

IN SILICO PROFILING OF THE ADMET PROPERTIES AND INHIBITORY POTENTIALS OF ALKALOIDS AGAINST IFIT5 IN RENAL CELL CARCINOMA

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ABSTRACT:

Alkaloids from diverse classes have demonstrated efficacy in anticancer treatments. Interferon-induced protein with tetratricopeptide repeats 5 (IFIT5) is implicated in the pathogenesis of renal cell carcinoma (RCC). Less is known about the inhibitory effects of these pharmacologically relevant classes of alkaloids on IFIT5. Thus, we determined the ADMET properties of these alkaloids, as well as their inhibitory potentials on IFIT5. Fifty alkaloids were retrieved from PubChem. The structure of IFIT5 was obtained from Protein Data Bank and processed using Biovia Discovery Studio to eliminate nonstandard molecules. Molecular docking was performed using PyRx to assess the binding affinities of protein-ligand complexes, while ADMET analysis was conducted using AdmetSAR and swissADME. Docking results revealed that all 50 selected alkaloids demonstrated high IFIT5 binding effects, ranging from -7.1 to -11.0 kcal/mol, surpassing the di(hydroxyethyl)ether cocrystallized ligand (-3.9 kcal/mol), with nortopsentin A emerging as the most promising hit. Additionally, four of the top five IFIT5 binding alkaloids (nortopsentin A, stylopine, oxymatrine, and deoxytubulosine) displayed favourable drug-like properties. The propitious drug-like properties and strong IFIT5 binding impacts displayed by these alkaloids, particularly nortopsentin A underscore their potential for advancement into pre-clinical/clinical trials for developing selective IFIT5 inhibitors for targeted RCC treatment.

Keywords: Renal cell carcinoma, IFIT5, alkaloids, binding affinity, pharmacokinetics, toxicity

INTRODUCTION

Renal cell carcinoma (RCC) is an insidious neoplasm, accounting for approximately 2% of global cancer diagnoses and deaths (Padala et al., 2020). A unique characteristic of RCC is that many patients are often asymptomatic; it is estimated that more than 50% of patients are diagnosed with RCC incidentally during imaging for an unrelated issue (Rosner et al., 2021). Several major risk factors associated with RCC include smoking, excess body weight, alcohol consumption, hypertension, diabetes, chronic kidney disease, as well as genetic factors, such as mutations in the von Hippel-Lindau (VHL) tumour suppressor gene (Al-Bayati et al., 2019). Most RCCs occur in the cortex of the kidney, which is composed of the glomerulus, tubular apparatus and collecting duct (El-Zaatari et al., 2020). RCC cases in developed countries are often diagnosed through imaging, with only 10% presenting with the classic triad symptoms, including hematuria, flank pain, palpable masses, fever, weight loss, and leukocytosis (Satwikananda et al., 2023).

About 90% of RCCs are of the clear cell, papillary and chromophobe histological subtypes, with the clear cell being the most common and aggressive (Low et al., 2016). These subtypes have significant prognostic and treatment-predictive value. RCC etiology is a complex process that is regulated by several molecular variables (Keefe et al., 2013). The interferon-induced protein with tetratricopeptide repeats (IFIT) is one such factor that has attracted a lot of interest. (Rethnam, 2022). The IFIT family consists of a group of proteins that are upregulated in response to interferon signaling, primarily in the presence of viral infections (Tan et al., 2021). Tetratricopeptide repeat (TPR) motifs are commonly found in members of the IFIT family, including IFIT1, IFIT2, IFIT3, and IFIT5. These motifs are implicated in protein-protein interactions. (Pidugu et al., 2019). IFIT proteins now play a unique role in non-viral diseases including cancer, according to recent investigations (Kwon et al., 2022; Moulin et al., 2023)

IFIT5 has emerged as a pivotal player in RCC progression (Kang et al., 2022). IFIT5 acts solely as a monomer that can not only bind directly to viral RNA molecules via its convoluted RNA-binding cleft but also endogenous cellular RNAs with a 5'-end phosphate cap, including transfer RNAs (tRNA) (Lo, Pong, et al., 2019). IFIT5 has been implicated exclusively in an innate immune response. However, a newly identified mechanism of IFIT5 is regulation of the turnover of tumour suppressor microRNAs (miRNAs), including miR-363 and miR-128, resulting in increased expression of transcription factors of epithelial-to-mesenchymal transition (EMT) such as slug and ZEB1, thereby enhancing invasion in RCC (Lo et al., 2018). EMT plays an essential role in RCC pathogenesis, invasion and response to therapies (Guarino et al., 2007). It has also been shown that EMT correlated with an increased recurrence risk and worst overall survival (OS) in patients with RCC (Rasti et al., 2018).

Conventional chemotherapeutic drug therapy has shown low success against RCC, most of these treatment modalities are associated with complications such as diarrhoea, nausea, and mouth sores, that subsequently affect the quality of life and overall mental status of cancer patients (Regassa et al., 2022). Also, compounds with great specificity are the focus of contemporary drug discovery techniques including high-throughput screening and structure-based drug design (Vázquez et al., 2020). However, anticipating and minimizing off-target effects is still a challenging task, particularly in light of the intricate network of cellular pathways (Newman et al., 2020). IFIT5 is recognized for its intricate involvement in various cellular mechanisms, including antiviral defense and innate immune response (Bela-Ong et al., 2020; Chico et al., 2019; Wu et al., 2022; Zhang et al., 2021). However,

its role in cancer pathogenesis has only recently come to light (Huang et al., 2019; Lo, Bao, et al., 2019; Lo, Pong, et al., 2019; Pidugu et al., 2019; Tan et al., 2021). This could be responsible for the paucity of research attempts pursuing the development of selective inhibitors targeting the cancer-promoting effects of IFIT5. Renal carcinoma cells are among the cancer cells that can become resistant to targeted therapy through a variety of mechanisms, such as the activation of alternative signaling pathways or mutations in the target protein (Posadas et al., 2017). In addition, delivering drug compounds specifically to renal carcinoma cells while minimizing systemic toxicity and off-target effects presents a significant challenge (Yang et al., 2022). Thus, searching for novel therapeutic strategies with minimum side effects has become an urgent requirement in the treatment of renal cancer and there is growing interest in the use of natural product compounds to search for useful candidates as a result of minimal side effects (Garrido-Laguna & Hidalgo, 2015; Gomez et al., 2016).

Natural products have attracted significant interest among researchers for the prevention and treatment of various human cancers. Natural products have been utilized in the discovery and development of drugs, especially for cancer and infectious diseases (Bernardini et al., 2018). Approximately 60% of current cancer chemotherapeutic drugs were derived directly or indirectly from natural sources (Cragg & Pezzuto, 2016). Examples of the associations between natural products and anticancer agents include the vinca alkaloids (vincristine and vinblastine) isolated from the Madagascar periwinkle plant, taxanes (paclitaxel) derived from the bark of a Pacific yew tree, and camptothecins (irinotecan and topotecan) isolated from a Chinese ornamental tree (Nerkar et al., 2021). Natural products like alkaloids have been found to provide therapeutic benefits by modulating a wide variety of cellular processes, such as apoptotic pathways, glucose metabolism, cell cycle progression, DNA synthesis and damage repair pathways, and redox regulation pathways (Braicu et al., 2022). Alkaloids encompass an enormous class of approximately 12,000 natural products (Bribi, 2018). The principal requirement for classification as an alkaloid is the presence of a basic nitrogen atom at any position in the molecule, which does not include nitrogen in an amide or peptide bond. Alkaloids sourced from various classes have exhibited notable anticancer and anti-proliferative properties across different cancer types. For instance, compounds such as berbamine, lycorine, and berberine, derived from natural sources, have demonstrated efficacy against glioblastoma and gastrointestinal cancers, including colon cancer. They achieve this by targeting crucial signaling pathways such as Wnt/ β -catenin, inducing cell cycle arrest, and promoting apoptosis. Moreover, alkaloids like colchicine, vinblastine, and vincristine exert their anticancer effects by modulating key signaling pathways. The diverse chemical structures of these alkaloids hold promise for future anticancer therapies, particularly in the context of gastrointestinal cancers (Byun et al., 2022; Dhyani et al., 2022; Kadir & Murugappan, 2022; Khan et al., 2022; Varela et al., 2023). Despite the role of the IFIT5 in the progression of RCC, there is a dearth of research that has attempted to develop inhibitors from natural products to selectively counteract its cancer-promoting effects (Gorgulla et al., 2021; Lane, 2018). Given the fascinating and pharmacologically relevant anticancer properties of alkaloids, this study will assess the pharmacokinetic, and toxicity properties, as well as the inhibitory potentials of different classes of alkaloids against IFIT5 to identify potential compounds, which could be developed further as potent, selective IFIT5 inhibitors in

(pre)clinical trials for targeted RCC treatment.

MATERIALS AND METHODS

Identification and Preparation of IFIT 5

IFIT5 was retrieved from the Research Collaboratory for Structural Bioinformatics (RSCB) Protein Data Bank (PDB). This online free-access depository stores thousands of protein structures (Rose et al., 2016). The protein was prepared following the method described by Kanmodi, Bankole, et al. (2023). Briefly, the 3D structure of the protein, IFIT 5 (PDB ID: 3ZGQ, resolution: 2.20 Å) was downloaded in PDB format and prepared using Biovia Discovery Studio 4.5 software (<https://discover.3ds.com/discovery-studio-visualizer-download>) to remove water molecules and hetatoms, and also to add polar hydrogen atoms. Prior to molecular docking, the PDB format of the protein was converted to the Protein Data Bank, Partial Charge (Q), and Atom Type (T) format (PDBQT) using the integrated Autodock wizard tool in PyRx.

Identification and Preparation of Ligands for Docking

The 3D structures of fifty (50) alkaloids of various classes with reported anticancer properties (Mondal et al., 2019) were downloaded in structured data format (SDF) from PubChem (Kim et al., 2016) (<https://pubchem.ncbi.nlm.nih.gov>); a free, user-friendly database storing millions of chemical compounds. These alkaloids include: indoles (aplicyanins B (CID: 16718384), arctigenin (CID: 64981), camptothecin (CID: 24360), coronaridine (CID: 73489), isoplysin A (CID: 135465870), 9-methoxycamptothecin (CID: 123617), moschamine (CID: 5969616), nortopsentins A (CID: 179268), nortopsentins B (CID: 456387), pericalline (CID: 6436240), sewarine (CID: 5458504), tetrahydrosecamine (CID: 169527), vallesiachotamine (CID: 5384527)); isoquinoline (berberine (CID: 2353), chelerythrine (CID: 2703), chelidonine (CID: 197810), cribostatins 1 (CID: 10330480), cycleanine (CID: 121313), jorumycin (CID: 9849761), liriodenine (CID: 10144), mimosamycin (CID: 4198), sanguinarine (CID: 5154), stylophine (CID: 6770)); pyrrole and pyrrolizidine (homoharringtonine (CID: 285033), prodigiosin (CID: 135455579), clivorine (CID: 5363807), clathrodin (CID: 5388709), dibromophakellstatin (CID: 10500579), Discorhabdin L (CID: 135451013), discorhabdin W (CID: 136117846), tambjamine I (CID: 381030), tambjamine K (CID: 135934866), indicine N-oxide (CID: 280564)); phenanthroindolizidine alkaloids (antofine (CID: 639288), tylophorine (CID: 92114), tylophorinidine (CID: 161749), hypoestestatin 2 (CID: 126663)); indoloquinoline alkaloids (5,11-dimethylindolo[2,3-b]quinoline (CID: 133982), 3,11-dichloro-6H-indolo[2,3-b]quinoline (CID: 42637308), cryptolepine (CID: 82143), 6H-indolo[2,3-b]quinoline (CID: 67484), neocryptolepine (CID: 390526) and β -Carboline – benzoquinolizidine (harmine (CID: 5280953), harmone (CID: 5281404), harmalol (CID: 3565), harmaline (CID: 35634), tryptoline (CID: 107838), deoxytubulosine (CID: 165003), 1',2',3',4'-tetrahydrotubulosine (CID: 21668793), and oxymatrine (CID: 114850)). Additionally, we downloaded the 3D-SDF format of the co-crystallized ligand di(hydroxyethyl)ether (CID: 8117) of IFIT 5 from PubChem. Before molecular docking (blind docking), energy minimization was carried out, thereby converting the ligands from SDF to PDB format; lastly, we converted them to PDBQT format.

Molecular Docking

Autodock Vina, an integral component of the PyRx software

package (<https://pyrx.sourceforge.io/>), was employed to carry out the multiple docking of ligands against the IFIT5 protein. PyRx, a computer-based drug discovery software, is capable of screening compound libraries against potential therapeutic targets and stands out as one of the few docking software packages suitable for multiple docking. In terms of optimization and multithreading, the integrated Autodock Vina in PyRx demonstrates significantly enhanced speed and efficiency. It internally determines grid charges and establishes the docking space (Lobo, 2020). Following the preparation of the ligands and protein, the docking process was executed using Vina Wizard. The residues in the active site of the target protein were chosen to create a grid box, and the Vina Wizard was employed to complete the docking procedure. Subsequently, the binding energy scores and root mean square deviation (RMSD) of the docked complex were generated and downloaded in CSV format.

Absorption, distribution, metabolism elimination, and toxicity (ADMET) investigation.

The ADMET properties are crucial to the discovery and development of industrial chemicals, insecticides, food additives, consumer goods, and pharmaceuticals (Trott & Olson, 2009). The top five (5) ligands with the lowest binding energies were chosen, and canonical SMILES were then generated and uploaded to admetSAR and SwissADME servers (<http://lmmd.ecust.edu.cn/admetSar2>) and (<http://www.swissadme.ch>) respectively, for analysis of their druglike characteristics and other pharmacokinetic parameters. admetSAR is a completely free web service tool for estimating chemical characteristics such as absorption, distribution, metabolism, excretion, and toxicity (Cheng et al., 2012). SwissADME is a free online tool to assess the pharmacokinetics, drug-likeness, and medicinal chemistry friendliness of small molecules (Daina et al., 2017).

Analysis of Ligand-Protein Interaction

After docking with the target protein, ligands that showed the lowest binding energy and hence highest binding affinities were found and chosen to examine the associated protein-ligand complex structures and bond interactions. The hydrogen bonding and hydrophobic interactions between the ligand and amino acid residues of the protein-ligand complex were visualized using the Biovia Discovery Studio software. The Biovia Discovery Studio software was also used to obtain the 2D structures illustrating the interactions of the protein-ligand complex.

RESULTS AND DISCUSSION

Binding Affinities

The pharmacological pipeline benefits from in-silico modelling in many ways, such as reduced failure rates, shorter clinical trial durations, and lower costs for research and development (Pushpakom et al., 2019; Roessler et al., 2021). As a result of earlier studies demonstrating the anticancer actions of the various alkaloid ligands (Mondal et al., 2019), we assess the binding energies of the alkaloids with IFIT5 in [Table I](#).

The best five IFIT5 binding ligands were selected, and their binding affinities were compared to the co-crystallized ligand [Table II](#). The results showed that all the ligands exhibited low binding energies (ranging from -11 to -9.8 Kcal/mol), hence, high binding affinities for IFIT5 compared to the co-crystallized ligand (-3.9 kcal/mol).

Table 1: Binding energies (ΔG) in Kcal/mol of the interactions of the fifty alkaloids with IFIT5

Ligands	Binding energies (Kcal/mol)
Indole Alkaloids	
Arctigenin	-8
Aplicyanin B	-7.5
Camptothecin	-9.7
Coronaridine	-8.2
Isoplysin A	-7.4
9-Methoxycamptothecin	-9
Moschamine	-8.8
Nortopsentin A	-11
Nortopsentin B	-9.4
Pericalline	-8.3
Sewarine	-8.3
Tetrahydrosecamine	-8.6
Vallesiachotamine	-8.2
Isoquinoline Alkaloids	
Berberine	-8.9
Chelerythrine	-7.4
Chelidonine	-9
Cribostatin	-7.4
Cycleanine	-9.2
Jorumycin	-8.1
Liriodenine	-9.5
Mimosamycin	-8
Sanguinarine	-8.5
Stylopine	-10.6
Homoharringtonine	-8.5
Prodigiosin	-9.5
Pyrrole and Pyrrolizidine	
Clivorine	-8.2
Clathrodine	-7.5
Dibromophakellstatin	-8
Tamjamine I	-7.4
Discorhabdin W	-10.7
Discorhabdin L	-8.7
Tamjamine k	-7.1
Indicine N-oxide	-7.2
Phenanthroindolizidine	
Antofine	-9.3
Tylophorine	-8.1
Tylophorinidine	-8.4
Hypoestestatin 2	-8.6
Indoquinoline	
3,11-dichloro-6H-indolo[2,3-b]quinoline	-9.6
Cryptolepine	-9.5
Neocryptolepine	-9.8
6-H-indolo [2,3-b]quinoline	-9.5
5,11-dimethylindolo[2,3-b]quinoline	-9.4
β-Carboline – benzoquinolizidine	
Harmine	-8.3
Harmame	-8.2
Harmalol	-8.2
Harmaline	-8.4
Tryptoline	-7.5

Deoxytubulosine	-9.8
1',2',3',4' - tetrahydrotubulosine	-9.7
Oxymatrine	-10

the ligand binding with other proteins in the body is lower and it is more likely to bind precisely with the target protein.), and longer duration of action (due to the formation of exceptionally stable complex with the target which takes longer to dissociate). Compounds demonstrating potent activity often display selectivity towards their target protein. For instance, imatinib demonstrates notable selectivity for ABL and its activated derivatives like v-ABL, BCR-ABL, and TEL-ABL, as evidenced by in vitro kinase assays using purified proteins, with IC₅₀ values ranging from 0.25 to 0.5 μM. Conversely, the IC₅₀ values for numerous other tyrosine and serine/threonine kinases were generally at least 100-fold higher. Furthermore, Cellular studies showed that imatinib specifically inhibited the proliferation of myeloid cell lines that express BCR-ABL with complete inhibition of proliferation occurring between 0.5 and 1 μM (Druker, 2004).

The implications of the low binding energies and hence high binding affinities of the best five ligands are a tendency for increased potency (requiring low concentrations to achieve a significant effect on the target protein), specificity (the likelihood of

Table 2: Binding energies (ΔG) in Kcal/mol of the interaction of the best five alkaloids with IFIT5 compared to that of the co-crystallized ligand.

S/N	Ligands	PyRx
1.	Nortopsentin A	-11
2.	Discorhabdin W	-10.7
3.	stylopine	-10.6
4.	Oxymatrine	-10
5.	deoxytubulosine	-9.8
Cocrystallized Ligand		
1.	di(hydroxyethyl)ether	-3.9

Analysis of ADME/T Properties

ADME/T evaluation revealed that all the ligands except discorhabdin W complied with Lipinski rule of five [Table III](#).

Table III: Drug-likeness of the best five (5) ligands

S/N	Ligands	Lipinski's Rule of Five
1.	Nortopsentin A	Yes; 1 violation: AlogP>5
2.	Discorhabdin W	No; 2 violations: MW>500, HBA>10
3.	stylopine	Yes; 0 violation
4.	Oxymatrine	Yes; 0 violation
5.	deoxytubulosine	Yes; 1 violation: AlogP>5

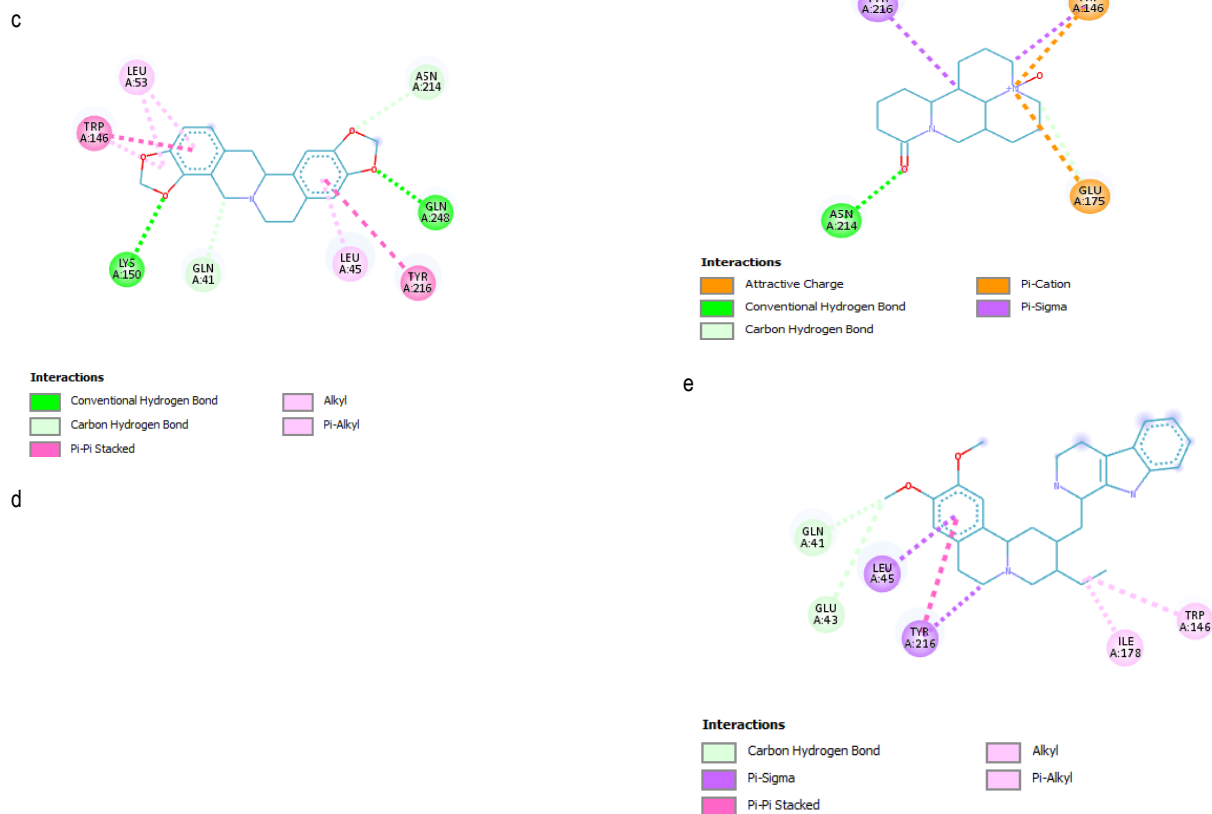


Figure 1: 2D protein-ligand interactions of nortopsentin A and IFIT5 (a); Discorhabdin W and IFIT5 (b); stylophine and IFIT5 (c); oxymatrine and IFIT5 (d); and deoxytubulosine and IFIT5 (e).

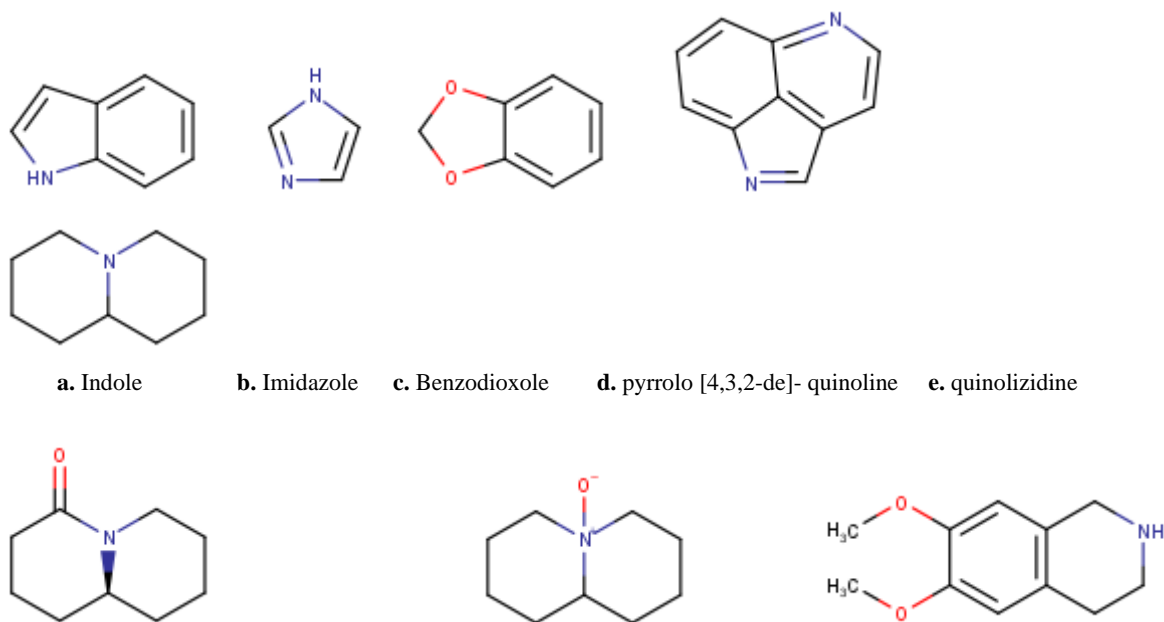


Figure 2: The various pharmacological scaffolds observed to be responsible for the binding interactions of the best five ligands with IFIT5.

DISCUSSION

Targeted therapy has revolutionized the way we approach developing advanced and potent anti-cancer drugs (Kanmodi, Oddiri, et al., 2023). The pharmacological pipeline benefits from in-silico modelling in many ways, such as reduced failure rates, shorter clinical trial durations, and lower costs for research and development (Pushpakom et al., 2019; Roessler et al., 2021). As a result of earlier studies demonstrating the anticancer actions of the various alkaloidal ligands (Mondal et al., 2019), we assess the binding energies of the alkaloids with IFIT1 in this study. Based on our findings, Nortopsentin A had the most desirable binding effect on IFIT5 (-11 Kcal/mol) of the best five ligands and co-crystallized ligands as shown in [Table II](#). Compounds exhibiting low binding energy tend to effectively inhibit their targets at lower concentrations, resulting in stronger inhibitory effects (Umamaheswari et al., 2012).

The interactions leading to the superior binding effects observed in the best ten ligands on IFIT5 are illustrated in the 2D and diagrams of the protein-ligand complexes shown in [Fig.1](#). The presence of alkyl, pi-alkyl bonds, and pi – pi stacked bonds characterized the interaction between aliphatic (valine, isoleucine, and leucine) and aromatic (tyrosine and tryptophan) amino acid residues of IFIT5 and the indole ring (Fig 2a) of nortopsentin A. Further, conventional hydrogen bonds were observed between IFIT5 polar (asparagine), negatively charged (glutamate) amino acid and the imidazole nitrogen and bromine atom attached to the indole ring of nortopsentin A respectively. Imidazole and indole rings have been reported to be crucial rings in the development of anticancer drugs (Dhingra et al., 2022; Godge et al., 2023; Mehra et al., 2022; Salerno et al., 2023). Stylopine benzodioxole ring interacted with IFIT5 amino acid residues via alkyl, pi – alkyl, and pi – pi stacked interactions. A conventional hydrogen bond is observed between the benzodioxole oxygen and lysine. Compounds containing the benzodioxole moiety exhibit a spectrum of biological activities, including anticancer, anti-tuberculosis, antimicrobial, analgesic, and anti-epileptic effects, reflecting their multifaceted pharmacological potential within scientific research and drug discovery endeavours (Hawash et al., 2020).

The pyrrolo [4,3,2-de]- quinoline ring of discorhabdin W (Fig 2) interacted with IFIT5's glutamate residue via the pi-anion bond while interacting with the aromatic phenylalanine residue via pi-pi stacked bonds. Additionally, the disulfide bond of discorhabdin W (a discorhabdin dimer), is observed to interact with IFIT5's phenylalanine residue via a pi-sulfur bond. Numerous derivatives of pyrroloquinoline have exhibited promising pharmacological properties, particularly demonstrating strong antitumor effects across a broad spectrum of cancer cell lines. This underscores their potential as candidates for therapeutic applications in oncology (Francesco et al., 2023). The presence of pi-sigma and carbon-hydrogen bonds characterised the interaction between TYR and GLU residues of IFIT5 and the quinolizidine ring of oxymatrine (Fig 2). The oxo group of (9aS)-octahydro-1H-quinolizin-4-one (a modification of the quinolizidine ring) (Fig 2) interacted with the polar uncharged side chain of an asparagine residue through a conventional hydrogen bond. The octahydro-1H-quinolizin-5-ium-5-olate of oxymatrine (Fig 2) interacted with the negatively charged side chain of GLU residue, and the indole ring of TRP residue via attractive charge interaction and pi-cation bond respectively. Compounds containing quinolizidine demonstrate diverse pharmacological activities, encompassing a wide array of bioactive properties including anticancer, antiviral, anti-inflammatory, and

antibacterial effects as discussed by Tang et al and Zhang et al, etc. (Huang et al., 2022; Tang et al., 2023; Zhang et al., 2023). The heliamine moiety of deoxytubulosine interacted with the aromatic amino acid residue TYR via pi-pi stacked and pi-sigma bonds; the aliphatic side chain of LEU via pi-sigma bonds; and the residues GLN and GLU via carbon-hydrogen bonds. Also, the ethyl group attached to the quinolizidine moiety of deoxytubulosine interacted with ILE and TYR residues using alkyl and pi-alkyl bonds, respectively.

Assessing the ADMET properties is pivotal in drug discovery and development. It serves to ascertain the safety profile and drug-likeness of chemical compounds, thereby guiding decisions throughout the drug development pipeline (Akinlalu et al., 2021; Guan et al., 2019). According to our results, only discorhabdin W did not comply with the Lipinski rule of five as shown in [Table III](#). Thus, the other four alkaloids in the best five category demonstrated propitious drug-likeness properties (Chen et al., 2020). The Lipinski Rule of Five provides a robust framework for predicting that compounds with two or more violations are likely to exhibit low oral bioavailability (Ibrahim et al., 2020). Furthermore, all other ligands ranked within the best five category except discorhabdin W displayed notable permeability across the blood-brain barrier (BBB), as indicated in [Table IV](#). This finding underscores their potential to elicit effects within central nervous system (CNS) regions (Wu et al., 2023). Based on our findings, deoxytubulosine, stylopine, and oxymatrine have high Caco-2 permeability indicating their ability to cross the human intestinal epithelial cell barrier, while only oxymatrine had a low human [intestinal absorption](#) of the best five alkaloids.

The status of a compound as either a P-glycoprotein (P-gp) inhibitor or substrate holds paramount importance in drug development, particularly in combatting multidrug resistance (MDR) within cancer therapy. P-gp, an ATP-binding cassette transporter, plays a pivotal role in restricting the absorption and bioavailability of drugs, thereby contributing to MDR. However, inhibitors of P-gp can counteract this resistance mechanism by impeding the efflux of drugs from cells, consequently augmenting their bioavailability and therapeutic efficacy (Rathod et al., 2022; Xing et al., 2020). Conversely, drug molecules that serve as substrates for P-gp undergo active transport out of cells, leading to a decrease in their intracellular concentration and subsequent efficacy (Lee et al., 2019; Rathod et al., 2022). Only deoxytubulosine, and Discorhabdin W, are inhibitors of the P-gp, while the others including nortopsentin A, stylopine and oxymatrine are non-substrates and non-inhibitors of P-gp, as shown in [Table 5](#). This implies that nortopsentin A, stylopine and oxymatrine may be retained in the cells for a longer time increasing their efficiency. Understanding how different compounds interact with CYP (cytochromes P450) is crucial. The metabolic biotransformation (including hydroxylation of aliphatic and aromatic carbon, epoxidation of the aromatic or olefinic double bond, heteroatom oxidation and dealkylation, and dehydrogenation) carried out by this superfamily of isoenzymes is crucial for the removal of drugs (Testa & Kraemer, 2008). According to several reports, it is estimated that between 50 and 90 percent of pharmaceutical compounds are substrates of one of five main isoforms (CYP1A2, CYP2C19, CYP2C9, CYP2D6, CYP3A4) (Di, 2014; Wolf et al., 2000). Different CYP isoforms have varying susceptibilities to inhibition, with 1A2 being the most susceptible and 2D6 being the least susceptible (Hayes et al., 2014). Keeping drug-metabolizing CYPs uninhibited is a common concern in the development of new

drugs (Lamb et al., 2007). The decreased clearance and buildup of the drug or its metabolites due to the inhibition of these isoenzymes is undoubtedly one of the main contributors to pharmacokinetics-related drug-drug interactions that can have toxic or other undesirable side consequences (Kirchmair et al., 2015). In our study, deoxytubulosine and oxymatrine exhibited low CYP inhibitory promiscuity, while nortopsentin A, stylopine and discorhabdin W showed high promiscuity. The broader the spectrum of Cytochrome P450 (CYP) isoforms inhibited by a specific small molecule, the greater the potential for it to engage in drug-drug interactions with a wide range of other medications (Cheng, Yu, et al., 2011). Oxymatrine and discorhabdin W are non-inhibitors of all the major CYP isoforms and are not likely to be involved in any adverse drug reaction related to drug-drug interactions. Deoxytubulosine inhibits only CYP2D6, a particularly important isoform due to its function in the metabolism of a variety of drugs, including antiarrhythmics, and anticancer treatments (Kumar & Surapaneni, 2001). Stylopine demonstrates inhibition of the CYP isoforms 1A2, 2D6, and 3A4, while nortopsentin A inhibits 1A2, 2C9, 2C19, and 3A4. Consequently, the likelihood of causing side effects or adverse drug reactions is highest with nortopsentin A, which inhibits four isoforms. Conversely, oxymatrine and discorhabdin W are less likely to induce such effects.

According to Cheng, Shen, et al. (2011), compounds with positive pIGC₅₀ values are generally considered toxic or weakly toxic to aquatic life. Thus, the best five IFIT5 binding ligands with pIGC₅₀ values ranging from 1.231 to 1.979 may exert toxic effects on aquatic life. However, our toxicity prediction showed that these five aforementioned compounds are neither carcinogenic nor Ames mutagenic. The Ames test provides valuable information about a potential drug candidate's ability to induce genetic mutations, which lead to cancer or other health problems. It suffices for the substance to be deemed an *in vitro* mutagen if this core test yields a positive result (Hakura et al., 2021; Savale, 2018). Additional investigations are required to evaluate the pharmacokinetic profiles and safety profiles of the best five ligands identified, to advance their candidacy for anti-IFIT5 drug development and targeted RCC therapy.

Conclusion

Our findings demonstrate that all ligands docked against IFIT5 exhibit high IFIT5 binding affinities (ranging from -11 to -7.1 kcal/mol) compared to the di(hydroxyethyl)ether cocrystallized ligand (-3.9 kcal/mol), with nortopsentin A emerging as the most promising hit. Additionally, four of the top five IFIT5 binding ligands—nortopsentin A, stylopine, oxymatrine, and deoxytubulosine—obeyed Lipinski's rule and displayed favourable drug-like properties. Furthermore, toxicity tests revealed that these hit compounds are neither Ames mutagenic nor carcinogenic. The propitious drug-like properties and strong IFIT5 binding impacts displayed by these alkaloids, particularly, nortopsentin A, underscores their potential for advancement into pre-clinical/clinical trials for developing selective IFIT5 inhibitors for targeted RCC treatment.

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