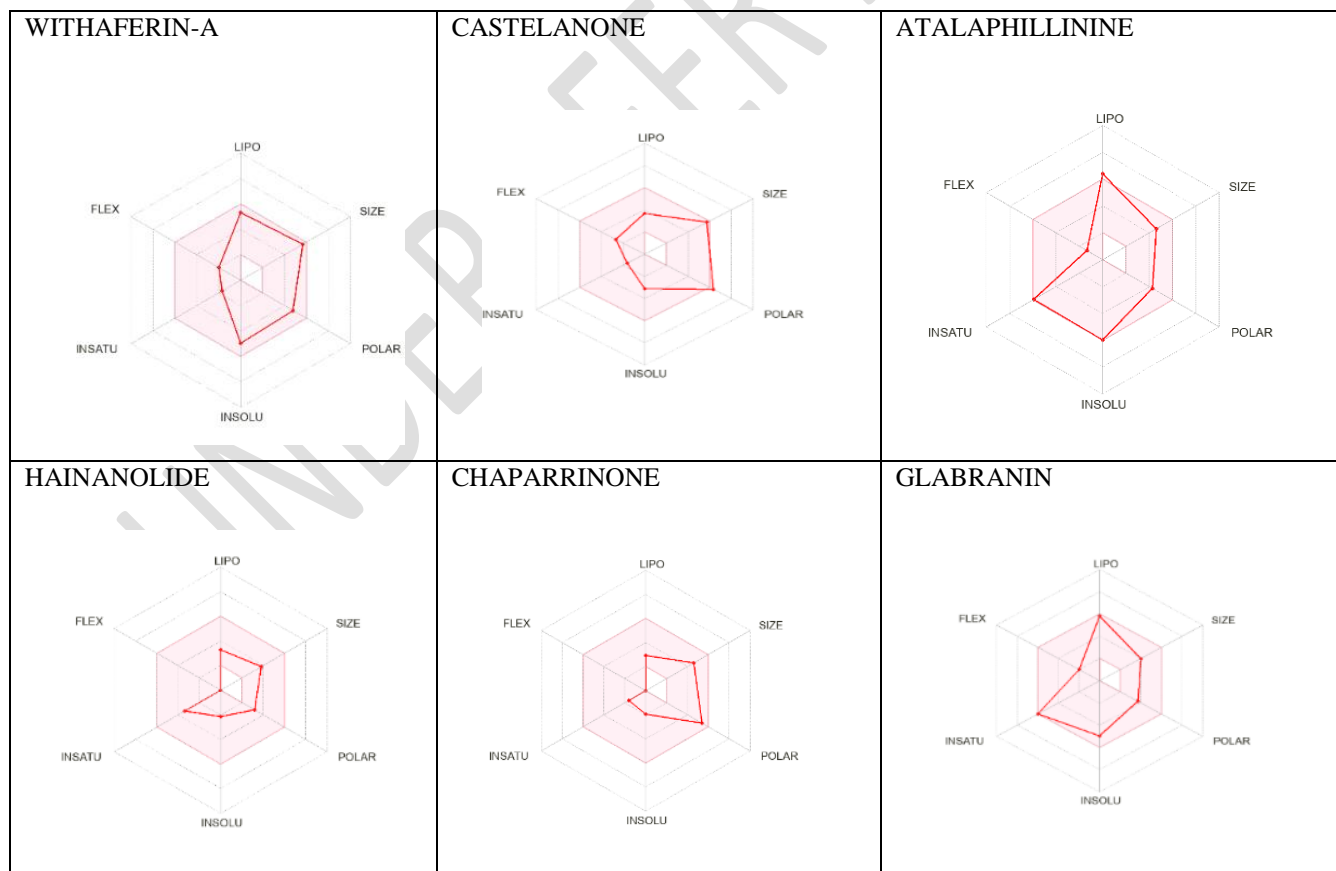
To determine how much the studied phytochemicals' data resembled pharmaceuticals, the Lipinski's rule of five was used. Lipinski's "rule of five," consists of a set of rules, that can be used to predict drug-likeness. According to this, molecules with molecular weights greater than 500, log P greater than 5, hydrogen bond donors greater than 5, and hydrogen bond acceptors greater than 10 have poor absorption or penetration. This rule only explains the molecular features of substances that are connected to their pharmacokinetics. ADME refers to the absorption, distribution, metabolism, and excretion of bioactive substances in a higher organism²⁰. Therefore, the hydrogen donor-acceptor bond content, molecular weight, and lipophilicity of the medicine are used to determine the rule's application. The drug-likeness of the 287 phytochemicals that showed a greater binding affinity to the selected proteins was assessed using Lipinski's rule of five. Chemicals that didn't follow one or more of Lipinski's rules were eliminated from the study, and the remaining substances went through further testing to find out how dangerous they were. The penetration, metabolism, and absorption of chemicals depend on hydrogen bonding, hence they are also crucial for drug preparation²¹.

3.3. Bioavailability Radar and Toxicity Prediction

A drug's water solubility is vital for oral bioavailability and absorption. Swiss ADME web tool is a software used to estimate the physicochemical qualities, absorption, distribution, metabolism, elimination, and pharmacokinetic features of molecules, which are important requirements to go forward with clinical experiments. It includes six essential physicochemical properties: flexibility, lipophilicity, saturation, size, polarity, and solubility²². The molecular weight should be in the range of 150 to 500 g/mol, and the saturation, or the fraction of carbons in the sp³ hybridization, should not be less than 0.25. The parameters for solubility, or LogS should not be greater than 6, flexibility, or XLOGP3, lipophilicity, or TPSA, should be between -0.7 and +5.0, and polarity, or TPSA, should be between 20 and 130 Å⁶. Compared to alternative forms of medication, oral drug formulations are more widely preferred, simpler to administer, and more cost-effective. They also impose fewer restrictions in terms of sterility. One major challenge for drug developers lies in the fact that a majority of new compounds exhibit low solubility in water, which diminishes their suitability for oral administration. Furthermore, the therapeutic efficacy of these compounds is influenced by their high lipophilicity. Resolving these issues becomes essential to enhance the bioavailability of the medication. The substances evaluated for their effectiveness against JEV have been found to be orally bioavailable. During the development process, computational techniques can be employed to assess the safety of a drug, surpassing the advantages offered by in vitro and in vivo experiments. The PROTOX-II webtool was used to conduct a toxicity analysis on the shortlisted chemicals. In order to determine their toxicity,

a number of parameters were used, including predicted LD50, cytotoxicity, carcinogenicity, hepatotoxicity, immunotoxicity, mutagenicity, and oral toxicity²³ Out of the 287 phytochemicals with the highest binding affinity scores for their respective receptors, only 13 ligands were identified to fall within the optimal range indicated by the pink colour on the bioavailability radar (Table 3). These 13 ligands were determined to be free from hepatotoxicity and mutagenicity, and they exhibited either active or inactive characteristics for the other assessed toxicity parameters. Out of all the ligands shown in (Table 4), Castelanone, Chaparinone, and Glaucarubolone belonged to toxicity class II and had the same LD50 value of 10mg/kg, showing their effect if consumed. The four ligands—Withaferin-A, Camptothecin, Codeine, and Cryptopleurine were classified as having Class III toxicity ($50 < LD50 \leq 300$), indicating that they would be slightly toxic and irritating if ingested. The six phytochemical medications Atalaphillinine, Hainanolide, Glabranin, Perivine, Arctigenin, and Deoxydopodophyllotoxin, on the other hand, were less hazardous than class II and III pharmaceuticals and fell into toxicity class IV ($522 < LD50 \leq 2000$)²⁴

Table 3: Bioavailability Radar plot of each shortlisted ligands



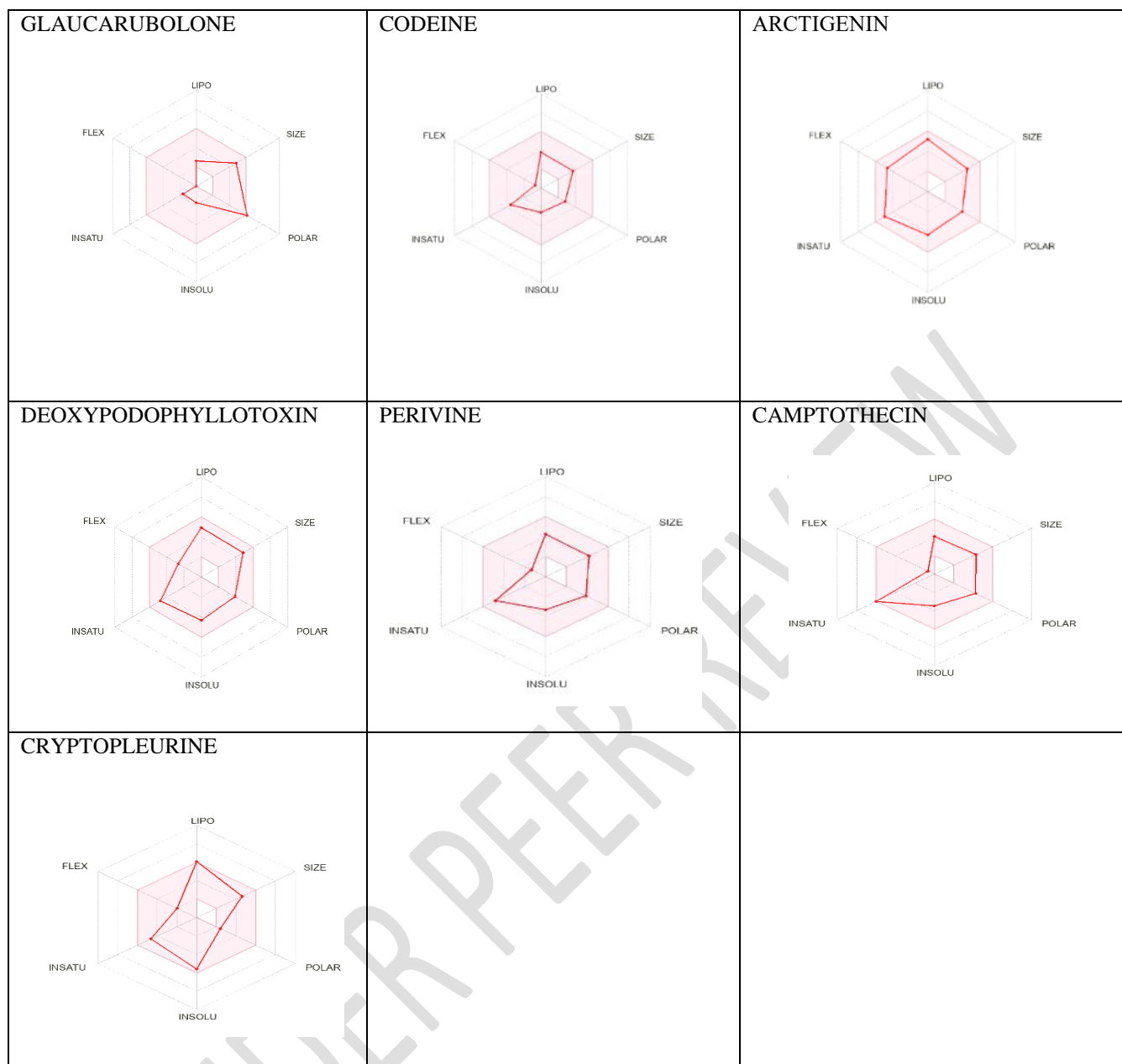


Table 4: Classes of toxicity

LIGAND	Predicted LD50	Predicted Toxicity Class	Hepatotoxicity	Carcinogenicity	Immunotoxicity	Mutagenicity	Cytotoxicity
ATALAPHILLININE	522mg/kg	4	INACTIVE	INACTIVE	ACTIVE	INACTIVE	INACTIVE
HAINANOLIDE	600mg/kg	4	INACTIVE	ACTIVE	ACTIVE	INACTIVE	INACTIVE
GLABRANIN	2000mg/kg	4	INACTIVE	INACTIVE	ACTIVE	INACTIVE	INACTIVE
PERIVINE	760mg/kg	4	INACTIVE	INACTIVE	INACTIVE	INACTIVE	INACTIVE
ARCTIGENIN	1500mg/kg	4	INACTIVE	INACTIVE	ACTIVE	INACTIVE	INACTIVE
DEOXYPODOPHYLLOTOXIN	899mg/kg	4	INACTIVE	ACTIVE	ACTIVE	INACTIVE	INACTIVE
WITHAFERIN-A	300mg/kg	3	INACTIVE	INACTIVE	ACTIVE	INACTIVE	ACTIVE
CAMPTOTHECIN	50mg/kg	3	INACTIVE	INACTIVE	ACTIVE	INACTIVE	ACTIVE

CODEINE	85mg/kg	3	INACTIVE	INACTIVE	INACTIVE	INACTIVE	INACTIVE
CRYPTOPLEURINE	100mg/kg	3	INACTIVE	INACTIVE	ACTIVE	INACTIVE	ACTIVE
CASTELANONE	10mg/kg	2	INACTIVE	INACTIVE	ACTIVE	INACTIVE	INACTIVE
CHAPARRINONE	10mg/kg	2	INACTIVE	INACTIVE	ACTIVE	INACTIVE	ACTIVE
GLAUCARUBOLONE	10mg/kg	2	INACTIVE	INACTIVE	ACTIVE	INACTIVE	ACTIVE

3.4 Molecular dynamic simulation analysis:

The analysis for RMSDs of the MD Simulation trajectories are shown above (Figure 2). Amongst, 4HDH as well as 4K6M complexed with withaferin A, a bioactive compound from *Aswagandha (Withania somnifera)* showed from all the complexes which showed minimal deviations throughout the time lapse of the simulation. These was followed by 5MV1 complexed with dihydrofesitin in our likeability as it showed some deviation after 70ns. Considering, the RMSDs of the ligand in the complexes as shown (Figure 3), we find that the ligands in all the complexes show comparatively sdttable deviation except the withaferin A molecule docked with 4K6M . This rules out this complexes as it shows a variable binding and may not have a strong reaction/response as a result. Amongst these Dihydrofesitin bounded with 5MV1 protein showed least deviation followed by withaferin A bounded with 3P54 at start of simulation, however they show larger deviations as the simulation progresses. This brings us to the withaferin A complexes with 4HDH , which showed a stable RMSD , which suggest a strong binding . Therefore, it is possible for it to possess a good physiochemical response on the protein. By following on the Radius of gyration(Rg) (Figure 4) we find that theprotein 4HDH shows the least Rg. Thus, we can conclude that the protein remains complex and holds on to the ligand. This may allow a strong physiochemical response. Along with this, by comparing the root mean square fluctuation (RMSF) of the protein targets, we find that 4HDH shows a very low fluctuation along its residues and thus we can explain the low Rg. However, the complex of 5MV1 with Dihydrofesitin shows a comparatively higher RMSF(Figure 5), thus it may not be as useful as a potential target for inhibiting proliferation of the virus. Lastly, by examining the SASA of the complexes, we find that 4HDH Complexed with withaferin A shows a decent area exposed to the solvent (water/cytosol), but is not as high as 4K6M as shown in (Figure 6), which might have served an advantage in holding the ligand bound for a longer period of time.

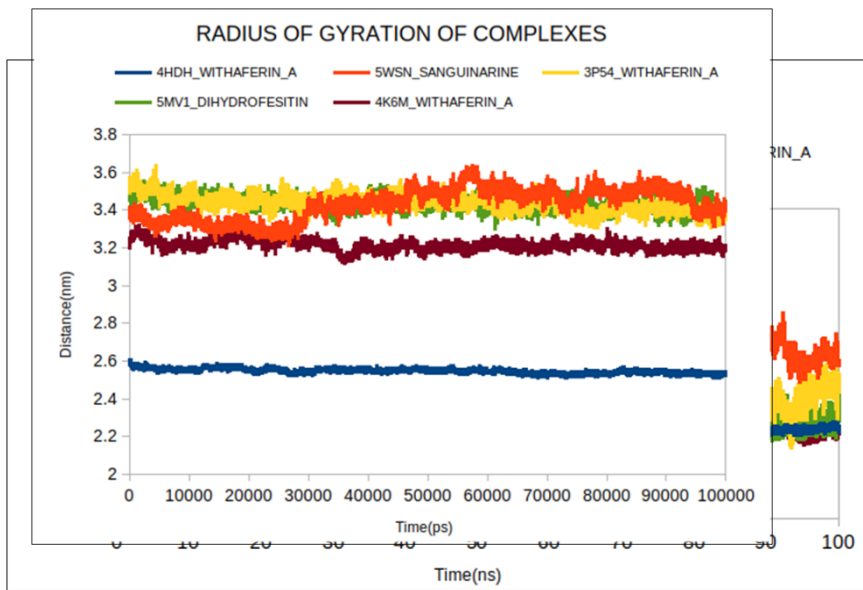


Figure 2: Root mean square deviations of complexes

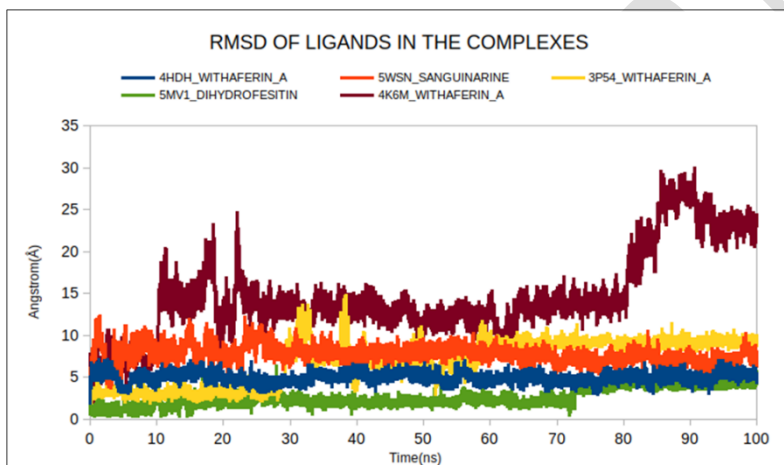


Figure 3: RMSD of ligands in the complex

Figure.4: Radius of gyration

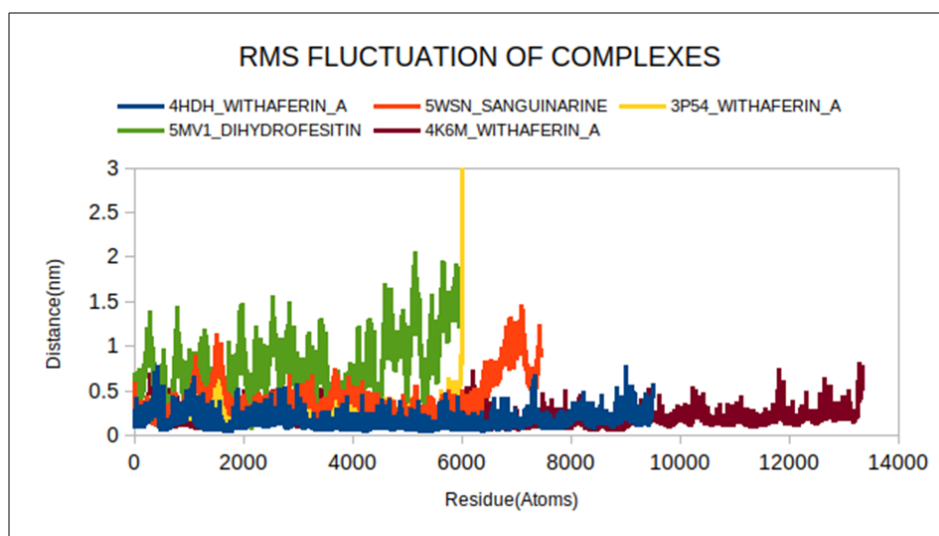
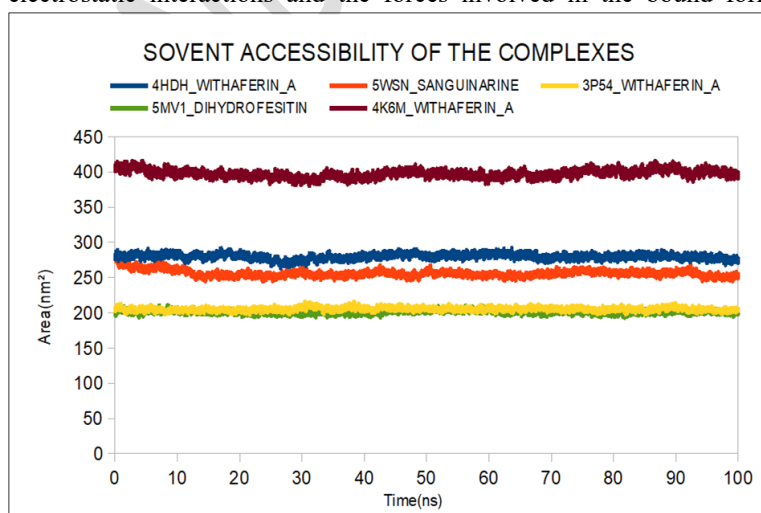


Figure 5: Root mean square fluctuation

Figure 6: Solvent accessible surface analysis

3.5 MM-GBSA END STATE FREE ENERGY CALCULATIONS:

By performing energy analysis we find the theoretical binding energy released at std. conditions. Out of which, the complex of 4HDH bound to withaferin A showed a good binding energy of -35.42 kJ/mol (Table 5) This gives us an indication that this good binding energy may be due to the spontaneity of the reaction leading to the formation of their complex. Above plots (Figure 7 & 8) relate to the factors/components that relate to the binding energy of the complex 4HDH_WITHAFERIN A. The Fig.7 deals with the energy associated with the electrostatic interactions and the forces involved in the bound formation/interaction as well as the energy



associated with solvation of the entire complex in water. The plot has significant negative energy which suggest

that it would readily dissolve in water and find stability relatively quickly.

The Fig.8 deals with the change in energies after formation of the complex, which states that the Delta (ΔG) is negative on totalling all the energies associated with complexation. These negative values denote that the structures are favourable and are most likely to lead to physiochemical changes after complex formation. Thus, may provide a therapeutic use to treat the viral infection. Over performing decomposition binding analysis we find the specific residues involve in the release of energies as noted(Figure 9). From the residues, the ligand (Withaferin A) has a high positive enthalpy(red) through the simulation. This enthalpy we can relate with the release of energy (negative enthalpies of some residues - blue). By relating to this we can state that the energy(enthalpy) needed for ligand to remain bound to the protein 4HDH is provided by the residues with negative energies. This can lead to inactivation of other processes that occur via those residues. Finally, by observing the Delta(ΔG) in the Decomposition Analysis (Figure 10), we find that the major contribution to change in the decomposition comes the ligand, Withaferin A, which validates the association with the protein 4HDH inhibits the functions of the protein. Visualization is essential for making sense of complex data from MD simulations. It helps understand molecular movement, structure changes, and interactions. Trajectory visualization creates animations to show molecular evolution. 3D structural visualization reveals atomic arrangements. Energy plots track system stability. Radial Distribution Functions analyze particle interactions. Free energy surfaces depict favorable regions. Software like VMD, BIOVIA Discovery Studio, PyMOL, Chimera aided in visualization for the trajectory (Figure 11&12). Meanwhile, the structures were extrapolate using GROMACS.

The analysis of Withaferin A within the complexes 4HDH and 4K6M, derived from *Withania somnifera*, provides essential insights into its interactions and potential therapeutic applications. Both complexes exhibit unique structures with Withaferin A, a bioactive compound known for its diverse pharmacological benefits. These complexes unveil how Withaferin A interacts with specific molecular targets, shedding light on its role in modulating biological pathways. Investigating binding sites and interactions within these structures offers a glimpse into possible mechanisms of action and their effects on cellular processes. Docking simulations visually demonstrate interaction orientations, while computational tools like Swiss ADME and Lipinski's rule evaluate the compound's drug-like properties and bioavailability. Molecular dynamics simulations enrich understanding by exploring dynamic behaviour over time, revealing stability and interactions. Visualizing these trajectories helps unravel intricate motions that drive the binding process. Safety assessment using tools like PROTOX-II provides insights into potential toxicity associated with Withaferin A.

Table 5: MM-GBSA END STATE FREE ENERGY CALCULATIONS

	Protein Ligand	Average (kJ/mol)	SD(Prop.)	SD	SEM(Prop.)	SEM
A	4HDH_withaferin A	-35.42	0.53	4.2	0.01	0.04
B	5WSN_sanguinarine	-32.88	0.51	4.59	0.01	0.05
C	3P54_withaferin A	-24.54	6.15	5.96	0.06	0.06
D	5MV1_dihydrofesitin	-23.73	3.83	4.77	0.04	0.05
E	4K6M_withaferin A	-21.36	3.36	8.96	0.03	0.09

[4HDH_withaferin A]

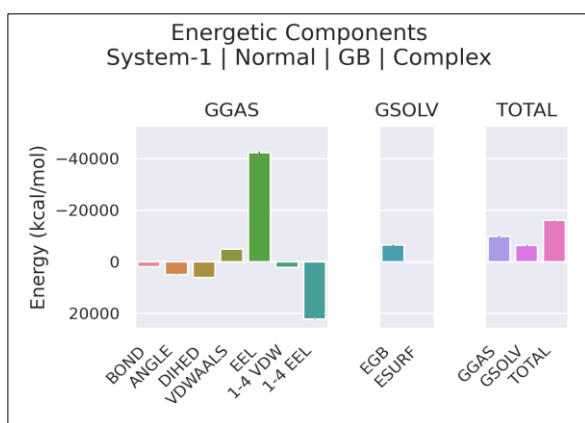


Fig.7: GB Energies for the Complex

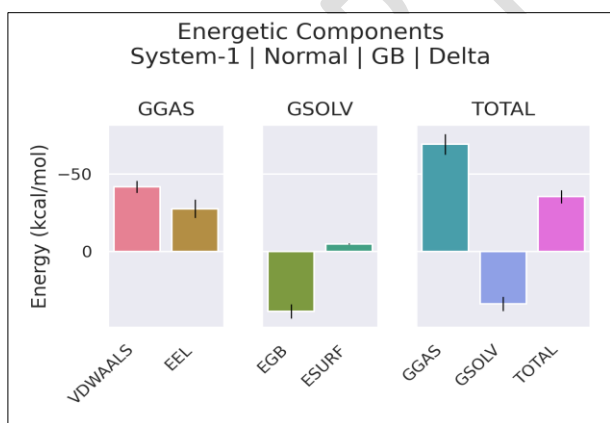


Fig.8: GB Energies for the Change in free energy

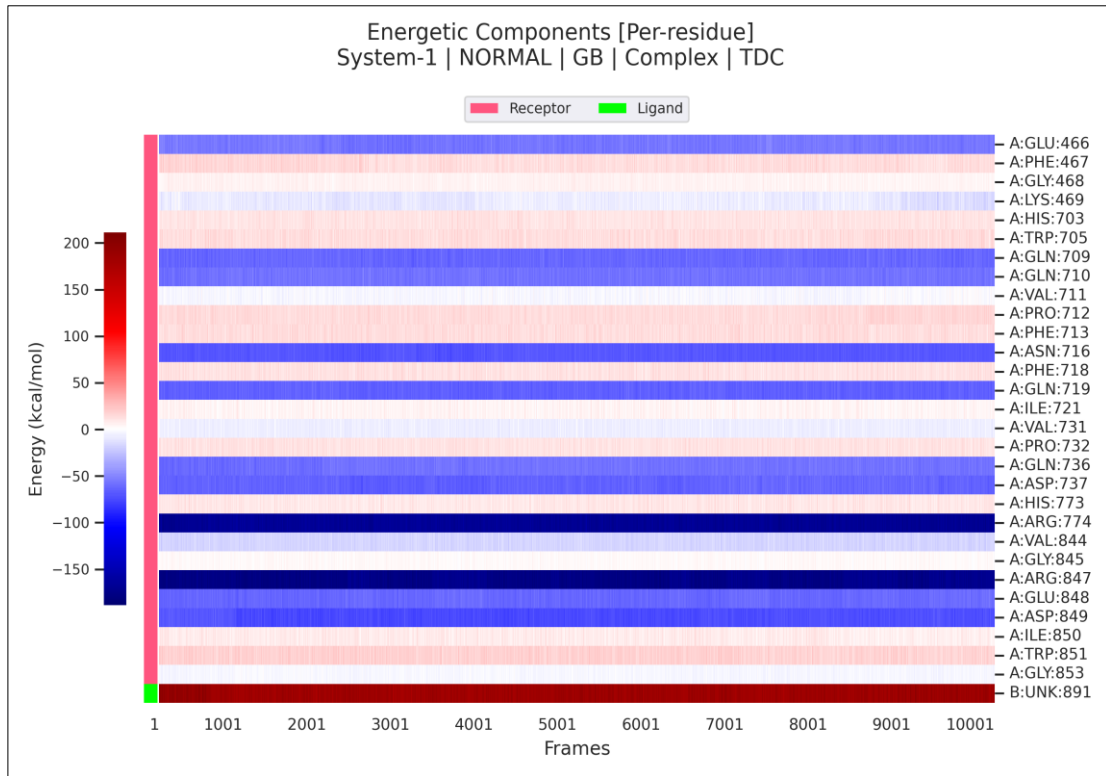


Figure 9: GB Decomposition Energies for the complex

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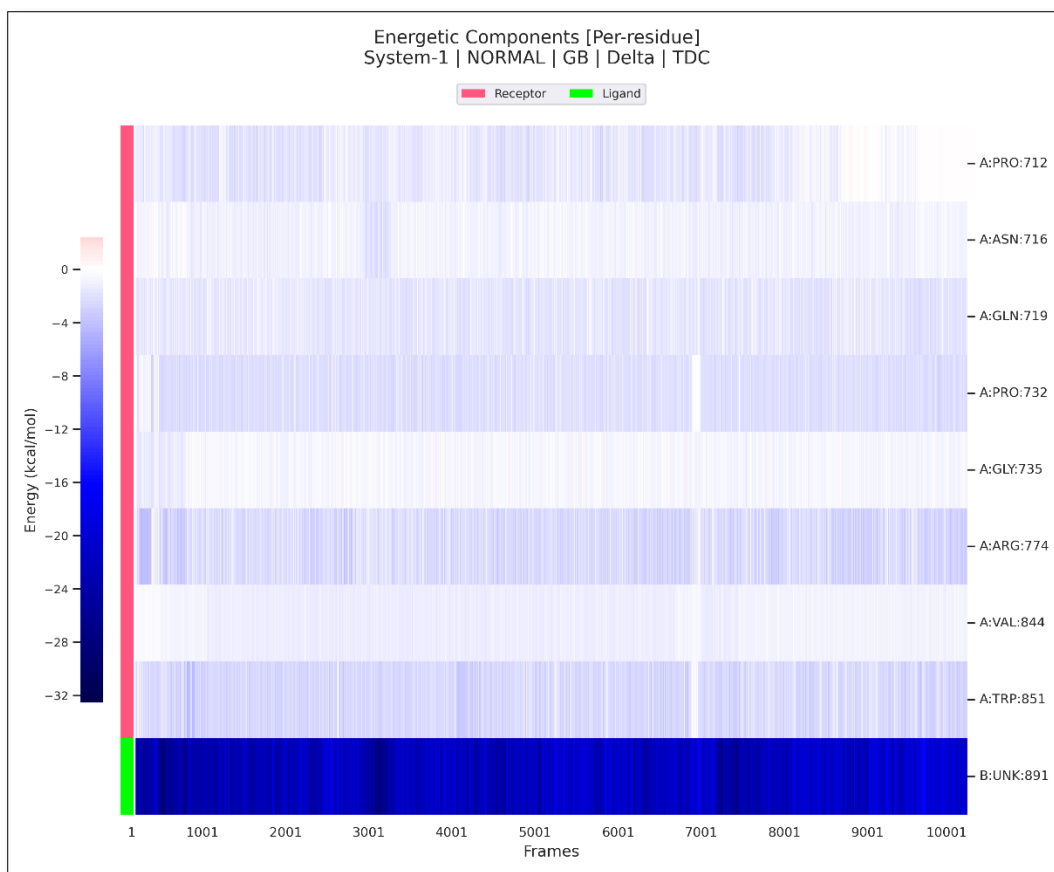


Figure 10: GB Delta decomposition for the complex

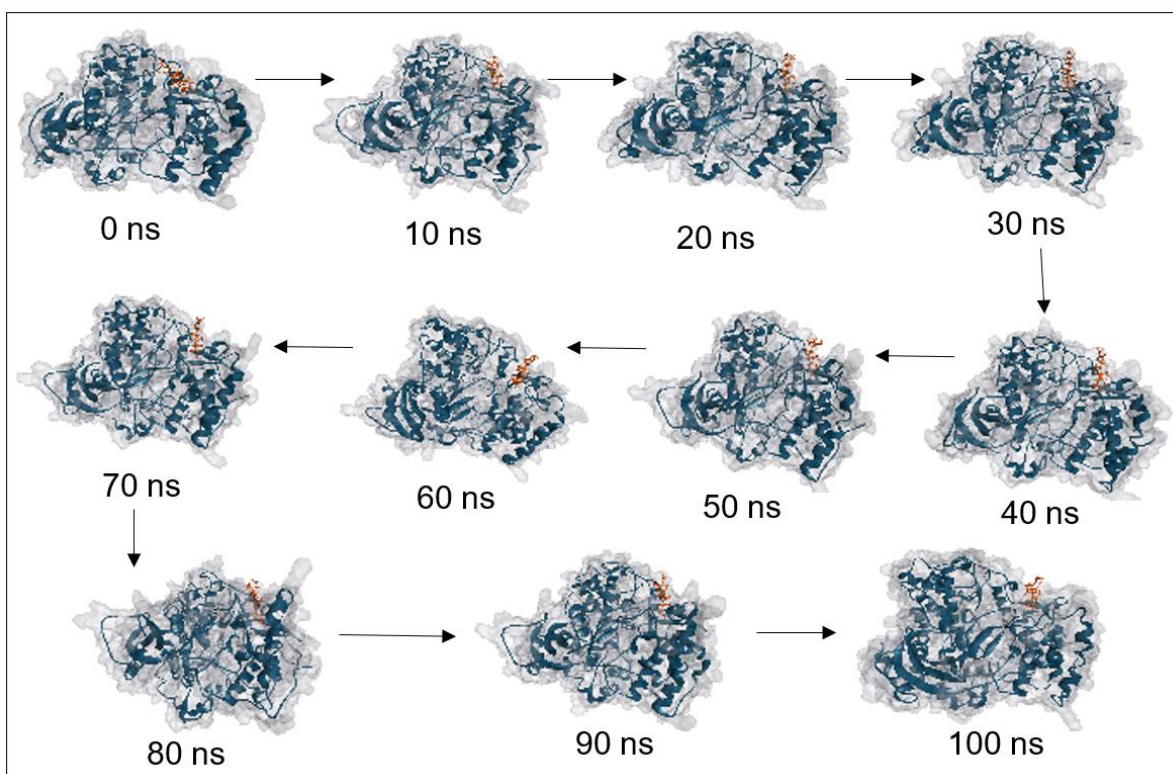


Figure 11 Visualization of Trajectory of 4HDH-WithaferinA

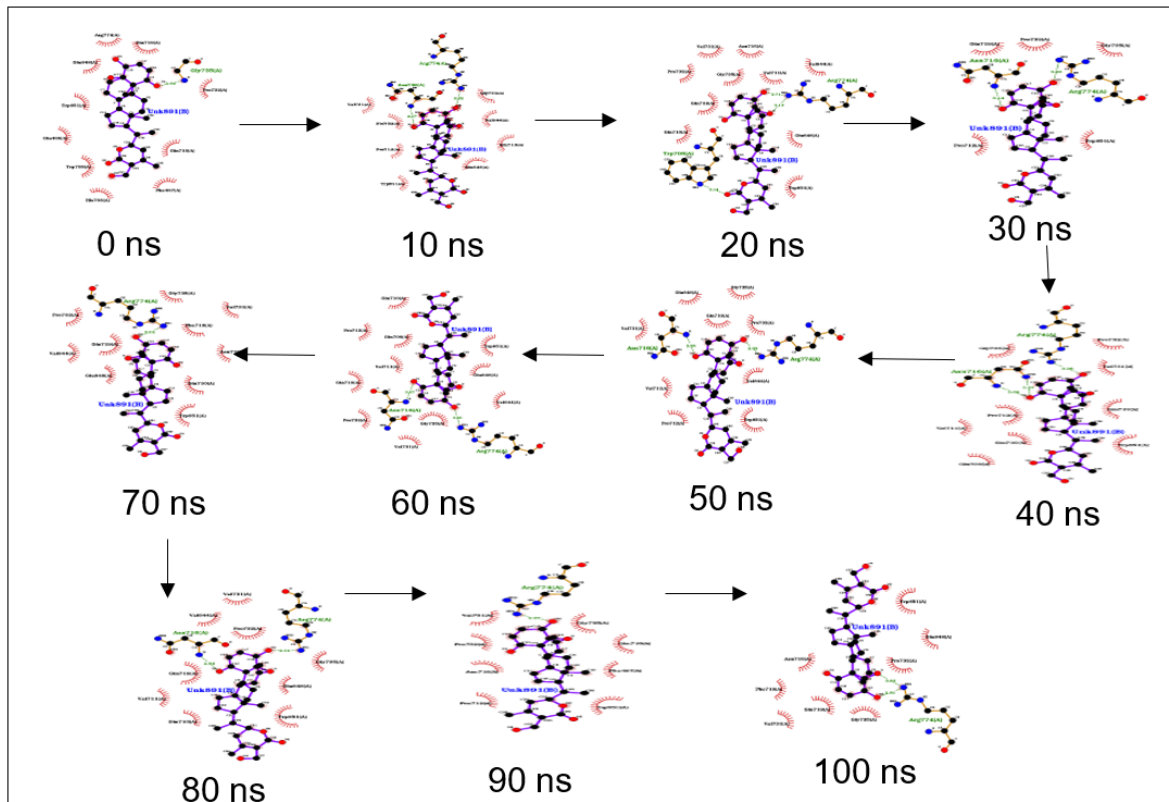


Figure 12 Visualization of Trajectory in 2-dimensional plot

4. CONCLUSION

The analysis of Withaferin A within the complexes 4HDH and 4K6M, derived from Ashwagandha, provides essential insights into its interactions and potential therapeutic applications. Both complexes exhibit unique structures with Withaferin A, a bioactive compound known for its diverse pharmacological benefits. These complexes unveil how Withaferin A interacts with specific molecular targets, shedding light on its role in modulating biological pathways. Investigating binding sites and interactions within these structures offers a glimpse into possible mechanisms of action and their effects on cellular processes. Docking simulations visually demonstrate interaction orientations, while computational tools like Swiss ADME and Lipinski's rule evaluate the compound's drug-like properties and bioavailability. Molecular dynamics simulations enrich understanding by exploring dynamic behaviours over time, revealing stability and interactions. Visualizing these trajectories helps unravel intricate motions that drive the binding process. Safety assessment using tools like PROTOX-II provides insights into potential toxicity associated with Withaferin A. Withaferin A shows strong potential as an effective drug against Japanese encephalitis virus (JEV), according to a detailed analysis. It demonstrates a robust ability to bind with the 4HDH and 4K6M proteins, indicating its capacity to disrupt viral processes. Its adherence to Lipinski's Rule of Five enhances its suitability as a potential drug. Its classification within a safe toxicity range (class 3) and its lack of activity in hypo-toxicity, carcinogenicity, and mutagenicity tests suggest a low risk profile. Notably, its physical characteristics, such as flexibility, lipophilicity, and polarity, align well with the requirements for stable drugs. Its active response in immunotoxicity and cytotoxicity tests suggests it could both modulate the immune system and eliminate infected cells. Molecular dynamics simulations show promising binding to five protein targets, with the 4HDH complex demonstrating particularly strong binding energy, indicating stability. Structural analyses further support the suitability of the 4HDH_withaferin A complex. In conclusion, these findings suggest that withaferin A holds promise as a potential treatment for JEV, though further research is needed to confirm its effectiveness and safety in clinical settings. While additional investigations are requisite for validation, these findings propose Withaferin A as a prospective JEV therapeutic option. In conclusion, Withaferin A's multifaceted interactions and characteristics position it as a candidate warranting further exploration for combatting JEV. Japanese encephalitis virus (JEV) is a mosquito-borne pathogen primarily impacting the central nervous system, causing brain inflammation and potential long-term neurological harm or fatality. Prevalent in rural Asian regions, preventive vaccination stands as the most effective safeguard. Numerous investigations encompass epidemiological analysis for transmission patterns, understanding the virus's pathogenesis, and the creation of vaccines and treatments. JEV remains a pressing public health issue across Asia, necessitating

continuous research to refine comprehension and bolster preventive and curative strategies. Analysing Withaferin A's interactions in Ashwagandha-derived 4HDH and 4K6M complexes provides pivotal insights into its therapeutic potential. These interactions illuminate the compound's role in impacting biological pathways, revealing its effects on cellular processes through binding site explorations and docking simulations. Computational assessments such as Swiss ADME and Lipinski's rule confirm its drug-like attributes, while molecular dynamics simulations unveil stability and interactions. Safety evaluation with PROTOX-II highlights potential toxicity linked to Withaferin A. Overall, Withaferin A showcases promise as a potential JEV treatment, demonstrating robust binding to 4HDH and 4K6M proteins, adherence to Lipinski's Rule of Five, and a favourable toxicity profile. Its active modulation of immune and cytotoxic responses underscores its therapeutic potential. A study on SARS-CoV-2 explores a natural compound Wi-A as potential inhibitors of TMPRSS2, crucial for viral entry. Wi-A binds to TMPRSS2's catalytic site, with stronger interactions. Wi-A's diverse content in *Withania somnifera* (Ashwagandha) suggests potential management of SARS-CoV-2 outbreak and drug development direction. Further research is needed for confirmation²⁵

ABBREVIATIONS :JEV- Japanese Encephalitis Virus; PDB- Protein Data bank; GRAS- Generally Recognized as Safe; SDF Structured Data File; RMSD- Root Mean Square Deviation; RMSF- Root Mean Square Fluctuations; Rg Radius of Gyration; SASAs- Solvent Accessible Surface Areas; MM-GBSA- Molecular Mechanics Generalized Born Surface Area; ADME- Absorption Distribution Metabolism Elimination; TMPRSS2- Transmembrane Protease, Serine 2 SARS-CoV-2- Severe Acute Respiratory Syndrome Coronavirus 2; Wi-A- Withaferin A ns- nanoseconds; fs- femtoseconds

ETHICS APPROVALS: This study does not involve any experiments on either animals or human subjects, and therefore no ethics approval was required.

DATA AVAILABILITY STATEMENT: All of the data generated or analysed during the course of this study have been included in the published article and its supplementary information files.

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