Scientiarum: A Multidisciplinary Journal
Volume 1, Issue 2, April 2025, pp. 43-64

DOI: 10.54646/SAPARS.2025.09

Exploring Molecular Interactions of Britanlin E: Targeting DNA Topoisomerase in Breast Cancer and p53 Binding Protein 1 in Head and Neck Cancer

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Abstract:

In this study, we employ AutoDock, widely-used molecular docking software, to investigate the molecular interactions of Britanlin E in the context of breast cancer and head and neck cancer. Britanlin E has shown promising anticancer properties, and understanding its binding mechanisms to specific target proteins is crucial for elucidating its therapeutic potential. Our computational approach involves docking simulations of Britanlin E with DNA Topoisomerase, a vital enzyme involved in DNA replication and repair pathways implicated in breast cancer progression, as well as with p53 Binding Protein 1, a critical regulator of cell cycle and apoptosis dysregulated in head and neck cancer. Through AutoDock simulations, we aim to elucidate the binding affinities, binding modes, and key amino acid residues involved in the interactions between Britanlin E and these target proteins. The insights gained from this study will contribute to a deeper understanding of Britanlin E's molecular mechanisms of action, paving the way for the development of novel therapeutic strategies for breast cancer and head and neck cancer.

Keywords: p53 binding protein, Britanlin-E, DNA Topoisomerase

1. Introduction

1.1 Cancer

A disease known as cancer occurs when some body cells proliferate out of control and invade other parts of the body. With trillions of cells making up the human body, cancer can begin almost anyplace. When the body needs new cells, human cells normally divide by proliferating and multiplying. New cells replace old ones when they die as a result of ageing or injury. This controlled mechanism can occasionally fail to function, causing damaged or aberrant cells to proliferate and expand when they shouldn't. Tumours are lumps of tissue that can be formed by these cells. Cancerous or benign tumours can both occur. Malignant tumours can metastasize, or spread into, neighbouring tissues, and can also generate new tumours by travelling to far-off regions of the body. Malignant tumours are another term for cancerous tumours. Blood cancers, including leukaemia's, typically do not develop into solid tumours, although many malignancies can. Benign tumours do not penetrate or spread to neighbouring tissues. Benign tumours seldom grow back after removal, while cancerous tumours occasionally do. However, benign tumours can occasionally grow to be rather enormous. Some, like benign brain tumours, are possibly deadly or cause severe symptoms. The WHO classifications serve as the basis for both cancer management and cancer diagnosis. The WHO began to incorporate biologic and molecular-genetic elements into its classifications in 2000. With the advancements in cancer genomes, these breakthroughs are having an increasingly significant impact on cancer diagnosis and treatment [1].

1.2 Types of Cancer

Cancer occurs in more than a hundred types. The organs or tissues where tumours originate are typically used to name different types of cancer. Cancers can also be classified according to the kind of cell that gave rise to them, such as squamous or epithelial cells.

- Carcinoma
- Sarcoma
- Leukaemia

- Lymphoma
- Myeloma
- Brain and Spinal Cord Tumour

2. Head and Neck Cancer

The five-year survival rate for head and neck cancer is still among the lowest for all major cancers, and it ranks as the sixth most prevalent illness worldwide. It is known that changes in the cellular molecules regulating apoptosis, invasion, DNA repair, proliferation, and angiogenesis play a role in the development of cancer at this anatomical location [2].

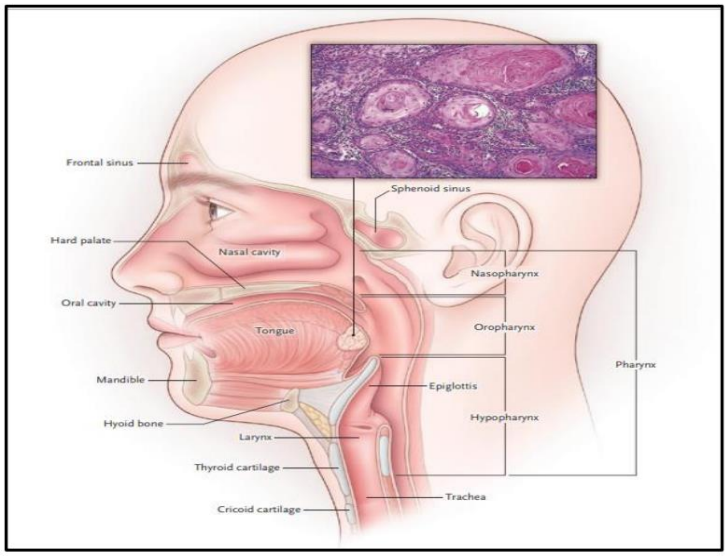


Fig 1: Major Anatomical Site of Squamous – Cell Carcinoma of the Head and Neck [3]

The primary anatomical sites of head and neck squamous-cell carcinoma. The lips, buccal mucosa, anterior tongue, floor of the mouth, hard palate, upper and lower gingiva, and retromolar trigone are all parts of the oral cavity. The pharynx is made up of the tonsillar area, tongue base, soft palate, posterior pharyngeal wall, and posterior surface of the larynx and postcricoid area, as well as the inferior posterior and inferolateral pharyngeal walls. The nasopharynx is located behind the nasal cavity. The oropharynx is made up of the tonsillar area, tongue base, and soft palate. The supraglottic larynx, glottic larynx (which consists of the voice cords and the anterior and posterior commissures), and subglottic larynx are all

parts of the larynx. The maxillary, ethmoid, sphenoid, and frontal sinuses are located in the nasal cavity and paranasal sinuses [3].

2.1 Causes of Head and Neck Cancer

Exposure to environmental contaminants, excessive alcohol use, and the use of tobacco products or betel quid (the leaf of Piper betel) and areca nut (Areca catechu) are the main risk factors for the development of HPV-negative head and neck squamous cell cancer (HNSCC). Particularly tobacco smoke and tobacco products are high in nitrosamines and polycyclic aromatic hydrocarbons, which are recognised human carcinogens and significantly raise the risk of HNSCC. Reactive metabolites are created when carcinogens undergo metabolic activation. If these metabolites are not eliminated by detoxification, they can cause damage to DNA, usually in the form of large DNA adducts. Should the damage to the DNA be faithfully and precisely repaired, there might not be any long-term effects. Permanent damage, including as mutations, deletions, and amplifications, can happen if the damaged DNA is not quickly repaired or is incorrectly repaired by lower fidelity repair processes. The development, advancement, and unfavourable prognosis of HPV-negative HNSCC are linked to the accumulation of mutations in important tumour suppressor genes (such TP53 and CDKN2A, which encode p53 and p16INK4A, respectively) or signalling pathways (including PI3K–AKT–mTOR and RAS–MAPK pathway genes) [4].

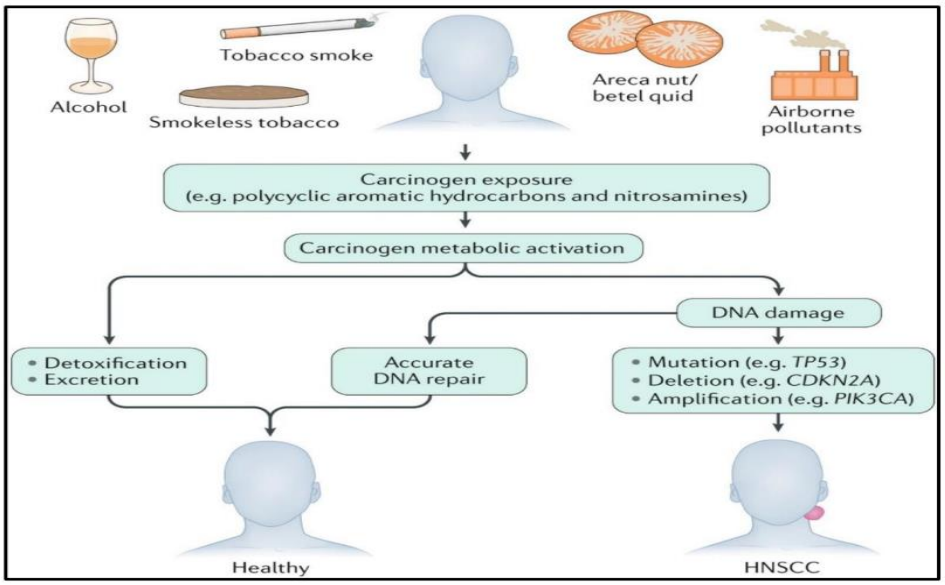


Fig 2: Development of Carcinogen – associated [4]

2.2 Symptoms

Symptoms of head and neck cancer can include pain during swallowing and mouth soreness. Depending on where the cancer begins, symptoms may vary. Malignancies that originate in the mouth, throat, sinuses, and salivary glands are classified as head and neck malignancies.

Signs in the throat and mouth:

- Might be able to feel a lump through the skin of your neck. The lump is usually not Uncomfortable.
- A mouth sore that refuses to heal away.
- Vomiting blood.
- Voice that is rough.
- Loose teeth.
- Discomfort during swallowing.

2.3 Mechanism of Head and Neck Cancer

Head and neck squamous cell carcinoma (HNSCC) is a synonym for the majority of head and neck malignancies, which originate from the mucosal epithelium of the oral cavity, pharynx, and larynx. While pharynx cancers are increasingly linked to human papillomavirus (HPV),

namely HPV-16, oral cavity and larynx cancers are typically connected with tobacco smoking, alcohol addiction, or both. As a result, HNSCC can be classified as HPV-positive or HPV-negative. Even though histological data shows that cellular atypical progresses via different degrees of dysplasia to invasive HNSCC, the majority of individuals with late-stage HNSCC are not diagnosed with a clinically noticeable premalignant lesion [4].

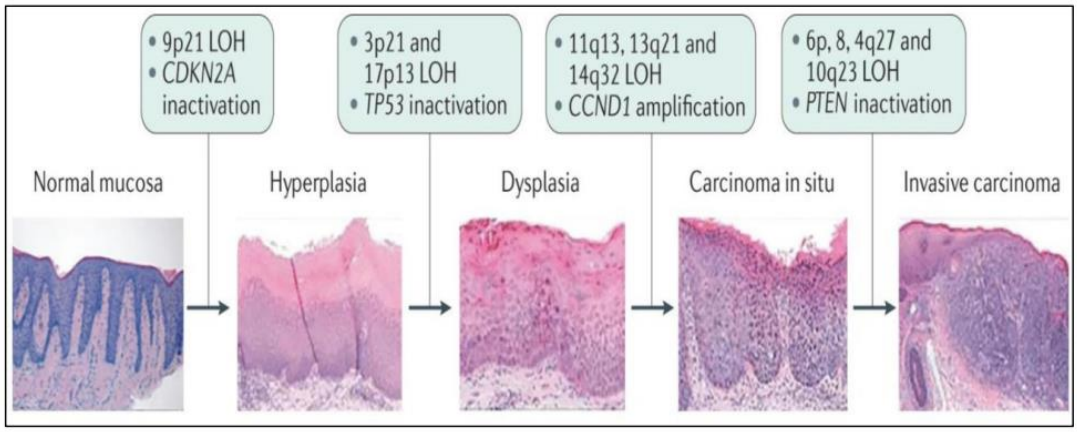


Fig 3: HNSCC progression and important genetic events [4].

Head and neck squamous cell carcinoma (HNSCC) originates in the mucosal epithelium lining the oral cavity, pharynx, larynx, and sinonasal tract. According to a model of the ordered histological evolution of HNSCC68, carcinoma in situ develops before invasive carcinoma, and mucosal epithelial cell hyperplasia is followed by dysplasia. It has been discovered that some genomic events are enriched at every stage of development and are listed. In particular, HNSCC formation typically entails turning off tumour suppressor genes including TP53 and CDKN2A, which encode p16INK4A and p53, respectively) in early stages and PTEN (encoding phosphatase and tensin homologue 14 (PTEN)) in later stages. This is in contrast to most cancers, where oncogenic mutations typically drive tumorigenesis [4].

Protein changes, such as altered or increased expression, can result from genetic and epigenetic modifications. A cancer may develop as a result of the aggregation of these changes in tumour suppressors, proto-oncogenes, and oncogenes. Among the other significant molecules that may be used as therapeutic targets are p53, EGFR, VEGFR, signal transducer and activator of transcription 3 (STAT3), and epidermal growth factor receptor (EGFR), which are among the critically changed pathways in HNSCC [5].

2.4 Pathogenesis of p53 Binding protein – I

The most common molecular events that lead to transformation are changes in EGFR and p53, which show up as enhanced migration, angiogenesis, survival, and proliferation as well as a lack of growth control. Over 50% of head and neck cancer cases have mutations in the p53 gene, making it one of the most frequently altered genes in the disease. When the tumour suppressor p53 on chromosome 17q13 is inactivated, cells are unable to respond to stress or damage to their DNA, which results in a lack of growth control. The p53 pathway is frequently dysregulated or altered in addition to p53, which results in additional p53 mutations [5]. There are 11 exons in the TP3 gene, the first of which is noncoding. With 393 amino acids, the p53 protein is divided into four regions, each with a distinct function: the C-terminal tetramerization domain (amino acids 319–360), the Nterminal transactivation domain (amino acids 20–42), the central DNA-binding domain (amino acids 103–292), and the C-terminal regulatory domain (amino acids 364–393). Known as the "guardian of the genome," wild type p53 is an essential tumour suppressor that keeps the genome stable, preventing the onset of cancer. As a transcription factor, P53 suppresses tumours by controlling the transcription of multiple downstream target genes related to cell cycle arrest, apoptosis, senescence, DNA repair, and metabolism. The primary mechanism by which the p53 protein is kept at a low level in normal, unstressed physiological settings is by degradation by its E3 ubiquitin ligase, MDM2, pirh2, and COP1. Following genotoxic stress exposure, p53 is stabilized and post translationally modified through phosphorylation, acetylation, and other modifications. This leads to a sharp increase in p53 levels, which in turn activates and transcriptionally regulates hundreds of genes involved in cell cycle arrest, senescence, apoptosis, metabolism, and differentiation. When combined, these actions guarantee that damaged DNA does not spread across damaged cells [6].

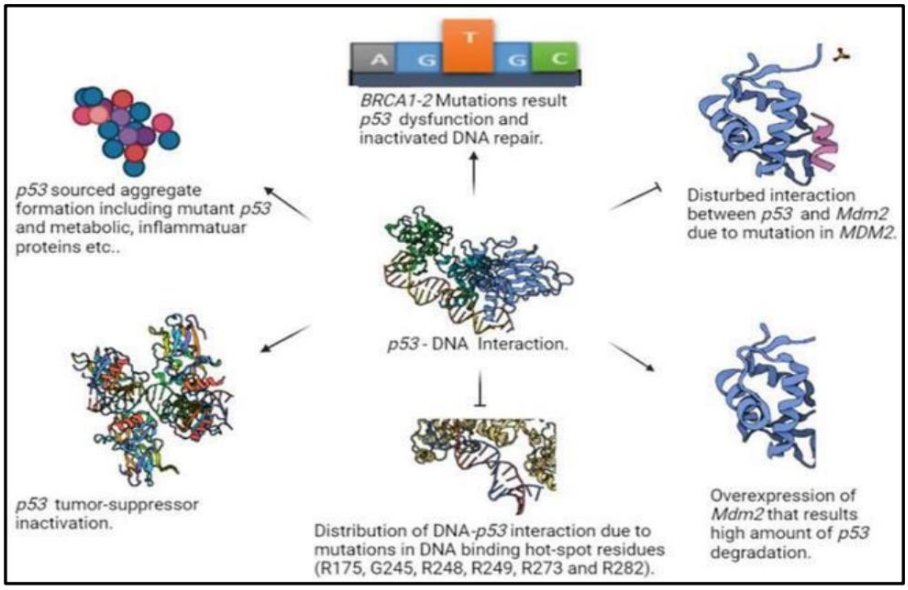


Fig 4: Overview of inactivation of p53 with distant mechanism [7]

A protein known as MDM2, or the murine double minute 2, interacts with p53, lowers its activity, and moves p53 from the nucleus to the cytoplasm. Moreover, MDM2 functions as a ubiquitin ligase. By delivering p53 to the ubiquitin proteasomal system (UPS), this activity of MDM2 aids in the breakdown of functional p53 and reduces the quantity of p53 in the cell. Cell growth stops when genetic damage occurs, and p53 triggers apoptosis, a planned cell death. Due to its capacity to control malignancy, cancer cells have evolved to p53 function in various ways and evade senescence and apoptosis through unique pathways [7]. These p53 gene characteristics and mutations aid in the transformation of cancer by allowing cells to avoid cell cycle checkpoints and death. Consequently, the majority of cancer cells depend on p53 mutations to continue existing. This explains the observation of high-frequency p53 mutations in the majority of malignant cell types. All cancer types, however, are known to undergo distinct genomic rearrangements and adaptations in response to unique changes and environmental stimuli. P53 functions and mutations vary depending on the type of cancer, each having its own unique mechanism [7].

3. Breast Cancer

As the most frequent tumour worldwide, breast cancer continues to be a global public health concern. Breast cancer detection and screening have improved as a result of increased public awareness of the disease, increased attention from the general population, and advancements in breast imaging. Breast cancer is the most common cause of death for women and a potentially fatal illness for women. Over the past 20 years, research on breast cancer has led

to a remarkable progress in our knowledge of the disease and the development of more effective treatments [8]. The milk ducts and/or the breast's milk-producing lobules are where breast cancer cells first proliferate. There is no risk to life from the early form (in situ). It is possible for cancer cells to invade neighbouring breast tissue. Tumours produced by this result in thickening or lumps. Metastasis is the process by which invasive tumours move to neighbouring lymph nodes or other organs. One can die from metastasis. Treatment is determined by the patient, the cancer's type, and its extent of dissemination. Medication, radiation therapy, and surgery are all used in treatment. Current evidence-based medicine indicates that the fight against breast cancer has advanced slowly over the last ten years, despite recent advancements in cancer therapy. In the metastatic field, this translates to a few months of survival prolongation. Taking into account the significant drawbacks of the targeted treatments that are already on the market, this is not shocking. The transient anticancer effect of currently 7 available targeted medications and the disregard for interpatient and intratumor heterogeneity are the causes of the high rates of intrinsic and acquired resistance to these medications. Understanding this incredibly complicated heterogeneity is essential to winning the "war" against metastasis and breast cancer. Particularly to be overlooked is the significant advancements in the treatment of HER2-positive breast cancer, which affects 20% of cases of breast cancer. The determination of the HER2 pathway's malfunction caused by an increased HER2 gene gave rise to the discovery of the well-known antiHER2 monoclonal antibody (mAb), trastuzumab [9]. Mutations in DNA and/or RNA cause normal cells to develop into cancerous ones. Due to heat, chemicals in the air, water, and food, mechanical cell-level injury, free radicals, evolution and ageing of DNA and RNA, viruses, bacteria, fungi, and parasites, these modifications / mutations can occur spontaneously (Law of Thermodynamics - increase of entropy) or they can be induced by other factors such as electromagnetic radiation (microwaves, X-rays, Gamma-rays, Ultraviolet-rays, etc. Any of these can result in mutations that could lead to cancer [10].

3.1 Types of Breast Cancer

It is divided into Invasive and Non- Invasive Breast Cancer.

Non-Invasive Breast Cancer Cells: These cells stay within the ducts and do not spread to the breast's surrounding connective and fatty tissues. The most frequent non-invasive breast cancer kind, accounting for 90% of cases, is ductal carcinoma in situ (DCIS). Less frequently

occurring lobular carcinoma in situ (LCIS) is thought to be a sign of an elevated risk of breast cancer.

Invasive Breast Cancer: Breast cancer cells that spread to the surrounding fatty and connective tissues of the breast after breaching the duct and lobular wall. It is possible for cancer to be invasive without also spreading to other organs or lymph nodes [10].

3.2 Causes of Breast Cancer

Genetic Factor

Breast cancer risk factors have long been associated with family history. It matters to have maternal and paternal relatives. The afflicted relative's risk is greater if she is a close relative, had cancer in both breasts, or acquired breast cancer at an early age. When evaluating risk, first-degree relatives—mother, sister, and daughter—are the most significant. An additional risk factor could be multiple second-degree relatives (grandmother, aunt) who have breast cancer. When inherited, the aberrant genes BRCA1 and BRCA2 significantly raise the lifetime risk of breast cancer, which is estimated to be between 40 and 8S%. Breast cancer tends to strike women with the BRCA1 gene early in life.

Hormonal Reasons

Breast cancer may develop more quickly if the hormonal level changes. It can be treated by the menstrual cycle (beginning and ending of periods), early pregnancy, hormone replacement treatment, and oral medication use.

Dietary and lifestyle factors

Breast cancer may be brought on by a sedentary lifestyle, a high fat diet, and obesity, especially in postmenopausal women. Alcohol consumption is yet another factor contributing to breast cancer. The risk rises as alcohol use increases. Women who drink two to five drinks a day are approximately 1.5 times more likely to get breast cancer than non-drinkers.

3.3 Signs and Symptoms of Breast Cancer

A lump in the breast or underarm is the typical sign of breast cancer. Being familiar with the texture, size, cyclical variations, and skin condition of your breasts can be achieved by performing monthly breast self-examinations (BSEs). Breast cancer is generally indicated by symptoms like 9 breast swelling or lump (mass), swelling in the armpit (lymph nodes), clear or bloody nipple discharge, nipple pain, inverted (retracted) nipple, scaly or pitted skin on nipple, persistent breast tenderness, and unusual breast pain or discomfort. Underarm lymph nodes are found at the advanced stage (metastatic) of the disease along with other symptoms such unintentional weight loss, shortness of breath from lung metastases, bone pain from bone metastases, and a decrease in appetite from liver metastases [10].

3.4 DNA Topoisomerase-I in Breast Cancer

The most frequent cancer in women and a major global cause of death is breast cancer (BC). A diverse collection of tumours, BC has a wide range of prognoses and therapy sensitivity. In order to stratify BC for customised treatment, more biomarkers must be found. DNA topology can be altered by the topoisomerases (TOP) to aid in transcription and replication. Topoisomerase I (TOP1) and Topoisomerase II (TOP2) are the two different forms of TOPs. They are categorised based on their capacity to create temporary single- or double-stranded breaks in DNA. TOPs are important for DNA function and may be targets for cancer treatments. A number of TOP inhibitors are employed in therapeutic settings [11]. Enzymes known as DNA topoisomerases are responsible for altering the torsional and flexural strain of DNA molecules. These enzymes have been linked in previous research to a number of eukaryotic and prokaryotic processes, including as chromosome segregation, transcription, recombination, and DNA replication [12].

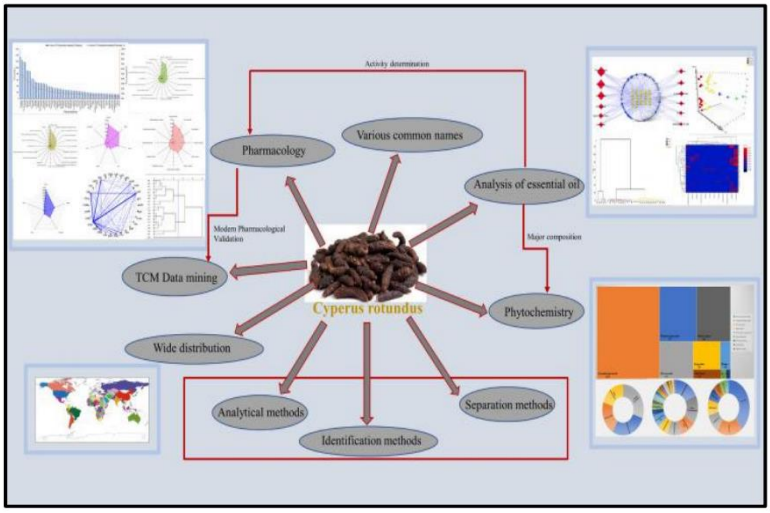
DNA topology can be altered by the topoisomerases (TOP) to aid in transcription and replication. Topoisomerase I (TOP1) and Topoisomerase II (TOP2) are the two different forms of TOPs. They are categorized based on their capacity to create temporary single- or double-stranded breaks in DNA. TOPs are important for DNA function and may be targets for cancer treatments. A number of TOP inhibitors are employed in therapeutic settings. One of the many widely acknowledged chemical pathways can inhibit the DNA topoisomerase enzymes. Substrate competitive inhibition, which is the binding of an inhibitory chemical to the topoisomerase active site to prevent the binding of the DNA substrate, is one possible method. Though recent reports of DNA-competitive inhibitors of other DNA-binding proteins imply that this mechanism may also be viable in DNA topoisomerases, there are no

noteworthy instances of topoisomerase-specific inhibitors that function by this manner. The creation of "topoisomerase poisons," which are made up of ternary protein-DNA-drug complexes that obstruct DNA re-ligation and imprison the enzyme in a "cleavage complex," is another frequent approach. Because of this compound, the cell's cytotoxic cleavage complex accumulates to high levels and enzyme turnover is inhibited. The type II topoisomerases are the only ones that exhibit competitive inhibition of the ATP binding site, a third mechanism that stops the enzymatic action powered by ATP hydrolysis. The mechanism of the topoisomerase poisons is of the utmost therapeutic significance. Through the formation of a locked ternary complex of cleaved DNA, protein, and medication that accumulates and has a cytotoxic impact, this method includes stabilising the cleavage complex. The anthracycline medicines were the first known class of topoisomerase inhibitors utilised in cancer treatment. When the anthracyclines were originally isolated from Streptomyces bacteria, it was found that they have both antibacterial and anticancer properties [13].

4. Cyperus Rotundus

The perennial nutgrass, Cyperus rotundus L. (Family: Cyperaceae), is a colonial herb that is commonly used in Ayurveda medicine to cure a variety of illnesses. It is thought to have originated in India 2000 years ago. Apart from its archaic applications, it finds application in multiple medical systems for the management of diverse illnesses. The combined effects of the chemicals in Cyperus provide an additional benefit over those of a single component. Over the last ten years, a multitude of studies have demonstrated the analgesic, anti-arthritic,

anti-candida, anti-cariogenic, anticonvulsant, anti-diarrheal, anti-emetic, anti-helminthic, anti-histamine, anti-hyperglycemic, antihypertensive, anti-inflammatory, anti-malarial, anti-obesity, antioxidant, anti-platelet, anti-pyretic, anti-ulcer, anti-viral, cardioprotective, cytoprotective, cytotoxic, gastroprotective, hepatoprotective, neuroprotective, and larvicidal properties of C. rotundus and its chemical constituents. Numerous secondary metabolites, which are essential to medicinal plants' survival as well as their ability to protect themselves

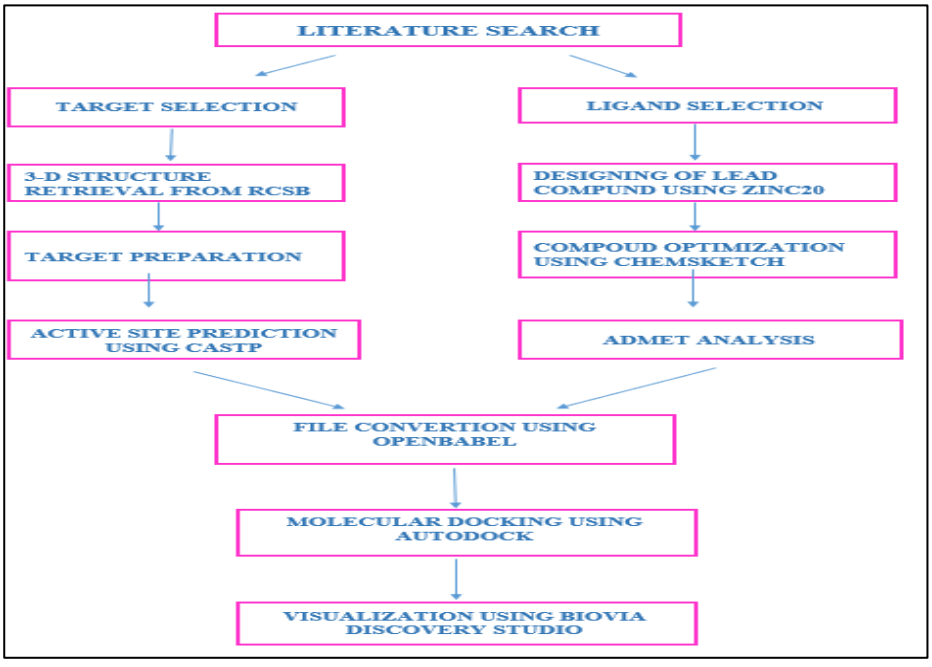


from animals, fungi, bacteria, and other plants, may be found in them. These metabolites are used as flavours, food additives, pharmaceutics, cosmetics, nutraceuticals, and industrially significant biochemicals. Medicinal herbs are the indirect source of many contemporary medications. The major constituents are α-cyperolone, β-cyperone, ρ-cymol, calcium, camphene, copaene, cyperene, cyperenone, cyperol, cyperolone, caryophyllene, cyperotundone, d-copadiene, d-epoxyguaiene, isocyperol, isokobusone, kobusone, limonene, linolenic acid, Patchoulenone, rotundene, mustakone, myristic acid, oleanolic acid, oleic acid, rotundenol, rotundone, β-selinene, selinatriene, sitosterol, stearic acid, sugeonol, and sugetriol [14].

Fig 5: Significance of Cyperus Rotundus in medical science [15]

Furthermore, it has been discovered that this plant contains a number of flavonoids, saponins, alkaloids, phenylpropanoids, quinonoid, diterpenoids, carbohydrates, aliphatic chemicals, and trace minerals. It clearly shows the variety of chemical components that make up C. Rotundus. This section summarises the 552 compounds from C. Rotundus that have been isolated or characterised, 350 and 202 compounds, respectively. Their chemical structures are shown in figure, and their complete chemical information—including name, formula, molecular weight, and the portions of the plant from which they originated—is included in the supplemental material. Based on the literature I have chosen the compound Britanlin E from this plant which has Anti- Tumour activity.

5. Workflow



6. METHODOLOGY

6.1 3DStructureretrieval

The Protein Data Bank is the database for the three-dimensional structure data of large biologicalmolecules,suchasproteinandnucleicacid.

a) The 3-D structure of protein DNA Topoisomerase I (1A36).

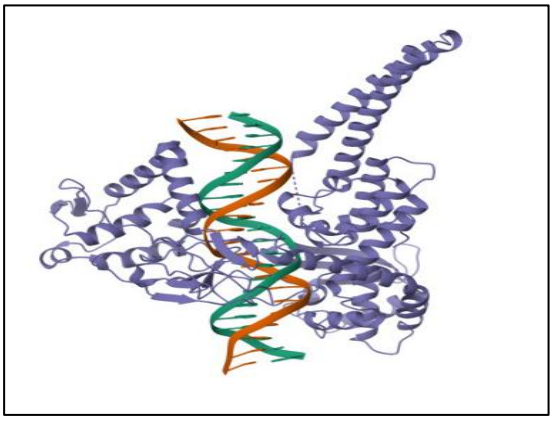


Fig 6: 3-D structure of protein DNA Topoisomerase I (1A36)

b) The 3-D Structure of protein p53 Binding Protein 1(6MY0)

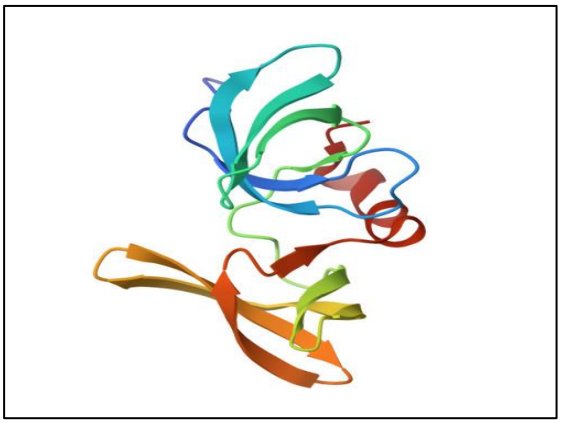


Fig 7: The 3-D Structure of protein p53 Binding Protein 1(6MY0)

6.2ACTIVE SITE USING CASTp

a) The active site of the target DNA Topoisomerase I (1A36) using CASTp.
Pocket no: 1

Area (SA): 4552.486

Volume (SA): 13321.385

b) The active site of the target p53 Binding Protein 1(6MY0)

Pocket no: 1

Area (SA): 12927.382

Volume (SA): 7412.037

6.3 ZINC20

The structure was designed based on literature review using ZINC SKETCH Tool in ZINC20 database.

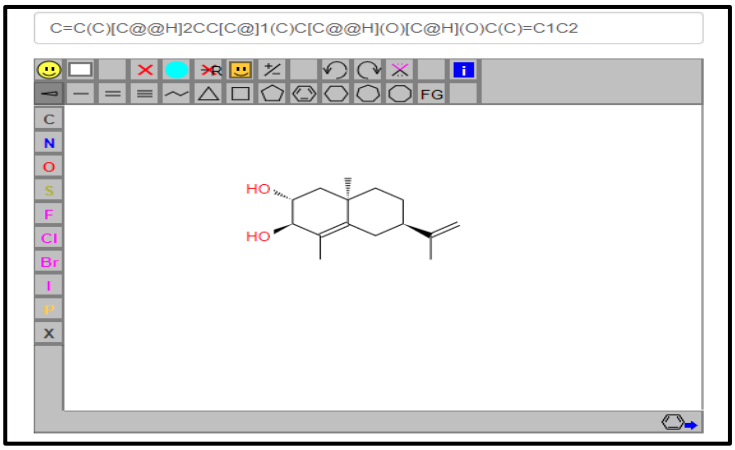


Fig 8: 2-D Structure of Britanlin E

6.4 CHEMSKETCH

Thecanonicalsmilesofthechemicalcompound Britanlin E isusedin ChemSketch for 3-D Optimization.

CanonicalSmiles: C=CC)[C@@H]2CC[C@]1(C)C[C@@H](O)[C@H](O)C(C)=C1C2

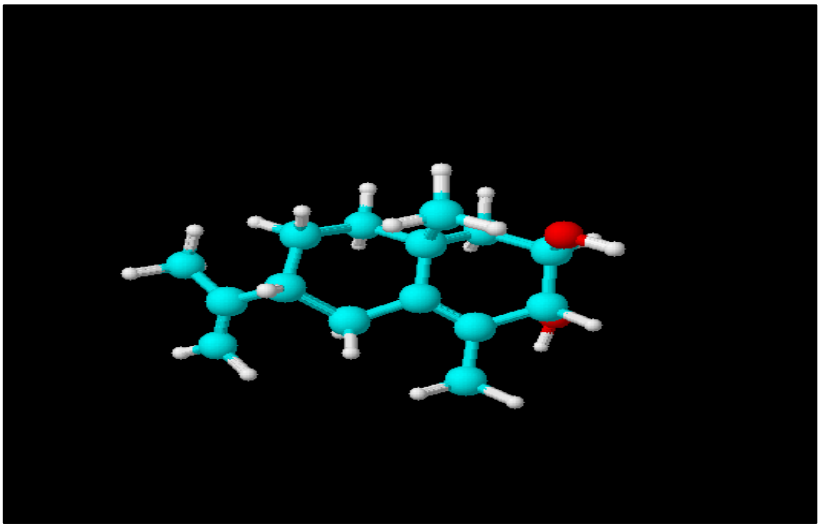


Fig 9: 3-D Structure optimization of Britanlin E

6.5 OPENBABEL

Openbabelisaformatconvertingtool,whichisusedtoconvertthemdlmolformatof chemical compound Britanlin E into the pdb format.

6.6 SWISS ADME

Thecanonicalsmilesof the chemical compound Britanlin Eare given as an input to view the validation of pharmacokinetic properties.

6.7 PKCSM

This is known as pharmacokinetic and pharmacodynamics (PK/PD) analysis. Britanlin E (toxicity) also was modelled effective. Thus, this platform may enable predictions of drug absorption, distribution, metabolism, excretion, and toxicity (ADMET).

6.8 MOLINSPIRATION

The canonical smiles of the chemical compound Britanlin E are used as an input in Molinspiration, and the output includes high quality molecule depiction, molecular database tools supporting substructure and similarity searches, and the calculation of various molecular properties needed in QSAR and drug design.

6.9 DOCKING

A crucial tool in computer-assisted drug design and structural molecular biology is molecular docking. Predicting the main binding mode(s) of a ligand with a protein that has a known three-dimensional structure is the aim of ligand-protein docking.

6.10 VISUALIZATION

Visualization in BIOVIA refers to the use of advanced graphical techniques and tools to explore, analyze, and present molecular structures, properties, and interactions within the software suite. It provides researchers with the means to visualize complex biological systems and chemical compounds**.** The result file is in the format of pdbqt , which is converted into pbq with help of open babel, a format converting tool,thepdb format isjoinedwith theinput filewhich is inpdb. Then finallythe pdb format file is visualized in the Biovia studio visualization tool. The molecular interaction, forces involved in it, distance between the molecules are noted.

7. RESULT AND DISCUSSION

7.1 SWISS ADME

Its gives a detailed information about the Physiochemical parameters, Lipophilicity, Water solubility, Pharmacokinetics and Drug likeness.

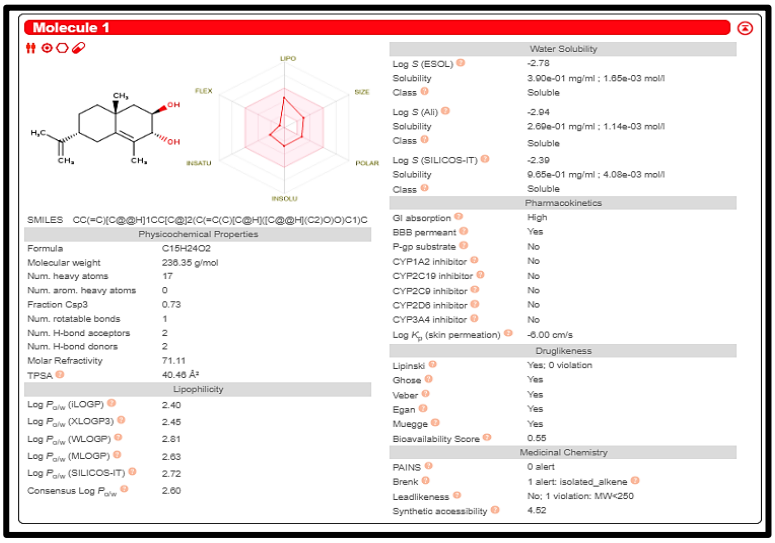


Fig 10 : Physiochemical parameters of Britanlin E

7.2 Molecular docking

It is a key tool in structural molecular biology and computer-assisted drug design. The goal of ligand-protein docking is to predict the predominant binding mode(s) of a ligand with a protein of known three-dimensional structure.

a) Molecular interaction between DNA Topoisomerase and Britanlin E against Breast Cancer is studied using Auto dock Tool. The binding Energy and geometry was also obtained.

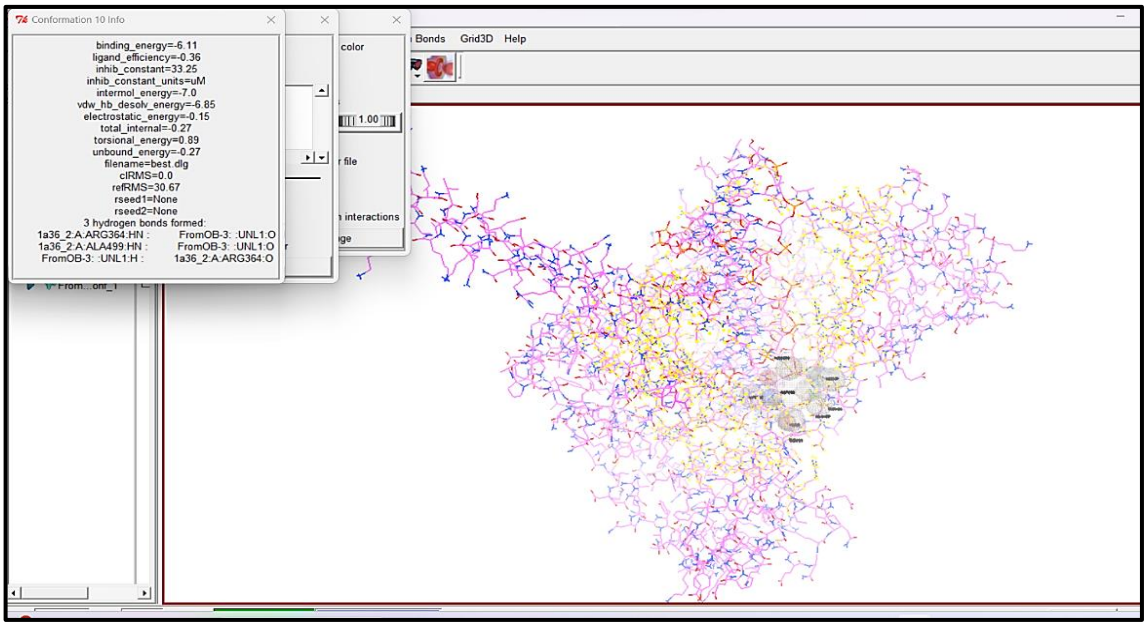


Fig 11: Molecular interaction between DNA Topoisomerase and Britanlin E

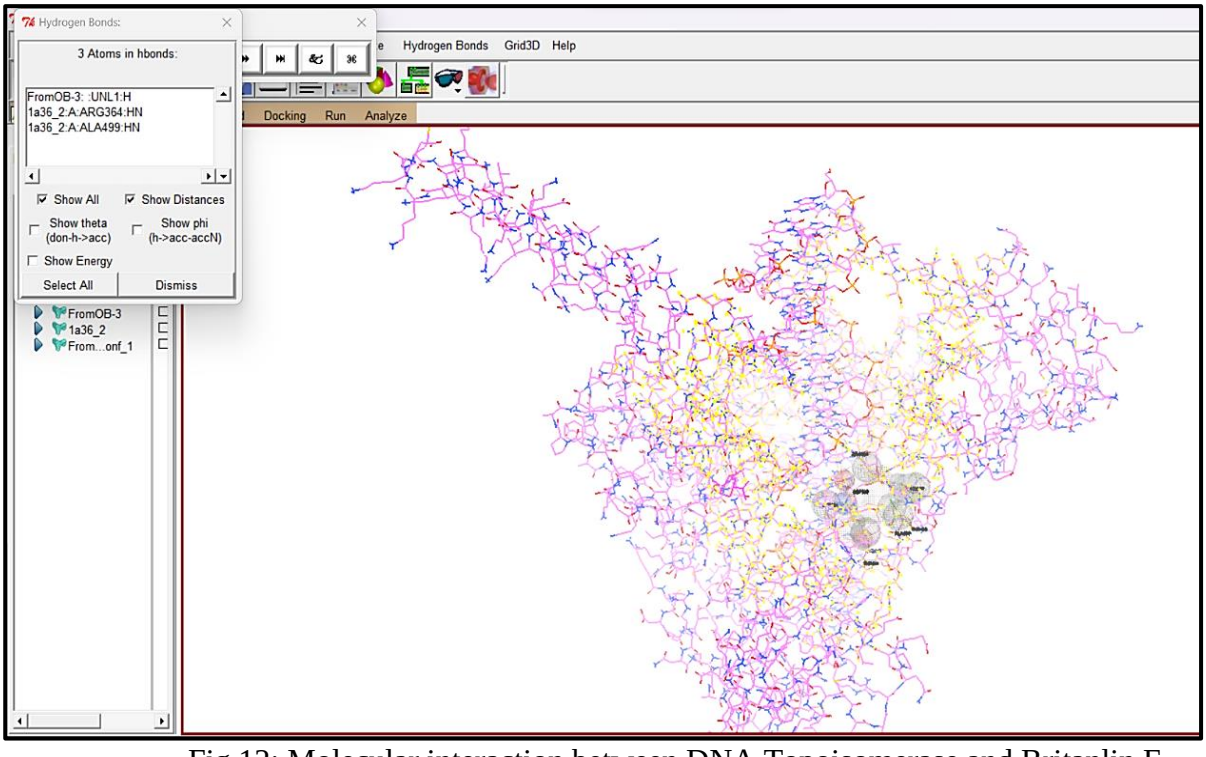


Fig 12: Molecular interaction between DNA Topoisomerase and Britanlin E

b) Molecular interaction between p53 Binding Protein-1 and Britanlin E against Head and Neck Cancer is studied using Auto dock Tool. The binding Energy and geometry was also obtained.

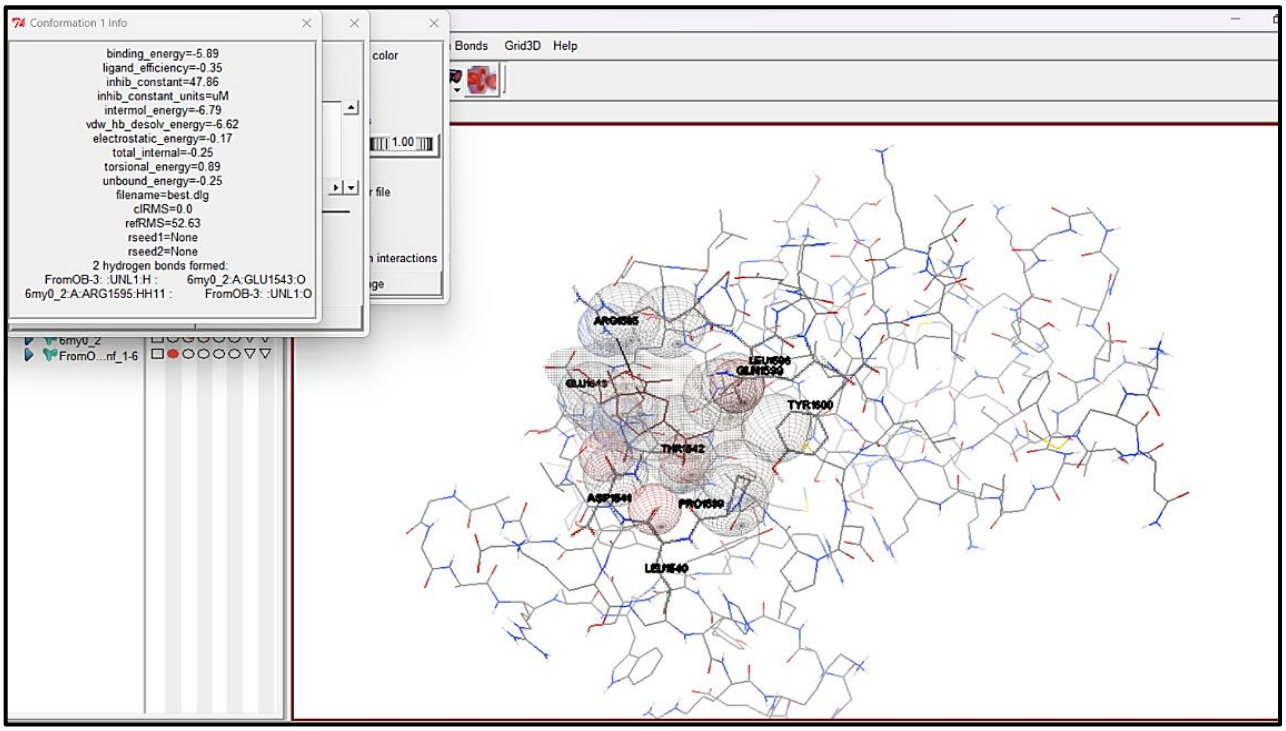


Fig 13: Molecular interaction between p53 Binding Protein-1 and Britanlin E

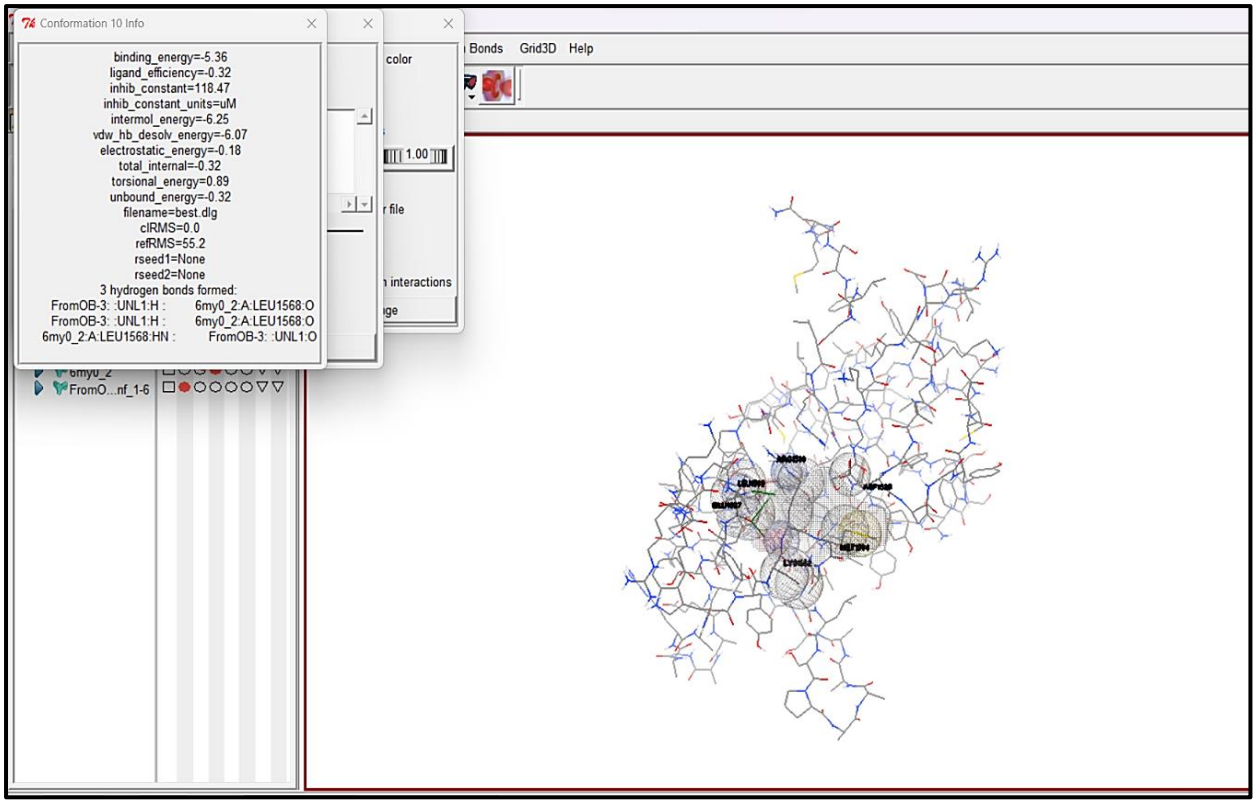


Fig 14: Molecular interaction between p53 Binding Protein-1 and Britanlin E

7.3 Visualization

Visualization of 3D structure and 2D structure of protein and ligand interaction in Biovia discovery tool.

a) Visualization between DNA Topoisomerase and Britanlin E against Breast Cancer is studied using Biovia.

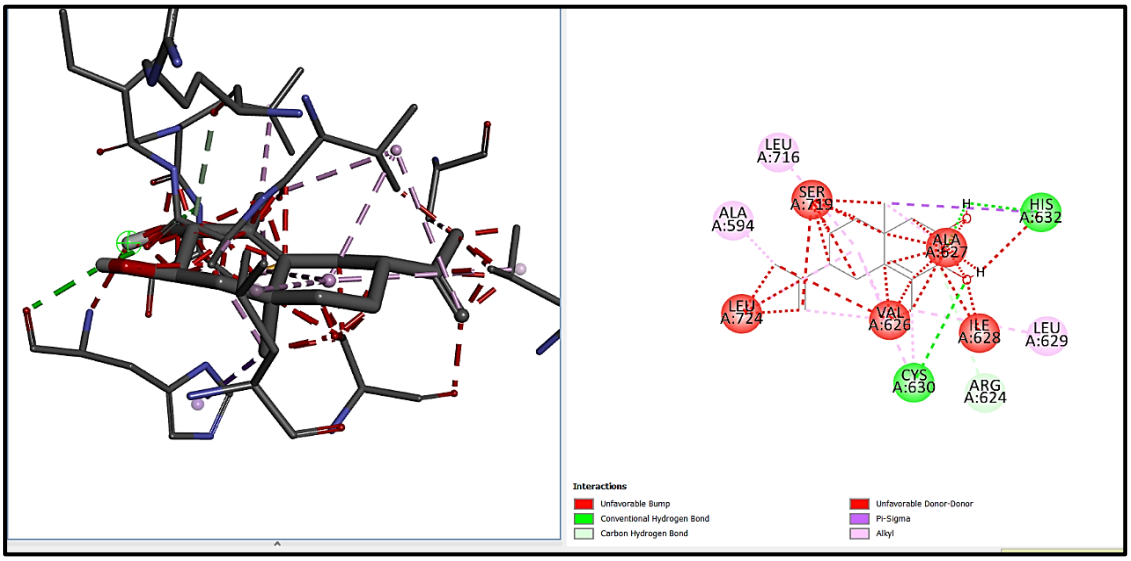


Fig 15: Visualization between DNA Topoisomerase and Britanlin E

b) Visualization between p53 Binding Protein-1 and Britanlin E against Head and Neck Cancer is studied using Biovia..

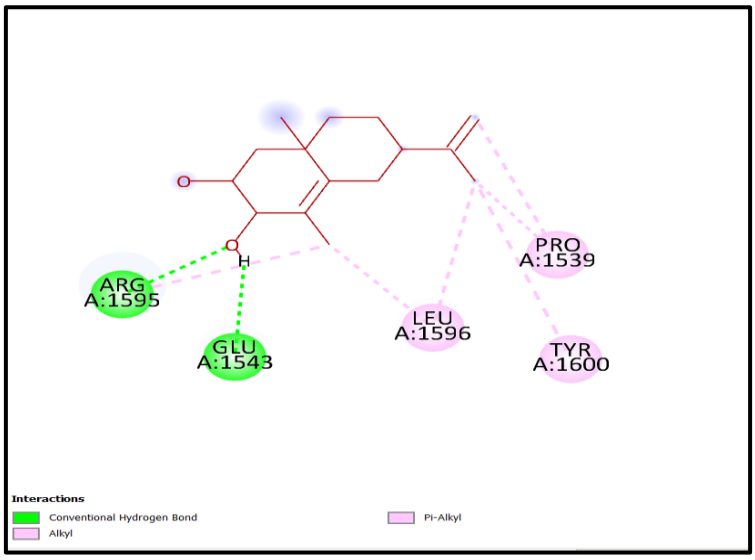


Fig 16: Visualization between p53 Binding Protein-1 and Britanlin E

8. Conclusion

In this comprehensive study, we have delved into the intricate molecular interactions of Britanlin E, shedding light on its potential as a promising anti-cancer agent. Through our investigations, we have achieved significant insights into its dual mechanisms of action targeting DNA Topoisomerase in breast cancer and p53 Binding Protein 1 (p53BP1) in head and neck cancer.

The analysis of Britanlin E's chemical properties and structural features has provided a solid foundation for understanding its interactions with key biomolecules. Our findings reveal compelling evidence of Britanlin E's ability to bind to DNA Topoisomerase, thereby inhibiting its enzymatic activity critical for DNA replication. This inhibition presents a promising avenue for disrupting cancer cell proliferation and growth in breast cancer.

Furthermore, our exploration of Britanlin E's interactions with p53BP1 has uncovered its potential as a modulator of this pivotal protein in head and neck cancer. By elucidating the binding affinities and modes of action, we have highlighted Britanlin E's capacity to interfere with signalling pathways crucial for cancer cell survival and progression.

The outcomes of this project underscore the importance of Britanlin E as a versatile agent capable of targeting distinct molecular targets in different cancer types. The inhibition of DNA Topoisomerase in breast cancer and the modulation of p53BP1 in head and neck cancer represent promising therapeutic strategies for combating these malignancies.

In conclusion, our study provides a solid foundation for further research and development of Britanlin E-based therapies. The insights gained here contribute significantly to the growing body of knowledge in the field of cancer biology and drug discovery. As we continue to unravel the complexities of Britanlin E's mechanisms of action, we move closer to the realization of more effective and targeted treatments for breast cancer and head and neck cancer.

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