

Synthesis, Antimicrobial Activity and *In Silico* Studies of Benzoxazole-Piperazine Hybrids Amide Linkages

2.1 Introduction

The heterocyclic molecule benzoxazole is composed of a fused benzene and oxazole ring system. Due to its planar and electron-rich structure, it exhibits significant pharmacological flexibility.⁵⁴ The resultant hybrid compounds frequently show increased bioavailability, higher solubility, and strong binding affinity to biological targets with the piperazine moiety.⁵⁵ The creation of new medicinal compounds with promise antibacterial,⁵⁶ antifungal,⁵⁷ anti-inflammatory,⁵⁸ anticancer,⁵⁹ and CNS-modulating qualities has resulted from this structural combination.⁶⁰

Benzoxazole derivatives containing piperazine have garnered considerable attention in medicinal chemistry due to their diverse range of biological activities and potential therapeutic applications.⁶¹ The addition of piperazine units to benzoxazole scaffolds has been shown in several investigations to impact the final products pharmacokinetic and pharmacodynamic characteristics substantially.⁶² In the case of CNS-active medication design, for example, piperazine derivatives are particularly appealing due to their recognized capacity to interact with a variety of neurotransmitter receptors and enzymes.⁶³ Consequently, benzoxazole derivatives containing piperazine have been investigated for use in anticancer, antifungal, and neuroprotective medications, demonstrating their promise as lead molecules in drug development.⁶⁴

Many common antibiotics are no longer effective due to the emergence of resistant strains of pathogens such *S. aureus*, *E. coli*, *B. subtilis*, *P. aeruginosa*, *A. niger*, and *C. albicans*.⁶⁵ This highlights the critical need for new therapeutic medicines.⁶⁶ As antibiotic and antimicrobial agent resistance, especially in gram-positive bacteria, poses serious problems for the healthcare and agricultural sectors, new medication classes are desperately needed.⁶⁷ The distinct structural and electrical characteristics of benzoxazole derivatives have attracted a lot of interest in drug development because they allow for a variety of biological functions.

A fundamental component of medicinal chemistry, amide bonds play a crucial role in enhancing the physicochemical characteristics of bioactive compounds.⁶⁸ They are

essential in hybrid drug design because they improve metabolic stability, molecular stiffness, and hydrogen-bonding interactions with biological targets.⁶⁹ The antibacterial activity of amide linkages has also been shown to be enhanced by better binding interactions with bacterial proteins.⁷⁰

Benzoxazole and piperazine frameworks joined by amide bonds are combined in hybrid compounds, which are intended to take use of each compound's distinct pharmacological characteristics.⁷¹ The amide bond guarantees the hybrid molecule's structural integrity while encouraging robust microbial target engagement, piperazine optimizes pharmacokinetics and promotes multi-target interactions, and benzoxazole improves specificity and binding affinity.⁷² The derivatives of the benzoxazole-piperazine combination provide a potential strategy by focusing on many microbial cell processes.⁷ It has been demonstrated that this multi-target strategy reduces the probability of resistance development while retaining effectiveness against resistant strains.⁷⁴

Numerous widely accessible drugs that include benzoxazole heterocycle show how important its derivatives are for creating novel compounds that may be used as medicinal agents.⁷⁵ Benzoxazole and piperazine are regarded as important biological active moieties with a variety of biological properties, such as anti-inflammatory (Flunoxaprofen, **1**),⁷⁶ (Benoxaprofen, **2**),⁷⁷ anti-psychotic (Salvianen, **3**),⁷⁸ anti-tubercular (Pseudopteroxazole, **4**),⁷⁹ nerve sparing agent (Tafamidis, **5**),⁸⁰ anti-cancer (Imatinib, **6**),⁸¹ anti-psychotic (Aripiprazole, **7**),⁸² CNS depressants (Eszopiclone, **8**),⁸³ Phosphodiesterase-5 (PDE5) inhibitor (Sildenafil, **9**),⁸⁴ anti-cancer (Quetiapine, **10**)⁸⁵ (**Figure 1**), underscoring these frameworks' adaptability in drug creation.

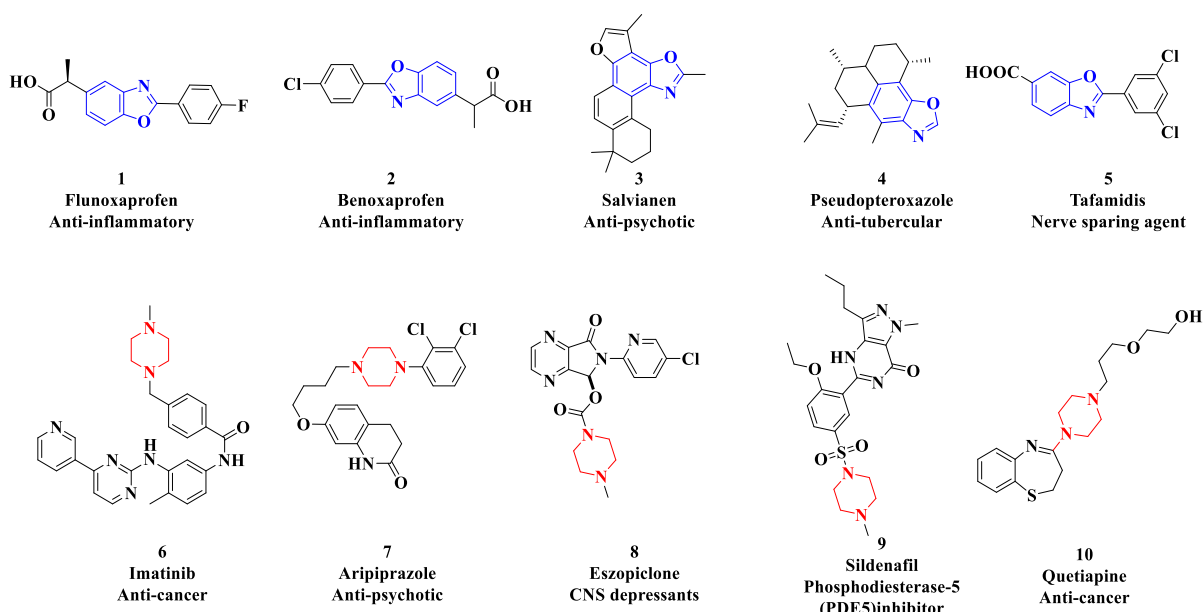


Figure 1: Marketed drugs containing Benzoxazole and piperazine motifs.

2.1.1 Synthetic methodologies for the substituted benzoxazole and piperazine framework and its biological significance

To a solution of 2-amino-4-chlorophenol (**11**) in ethyl acetate, substituted phenylisothiocyanate (**12**) and copper acetate were added and the reaction mixture was stirred at 25 °C for 5h. To get 5-chloro-*N*-phenylbenzo[*d*]oxazol-2-amine derivatives (**13**) with 80-90% yield (**Figure 2**).⁸⁶

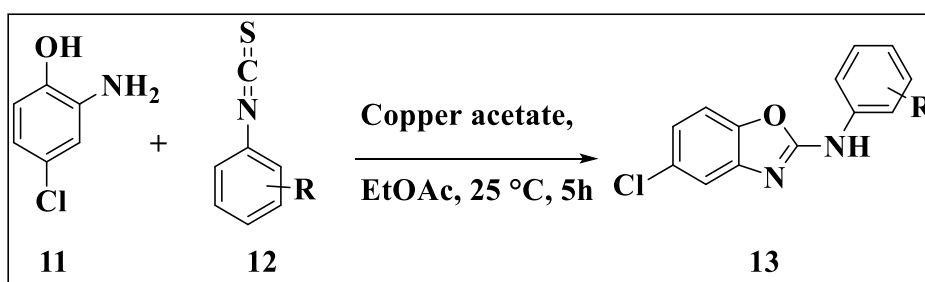


Figure 2

But-3-en-2-one (**15**) and 1,8-diazabicyclo[5.4.0]undec-7ene (DBU) were added to a solution to tert-butyl (2((5-chlorobenzo[*d*]oxazole-2-yl)amino)ethyl)carbamate derivatives (**14**) in DMF at 0-5 °C, and reaction was stirred at 25 °C for 16h. To get tert-butyl (2((5-chlorobenzo[*d*]oxazol-2-yl)(3-oxobutyl)amino)ethyl)carbamate derivatives (**16**) (**Figure 3**).⁸⁷

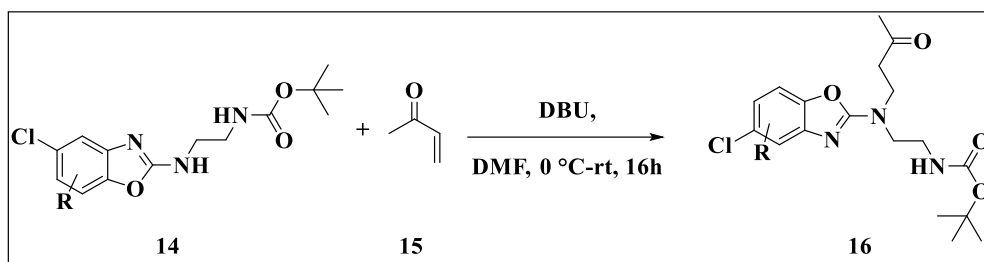


Figure 3

To a mixture of *o*-substituted anilines derivatives (**11**) and 1,3-diketones (**17**) in THF was added 30% w/w aqueous NaCl₂, and reaction was stirred at 70 °C for 2h. To get derivatized 5-chloro-2-methylbenzo[*d*]oxazole (**18**) (Figure 4).⁸⁸

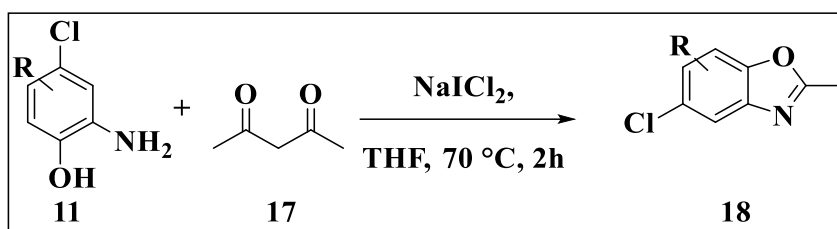


Figure 4

A mixture of some 2-amino-4-chlorophenol derivatives (**11**), potassium hydroxide, and carbon disulphide in ethanol and water and stirred at 80 °C for 3h to get derivatized 5-chlorobenzo[*d*]oxazole-2-thiol (**19**) (Figure 5).⁸⁹

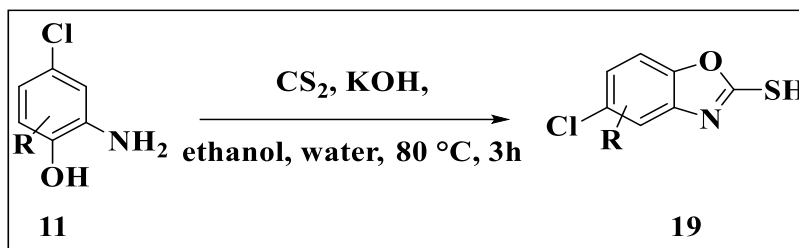


Figure 5

Compound 5-chlorobenzo[*d*]oxazole-2-thiol (**19**), 2-bromo-2-fluoro-1-phenylethan-1-one (**20**) and K₂CO₃ stirred in THF. The reaction was stirred for 25 °C for 2h for generate the 2-((5-chlorobenzo[*d*]oxazol-2-yl)thio)-2-fluoro-1-phenylethan-1-one (**21**) (Figure 6).⁹⁰

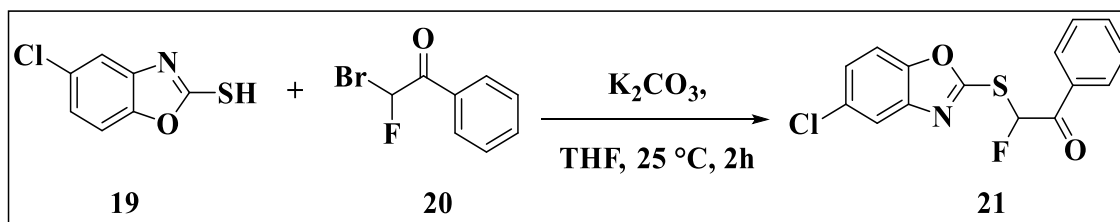


Figure 6

For the preparation of the derivatives 5-chlorobenzo[*d*]oxazol-2-amine (**23**) via cyclisation of derivatives 2-amino-4-chlorophenol (**11**) in methanol, cyanogen bromide (**22**) was added at 0°C in a dropwise and reaction was stirred at 25 °C for 16h (**Figure 7**).⁹¹

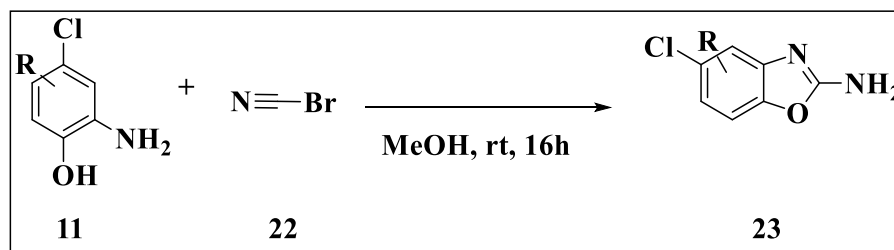


Figure 7

S-((5-chlorobenzo[*d*]oxazol-2-yl)methyl)ethanethioate (**24**) by using methanol:water (5:1) and K₂CO₃ and reaction was stirred at 25 °C for 2 h to generate the (5-chlorobenzo[*d*]oxazol-2-yl)methanethiol (**25**) (**Figure 8**).⁹²

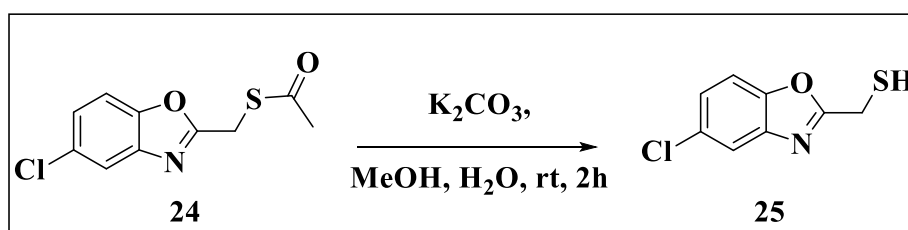


Figure 8

Some important benzoxazole derivatives having biological activity, such as anticancer (**26**),⁹³ antitubercular (**27**),⁹⁴ antibacterial (**28**),⁹⁵ antiprotozoal (**29**),⁹⁶ anthelmintic (**30**),⁹⁷ antiinflammatory (**31**),⁹⁸ and antibiotic (**32**)⁹⁹ (**Figure 9**).

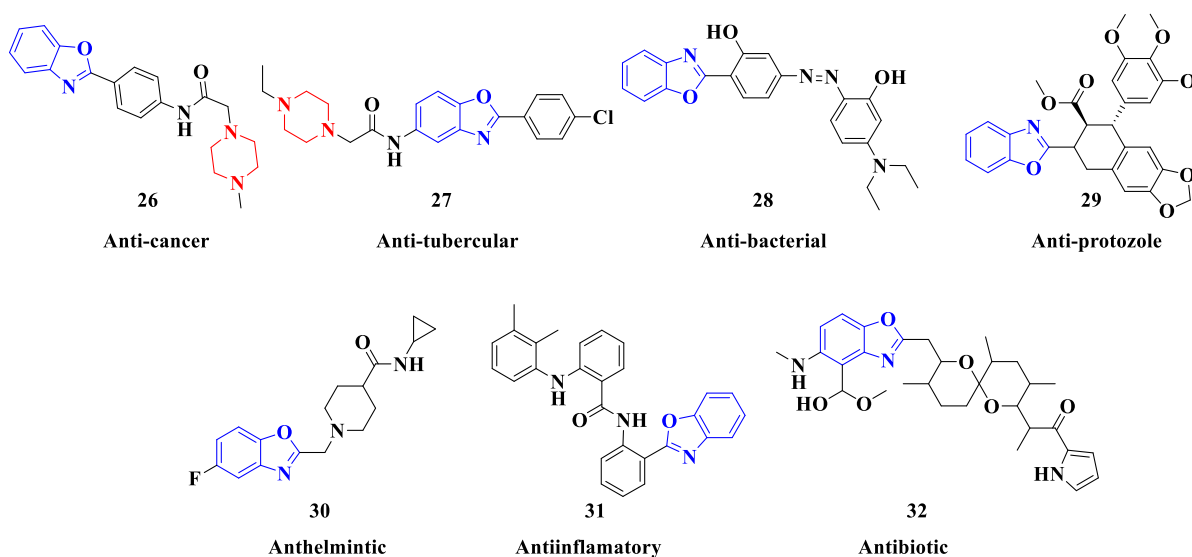
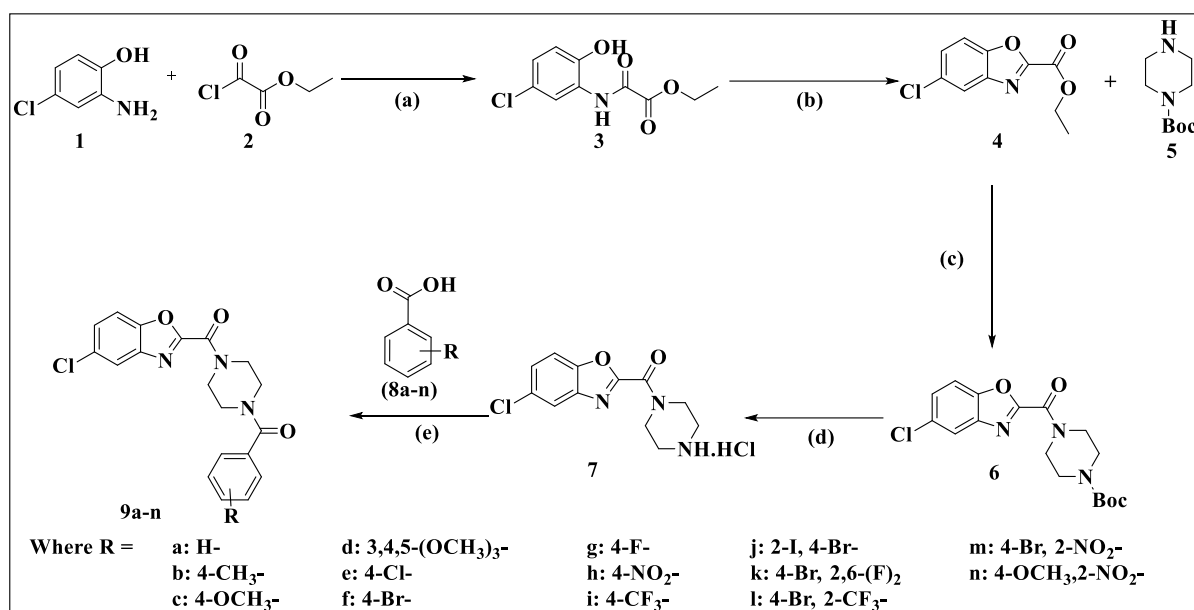


Figure 9: Important compounds containing Benzoxazole and piperazine motifs.

2.2 Results and Discussion

2.2.1 Chemistry

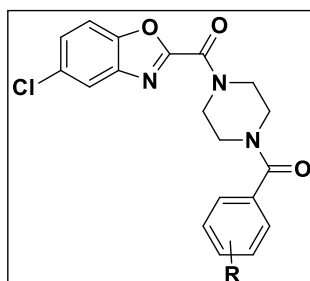
In order to investigate the various chemical and possible pharmacological characteristics of benzoxazole-piperazine hybrids with amide linkages (**9a-n**), a carefully designed series of procedures focused at functional group modification was used to create the final compounds (Scheme 1). Following a reported procedure, the process started with the amide formation of 2-amino-4-chlorophenol (**1**), which reacted with ethyl 2-chloro-2-oxoacetate (**2**) to yield ethyl 2-((5-chloro-2-hydroxyphenyl)amino)-2-oxoacetate (**3**) in 77% yield.¹⁰⁰ This was confirmed by figureits ¹H NMR data, which showed an amide proton singlet at δ 10.65 ppm and a phenol (OH) singlet at δ 9.65 ppm, both of which were exchangeable in D₂O. Under Mitsunobu conditions, compound **3** underwent intramolecular cyclization, yielding 81% ethyl 5-chlorobenzo[d]oxazole-2-carboxylate (**4**).¹⁰¹ Compound **4** was then reacted with 1-boc piperazine (**5**) via ester-amine coupling using trimethylaluminium (TMA, 2M in toluene) at 110 °C, yielding *tert-butyl* 4-(5-chlorobenzo[d]oxazole-2-carbonyl)piperazine-1-carboxylate (**6**) with a 54% yield and 97% purity as determined by LC-MS analysis.¹⁰² The *N*-Boc deprotection of compound **6** was performed using 4M HCl in dioxane, resulting in (5-chlorobenzo[d]oxazol-2-yl)(piperazin-1-yl)methanone hydrochloride (**7**) with a 90% yield.¹⁰³ The final compounds (**9a-n**) were synthesized through acid-amine coupling of compound **7** with substituted benzoic acids (**8a-n**) utilizing HATU and DIPEA in DMF as a solvent.¹⁰⁴ The synthesized compounds were isolated with purity exceeding 95% as confirmed by LC-MS, elemental analysis, ¹H NMR, ¹³C NMR, and FTIR spectroscopy.



Reaction conditions: a) TEA (2 eq), DMF, 0 °C, rt, 3h; b) triphenylphosphine (1.5 eq), DIAD (1.5 eq), THF, 0 °C, rt, 3h; c) TMA (1.5 eq), toluene, 110 °C, 16h; d) 4M HCl in dioxane, ethyl acetate rt, 16h; e) HATU (1.5 eq), DIPEA (3 eq), DMF, 0 °C, rt, 16h.

Scheme 1: Synthesis of benzoxazole-piperazine hybrid with amide linkage (**9a-n**).

Table 1: Physicochemical characteristics of the novel benzoxazole-piperazine derivatives **9a-n**.



Comp.	R	Molecular Weight	Molecular Formula	Yield (%)	Melting Point (°C)
9a	H	369.80	C ₁₉ H ₁₆ ClN ₃ O ₃	82	172-175
9b	4-Me	383.83	C ₂₀ H ₁₈ ClN ₃ O ₃	78	135-138
9c	4-OMe	399.83	C ₂₀ H ₁₈ ClN ₃ O ₄	83	127-130
9d	3,4,5-OMe	459.88	C ₂₂ H ₂₂ ClN ₃ O ₆	83	127-130
9e	4-Cl	404.25	C ₁₉ H ₁₅ Cl ₂ N ₃ O ₃	89	169-170
9f	4-Br	448.70	C ₁₉ H ₁₅ BrClN ₃ O ₃	85	172-175
9g	4-F	387.79	C ₁₉ H ₁₅ ClFN ₃ O ₃	90	199-202

9h	4-NO ₂	414.80	C ₁₉ H ₁₅ ClN ₄ O ₅	88	230-233
9i	4-CF ₃	437.80	C ₂₀ H ₁₅ ClF ₃ N ₃ O ₃	78	167-171
9j	2-I, 4-Br	574.59	C ₁₉ H ₁₄ BrClIN ₃ O ₃	71	187-191
9k	4-Br,2,6-F	484.68	C ₁₉ H ₁₃ BrClF ₂ N ₃ O ₃	73	160-164
9l	4-Br, 2CF ₃	516.70	C ₂₀ H ₁₄ BrClF ₃ N ₃ O ₃	83	129-132
9m	4-Br, 2-NO ₂	493.70	C ₁₉ H ₁₄ BrClN ₄ O ₅	94	147-150
9n	4-OCH ₃ , 2-NO ₂	444.83	C ₂₀ H ₁₇ ClN ₄ O ₆	95	197-200

2.3 Antimicrobial Activity

The nutrient agar disk diffusion technique was used to assess the antibacterial activity of the recently synthesized hybrid benzoxazole-piperazine derivatives with substituted amides (**9a-n**). Gram-positive bacteria (*B. subtilis* ATCC6051 and *S. aureus* ATCC12600), gram-negative bacteria (*P. aeruginosa* ATCC10415 and *E. coli* ATCC9637), and fungal strains (*A. niger* (ATCC 16888) and *C. albicans* (ATCC 10231)) were used to assess the synthetic compounds activity. The negative control was DMSO, while the positive controls for antibacterial and antifungal activities were chloramphenicol (30 µg/disc) and gentamicin (10 µg/disc) and nystatin, respectively. The zones of inhibition for each produced drug against the four bacterial strains and two fungal strains (**Figures 10 and 11**) in comparison to the reference standards gentamicin and chloramphenicol. Using the disc diffusion technique, the test was conducted on nutritional agar containing sodium chloride (5.0 g/L), yeast extract (10.0 g/L), and peptone (10.0 g/L) at a pH of 7.2.¹⁰⁵ Compound **9f** had the strongest antibacterial activity among the compounds tested against every bacterial species examined.

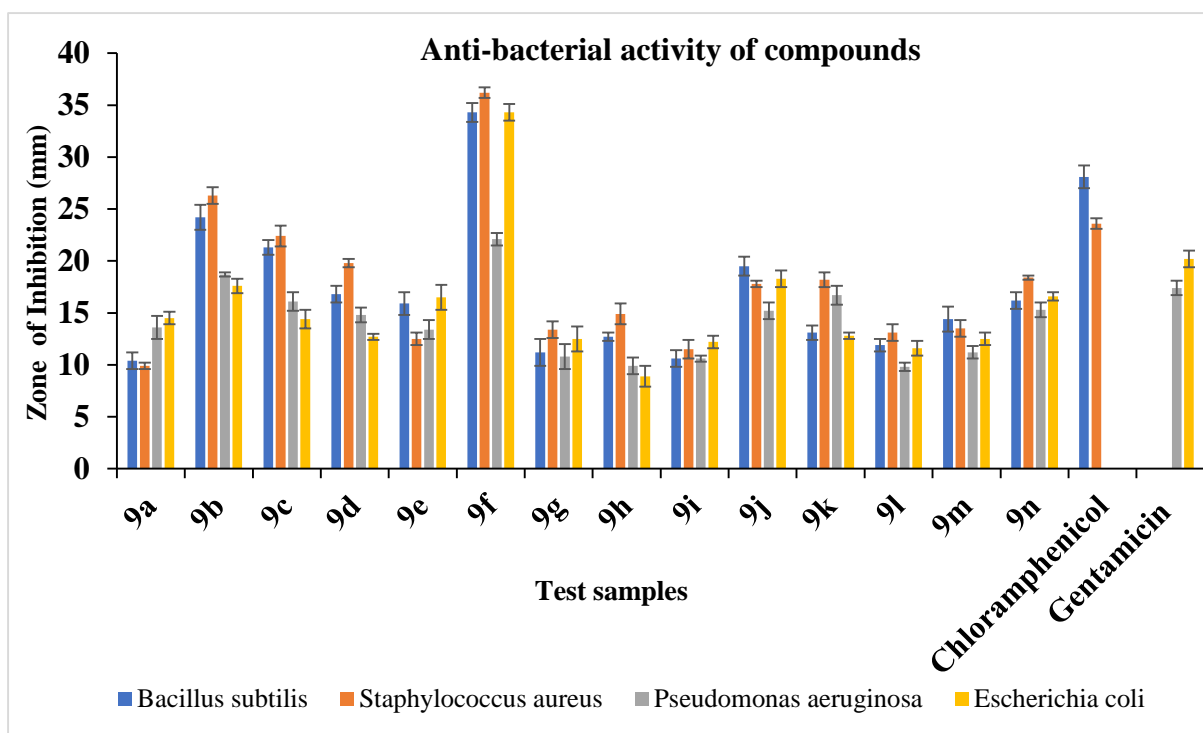


Figure 10: Graphical presentation of anti-bacterial activity data of newly synthesized benzoxazole-piperazine hybrid with amide linkage **9a-n**.

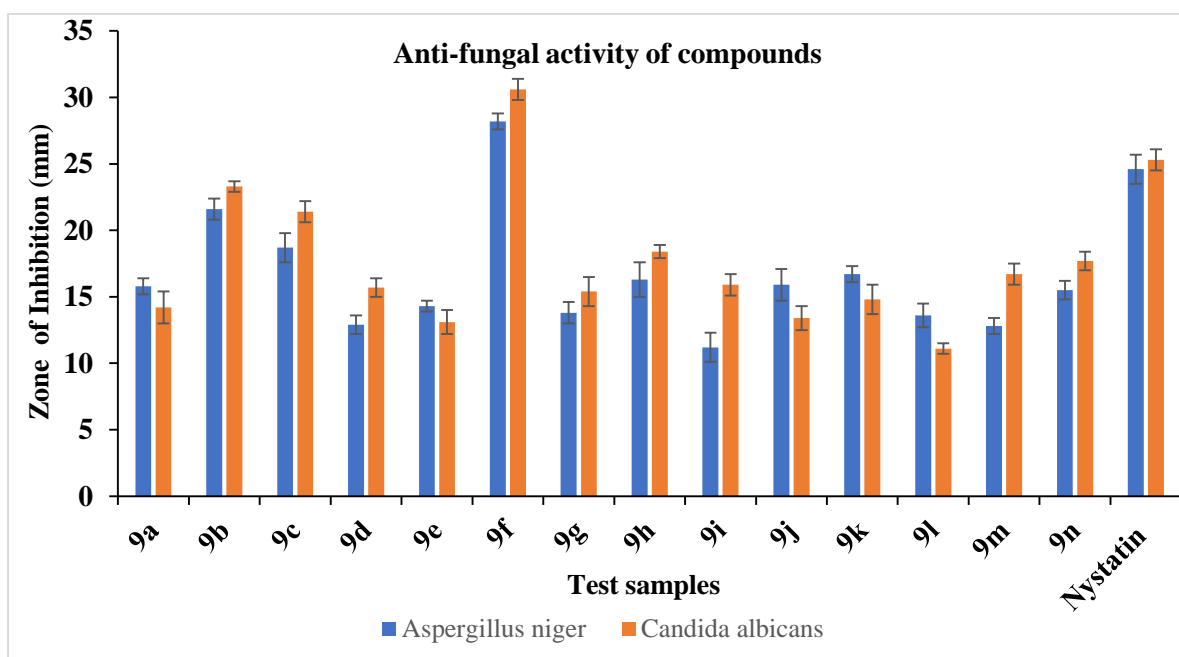


Figure 11: Graphical presentation of anti-fungal activity data of newly synthesized benzoxazole-piperazine hybrid with amide linkage **9a-n**.

2.4 Structure Activity Relationship (SAR)

B. subtilis (34.3 ± 0.9 mm) and *S. aureus* (36.2 ± 0.5 mm) were two gram-positive pathogens that compound **9f**, which has a para-position (4-Br) substitution, shown moderate to strong antibacterial activity. In contrast, the conventional medication chloramphenicol showed inhibition zones against the corresponding infections of 28.1 ± 1.1 mm and 23.6 ± 0.5 mm. Against gram-negative pathogens, compound **9f** demonstrated noteworthy antibacterial activity, with inhibition zones of 22.1 ± 0.6 mm for *E. coli* and 34.3 ± 0.8 mm for *P. aeruginosa*. Conversely, smaller inhibition zones of 17.4 ± 0.7 mm and 20.2 ± 0.8 mm were shown by the common medication gentamicin. In contrast to compound **9f**, compound **9j**, which has both an ortho-position (I) and a para-position (Br) substitution, showed less antibacterial efficacy against gram-positive and gram-negative microorganisms. In addition, out of all the compounds examined, compound **9a** with no modification (H) showed the least amount of antibacterial activity against both kinds of infections.

Furthermore, compound **9f** exhibited moderate to high antifungal activity against *A. niger* (28.2 ± 0.6 mm) and *C. albicans* (30.6 ± 0.8 mm), whereas the usual medication nystatin showed activity against the same pathogens of 24.6 ± 1.1 mm and 25.3 ± 0.5 mm, respectively. Comparing compound **9j** to compound **9f**, the former showed less antifungal efficacy against *A. niger* and *C. albicans*. Compound **9i**, which has a replacement for CF₃, on the other hand, showed the least amount of antifungal efficacy against both fungal strains after testing.

2.5 Molecular Docking

The molecular docking investigation gave important information about the chemicals' stability and possible strength of interaction inside the protein binding pocket.¹⁰⁶ With the highest negative binding affinity of -7.8 kcal/mol among the compounds examined, **9f** was the most promising candidate (Table 2). Its great affinity is consistent with its interaction profile's strong hydrogen bonding, ideal interaction distances, and notable hydrophobic interactions. The substantial binding affinities of **9b** (-7.7 kcal/mol) and **9c** (-7.5 kcal/mol) further highlighted their reliable and efficient interactions with the protein target. These compounds' durability and strong antibacterial activity are probably attributed to the many hydrogen bonds they establish with important residues while preserving advantageous hydrophobic interactions. Although it was somewhat

less efficient than compounds **9f** and **9b**, compound **9n** (-7.5 kcal/mol) showed a binding affinity similar to that of **9c**, indicating that it is another promising candidate for antibacterial action. Chemicals **9j** (-7.3 kcal/mol) and **9l** (-7.4 kcal/mol), on the other hand, had modest binding affinities. In contrast, the compounds with the least favorable binding affinities, **9d** (-6.6 kcal/mol), **9e** (-6.7 kcal/mol), and **9g** (-6.7 kcal/mol) showed poorer interaction patterns. These substances probably have fewer hydrophobic and hydrogen bonding interactions or have less-than-ideal interaction geometries, which lowers their stability and binding effectiveness inside the protein pocket.

To assess their potential for antimicrobial activity, the protein-ligand interactions for lead compounds **9b**, **9c**, and **9f** were examined (**Figures 12, 13, and 14**); similarly, the interactions for chloramphenicol were examined to assess their potential for antimicrobial activity (**Figure 15**). In order to determine binding stability and efficacy, the evaluation concentrated on the types and strengths of interactions, such as ionic, hydrophobic, and hydrogen bonding interactions. Compound **9b** stabilizes itself inside the binding pocket by forming hydrogen bonds with important residues, including ARG (3.23 Å) and THR (3.13 Å). Stability is further improved by hydrophobic interactions with residues such as LYS and PRO. Nevertheless, certain interactions (like 5.10 Å) take place near the upper end of the permissible distance range, suggesting perhaps less-than-ideal binding. Compound **9c** contributes to stable binding by forming hydrogen bonds with residues like ARG (3.20 Å) and GLU (3.14 Å). However, some interaction distances, like 5.39 Å, are outside of the ideal range, indicating that the compound is not as well anchored in the pocket. However, compound **9f** provides strong anchoring at the binding site by forming strong hydrogen bonds with important residues such as ARG (3.22 Å) and THR (3.19 Å). Furthermore, the binding is further stabilized by strong hydrophobic interactions with residues like PRO and LYS.

Table 2: Molecular docking results of the newly synthesized compounds (**9a-n**) against *E. coli* DNA gyrase B protein receptor (PDB: 4DUH).

Comp.	Binding affinity (kcal/mol)	Interacting residues (Å)	No. of H-Bonds
9a	-7.4	Asp17 (3.51), Arg20 (4.44), Arg20 (2.94), Thr175 (2.72), Arg204 (2.96), Thr30 (3.19)	04

9b	-7.7	Lys24 (4.67) Lys24 (4.04), Arg204 (3.23), Pro23 (5.39) Pro23(4.18), Thr175 (3.13), Arg20 (5.10) Arg20 (3.55)	03
9c	-7.5	Lys10 (4.10), Lys10 (4.60), Arg204 (3.20), Pro23 (4.14), Pro23 (5.39), Thr175 (3.14), Arg20 (5.08), Arg20 (3.54)	02
9d	-6.6	Gly75 (2.06), Ile94 (2.21), Gly101 (2.12), Glu50 (2.11), Gly102 (2.16), Thr 165 (2.83), Gly 77 (2.81)	03
9e	-6.7	Arg204 (3.23), Arg204 (3.03), Arg20 (3.44), Thr175 (3.58)	03
9f	-7.8	Lys21 (4.74), Lys21 (4.20), Arg204 (3.22), Pro23 (4.21), Pro23 (5.40), Thr175 (3.12), Arg20 (5.09), Arg20 (3.51)	02
9g	-6.7	Arg204 (3.23), Arg20 (3.05), Arg20 (3.59), Thr175 (3.38)	03
9h	-6.9	Ala100 (3.20), Phe104 (3.52), Gly103 (3.93), Gly117 (3.47)	03
9i	-7.5	Gly101 (2.83), Asn46 (3.20), Ala100 (3.20), Gly81 (3.33), Gly117 (3.34), Asp34 (3.34), Val44 (4.96), Ile94 (5.10), Ile78 (5.44), Ile113 (5.44), Val120 (4.96), Asn45 (3.78), Asp83 (3.83)	02
9j	-7.3	Thr175 (2.98), Thr175 (2.93), Arg20 (3.76) Lys21 (4.15), Pro23 (5.12), Pro23 (5.31), Arg20 (4.90)	03
9k	-7.0	Arg204 (2.24), Thr175 (3.00), Arg 20 (4.46), Thr30 (3.21) Asp17 (2.10), Asp17 (3.38) Lys21 (4.58), Pro23 (5.40), Pro23 (4.18)	03
9l	-7.4	Thr175 (3.07), Thr175 (3.01), Thr175 (3.81), Lys21 (4.27), Arg20 (4.75), Arg20 (3.56), Pro23 (5.31), Pro23 (5.17)	03
9m	-6.9	Thr175 (2.84), Lys21 (2.84), Arg204 (2.29), Arg20 (4.95), Arg20 (3.96), Arg204 (4.59), Pro23 (4.24), Arg22 (4.44), Arg22 (3.74), Pro23 (5.39)	03
9n	-7.5	Arg204 (2.44), Arg204 (2.94), Arg20 (2.97), Thr175 (3.54), Pro23 (5.40), Pro23 (4.19), Lys21 (4.06), Lys21 (4.64), Ser202 (3.46), Asp17 (3.36), Arg20 (4.22)	04
Chloramphenicol	-6.8	Gly101 (2.16), Glu50 (3.96), Ile78 (4.92), Pro79 (5.45), Lys103 (4.14), Arg76 (3.20), Gly77 (2.80), Thr165 (2.86)	04

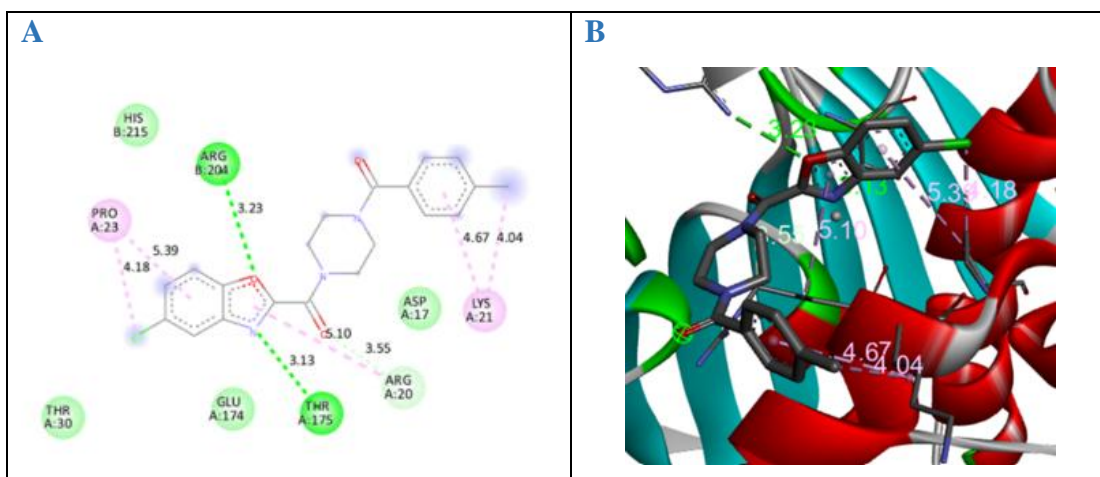


Figure 12: Docking pose of compound **9b** with 24 kDa domain of *E. coli* DNA gyrase. (A) Receptor-ligand interaction on a 2D diagram, (B) Receptor-ligand interaction on a 3D diagram.

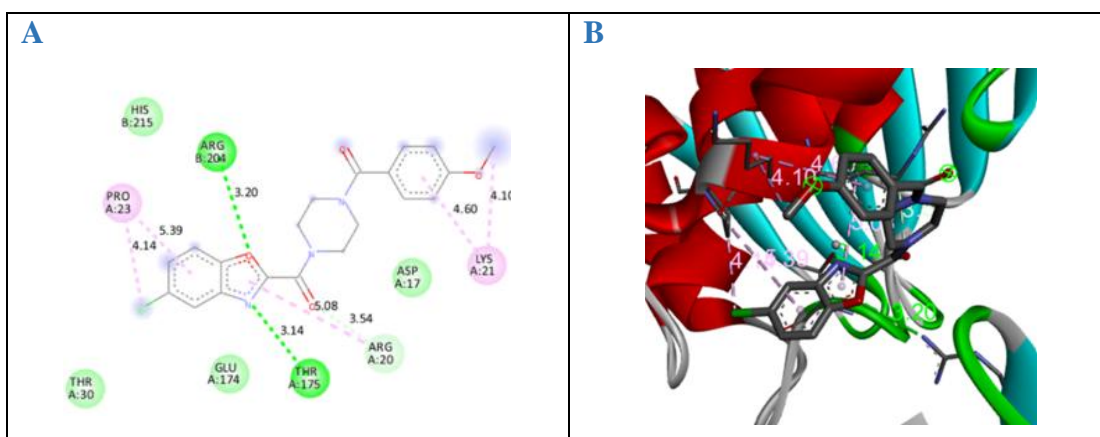


Figure 13: Docking pose of compound **9c** with 24 kDa domain of *E. coli* DNA gyrase. (A) Receptor-ligand interaction on a 2D diagram, (B) Receptor-ligand interaction on a 3D diagram.

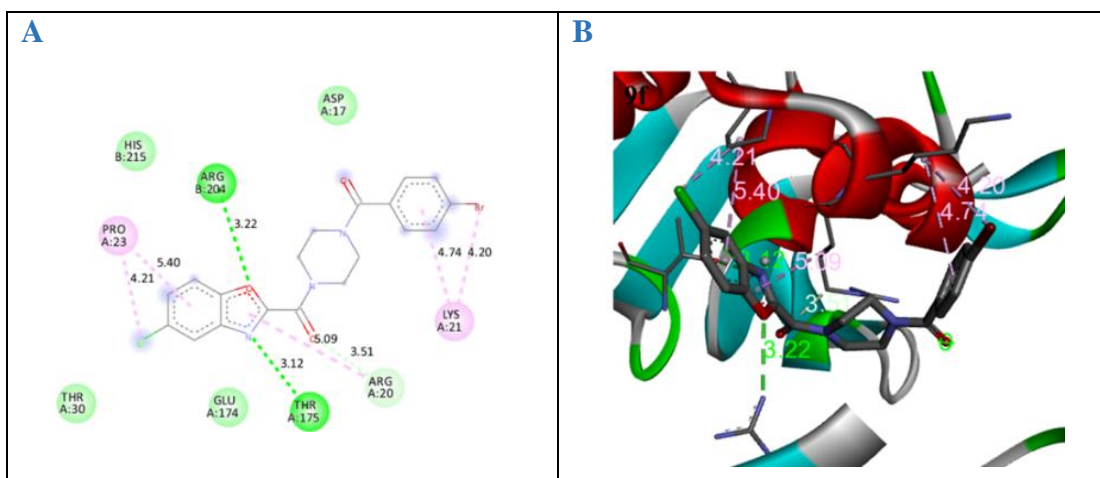


Figure 14: Docking pose of compound **9f** with 24 kDa domain of *E. coli* DNA gyrase. (A) Receptor-ligand interaction on a 2D diagram, (B) Receptor-ligand interaction on a 3D diagram.

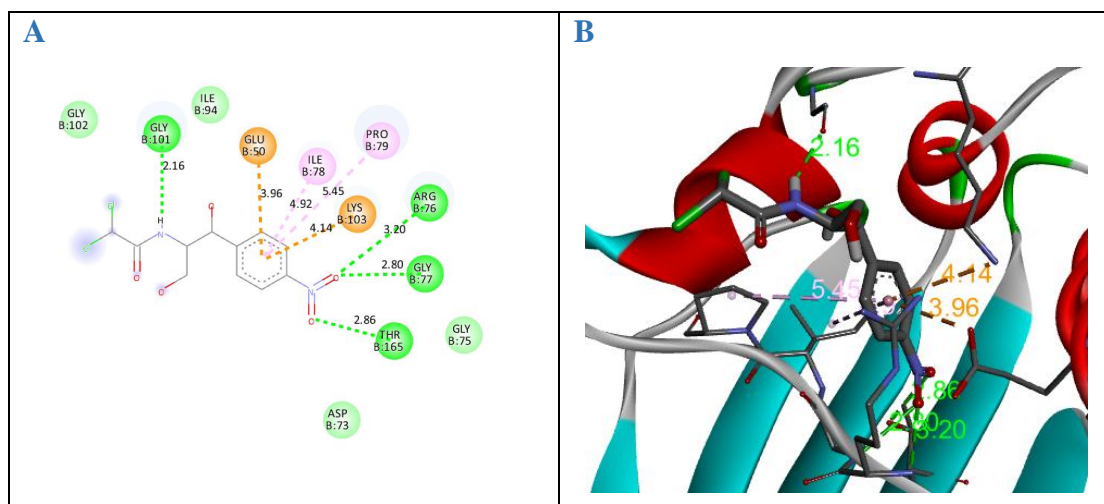


Figure 15: Docking pose of chloramphenicol with 24 kDa domain of *E. coli* DNA gyrase. (A) Receptor-ligand interaction on a 2D diagram, (B) Receptor-ligand interaction on a 3D diagram.

2.6 Molecular Dynamics Simulation Analysis

Compound **9f** was chosen for further examination by molecular dynamics simulation (MDS) based on the docking analysis. In MDS, the root mean square deviation (RMSD) and root mean square fluctuation (RMSF) offer complementary insights into the structural dynamics of the protein-ligand complex during the simulation duration.¹⁰⁷ The RMSD graph for compound **9f** illustrates the overall stability of both the protein and the ligand during the simulation (**Figure 16**). The protein RMSD stabilizes between 1.25 and 1.75 Å after the first 10 to 15 nanoseconds, signifying that the protein reached equilibrium and sustained a stable shape throughout the 100-nanosecond simulation. The ligand RMSD remained consistently low, oscillating between 1.0 and 2.5 Å, indicating that the ligand was securely attached inside the protein's binding pocket, without notable displacement or detachment. The lack of significant fluctuations in both the protein and ligand RMSD further confirmed the stability and dependability of the simulation.

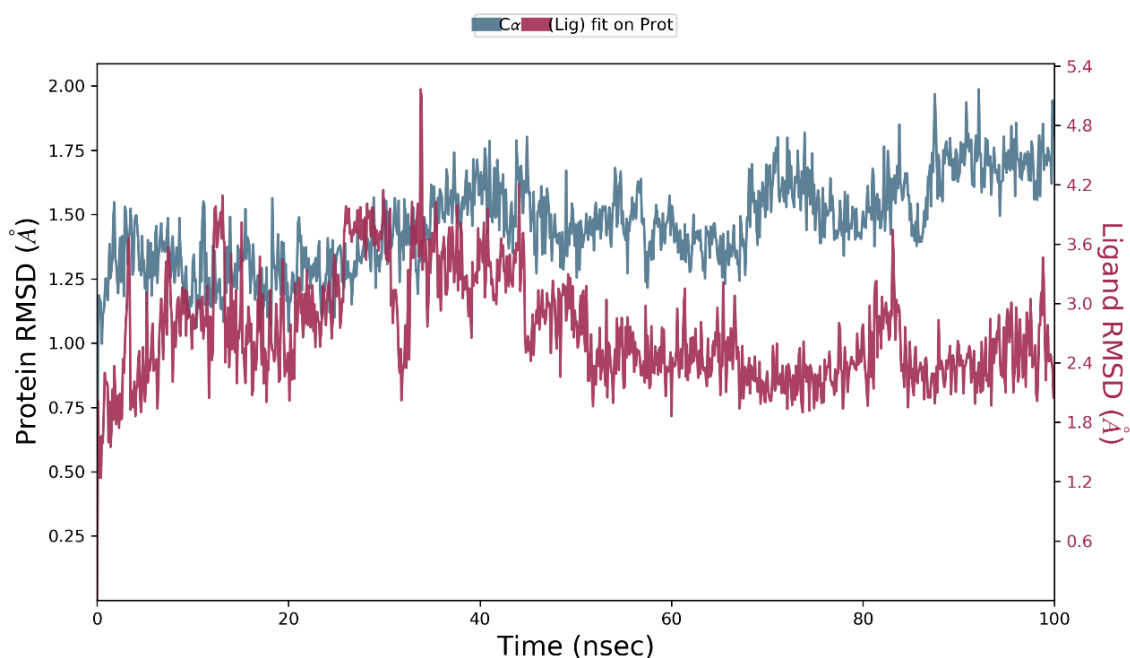


Figure 16: RMSD plot of compound **9f**-4DUH complex.

Conversely, the RMSF offered residue-specific insights regarding the protein's flexibility during the simulation.¹⁰⁸ The peaks on the RMSF graph indicate areas of increased flexibility, including terminal residues and loop regions, whereas other areas exhibited relative stability (**Figure 17**). The results validate that compound **9f** establishes a stable combination with the protein, positioning it as a robust contender for further advancement in antimicrobial applications. These regions generally display greater variability as they lack the constraints of secondary structural elements like alpha-helices or beta-sheets. Conversely, the central residues and secondary structural components have reduced RMSF values, often beneath 1.5 Å, signifying their stiffness and structural stability. Several residues near the midpoint and adjacent to the C-terminal exhibit moderate flexibility, with RMSF values nearing 3 Å. These probably relate to loop areas or dynamic domains. The interaction fraction graph emphasizes key residues, such as ARG_136, ARG_76, ASP_73, and LYS_103, which establish important hydrogen bonds and hydrophobic interactions. These acids are crucial for maintaining the protein-ligand complex and demonstrate persistent interactions during the simulation, confirming robust ligand binding (**Figure 18**).

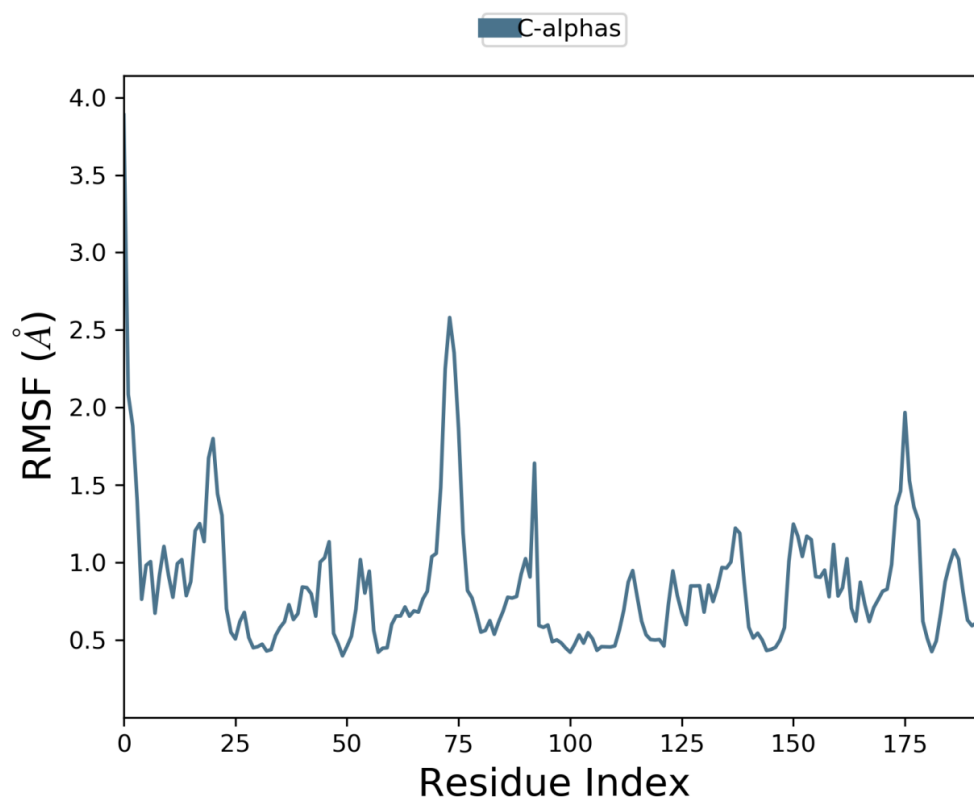


Figure 17: RMSF plot of compound **9f**-4DUH complex.

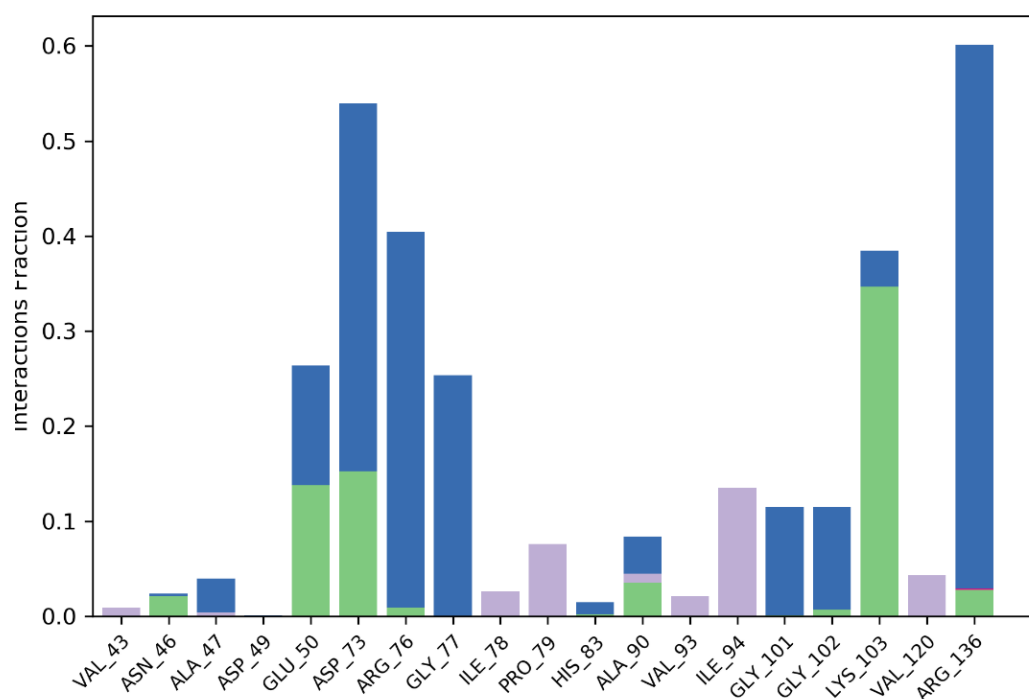


Figure 18: Interaction graph of compound **9f**-4DUH contacts.

2.7 ADMET evaluation

A multitude of prospective drug candidates do not advance in the drug development process owing to insufficient pharmacokinetic and physicochemical characteristics.¹⁰⁹ Utilizing SwissADMET methodologies to assess freshly synthesized compounds enables the early identification and rectification of these deficiencies in the first stages of research.¹¹⁰ The evaluation of the ADMET characteristics of the newly synthesized benzoxazole hybrid compounds, as shown in Table 3, indicated that the water solubility (Log S) values varied from -4.25 to -6.95, suggesting their potential bioavailability. The lipophilicity (Log Po/w) values were determined to be below 5, namely between 1.94 to 4.31, indicating advantageous membrane permeability. All produced compounds conformed to Lipinski's rule of five, except for compounds **9k** and **9l**, which possessed molecular weights more than 500. Moreover, all the benzoxazole hybrid compounds had lipophilicity scores between 1.94 and 4.31, underscoring their potential for drug-like characteristics.

Table 3: ADMET properties of newly synthesized benzoxazole-piperazine hybrid with amide linkage **9a-n**.

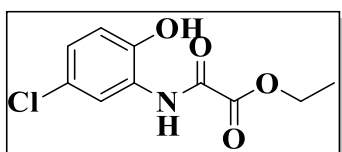
Comp.	Physicochemical properties						Pharmacokinetics		Medicinal chemistry	
	M.W. [#]	HBA	HBD	TPSA	Log Po/w	Log S	GIA	Log kp	ROF	SA
9a	369.80	4	0	66.65	2.69	-4.25	High	-6.35	0	2.87
9b	383.83	4	0	66.65	3.06	-4.56	High	-6.17	0	2.99
9c	399.83	5	0	75.88	2.73	-4.33	High	-6.55	0	2.96
9d	459.88	7	0	94.34	2.69	-4.49	High	-6.95	0	3.35
9e	404.25	4	0	66.65	3.25	-4.85	High	-6.11	0	2.88
9f	448.70	4	0	66.65	3.33	-5.17	High	-6.33	0	2.90
9g	387.80	5	0	66.65	3.02	-4.41	High	-6.39	0	2.89
9h	414.80	6	0	112.47	1.97	-3.93	High	-6.74	0	3.04
9i	437.80	7	0	66.65	3.71	-5.11	High	-6.13	0	3.00
9j	574.60	4	0	66.65	3.97	-6.34	High	-6.64	1	3.05
9k	484.68	6	0	66.65	3.92	-5.49	High	-6.41	0	2.96
9l	516.70	7	0	66.65	4.31	-6.03	High	-6.12	1	3.09
9m	493.70	6	0	112.47	2.59	-5.23	High	-6.73	0	3.22

9n	444.83	7	0	121.7	1.94	-4.39	High	-6.95	0	3.32
Doxycycline	444.43	9	6	181.62	-0.50	-2.35	Low	-8.63	0	5.25
[#] Hydrogen Bond Acceptors (HBA), Hydrogen Bond Donors (HBD), Topological Polar Surface Area (TPSA), Lipophilicity (Log Po/w), Water Solubility (Log S), Gastrointestinal Absorption (GIA), Skin permeation (Log Kp), Lipinski's rule of five (RoF) and Synthetic Accessibility (SA).										

2.8 Experimental Section

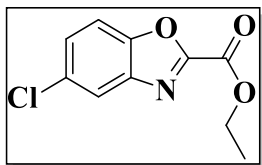
2.8.1 Chemistry

Synthesis of {Ethyl 2-[(5-chloro-2-hydroxyphenyl)amino]-2-oxoacetate} (3)



Compound {Ethyl 2-[(5-chloro-2-hydroxyphenyl)amino]-2-oxoacetate} (**3**) was synthesized using a previously reported method with yield: 77%. mp: 125-127 °C (Reported mp: 125-128 °C).¹⁰⁰

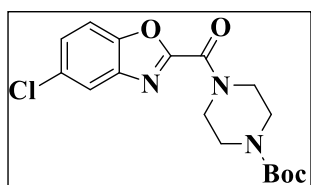
Synthesis of ethyl 5-chlorobenzo[d]oxazole-2-carboxylate (4)



TPP (32.34 g, 0.123 mol) and DIAD (24.98 g, 0.123 mol) were added to a solution of {Ethyl 2-[(5-chloro-2-hydroxyphenyl)amino]-2-oxoacetate} (**3**) (20 g, 0.082 mol) in THF (200 mL) in 3-neck RBF at 0 °C under a nitrogen environment. For three hours, the reaction was agitated at room temperature. Using the proper mobile phase and TLC, the product's formation and the starting material's consumption were tracked. After the reaction was finished, it was quenched with water and extracted twice or three times using ethyl acetate. To obtain the crude product, the mixed organic layer was dried over sodium sulfate, filtered, and the solvent was evaporated until it was completely dry. Column chromatography employing 60–120 silica gel was used to purify the crude product, which was then eluted using 0–20% ethyl acetate in hexane. Ethyl (5-chlorobenzo[d]oxazol-2-yl)carboxylate (**4**), off white (15 g, 81% yield).¹⁰¹ mp: 135–138 °C. Off-white solid. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3084 (aromatic-CH), 2912 (aliphatic-CH), 1725 (COO), 1638 (C=N), 1545 (C=O). ¹H NMR (400 MHz, *DMSO-d*₆): δ ppm

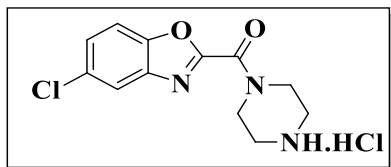
8.09-8.08 (d, $J=2\text{Hz}$, 1H, Ar-CH), 7.97-7.94 (d, $J = 8.8\text{ Hz}$, 1H, Ar-CH), 7.67-7.65 (q, $J = 6.5\text{Hz}$, 1H, Ar-CH), 4.46-4.41 (q, $J = 7.2\text{Hz}$, 2H, CH₂), 1.38-1.34 (t, $J = 6.8\text{Hz}$, 3H, CH₃). ¹³C NMR (100 MHz, *DMSO-d*₆): 155.98, 154.41, 149.41, 141.65, 130.44, 128.83, 121.70, 113.95, 63.26, 14.33. LC-MS (m/z): 97%, $[M]^+$: 226, $[M+1]^+$: 227. Anal. Calcd. C₁₀H₈ClNO₃ (225.63): C, 53.23; H, 3.57; N, 6.21%. Found C, 53.35; H, 3.49; N, 6.26%.

Procedure for synthesis of *tert*-butyl 4-(5-chlorobenzo[*d*]oxazole-2-carbonyl)piperazine-1-carboxylate (6)



At 0 °C, trimethyl aluminum (TMA, 2M in toluene) (63 mL, 7.20 g, 0.099 mol) was added to a solution of *tert*-butyl piperazine-1-carboxylate (**5**, 18.57 g, 0.099 mol) in toluene (150 mL) under a nitrogen environment. After 15 minutes of stirring, ethyl 5-chlorobenzo[*d*] oxazole-2-carboxylate (**4**, 15 g, 0.066 mol) was gradually added to the mixture. For 16h, the reaction was agitated at 110 °C, and TLC was used to track its development. After finishing, water was added and the liquid was allowed to cool to room temperature. Ethyl acetate was used three times to extract the mixture. To get the crude product, the mixed organic layer was cleaned with brine, dried on sodium sulfate, and then evaporated in a vacuum. Using 60–120 mesh silica gel, column chromatography was used to purify the crude product. 0–30% ethyl acetate in hexane was used to elute the product. *Tert*-butyl 4-(5-chlorobenzo[*d*]oxazole-2-carbonyl)piperazine-1-carboxylate (**6**), 16 g, 54% Yield.¹⁰² mp: 154-157 °C. Off-white solid that was produced as the pure end product. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 2996 (aromatic-CH), 2916 (aliphatic-CH), 1682 (C=O), 1653 (C=O), 1537 (C=N), 1125 (C-N). ¹H NMR (400MHz, *DMSO-d*₆): δ ppm 8.07 (s, 1H, Ar-CH), 7.94-7.92 (d, $J = 8.4\text{Hz}$, 1H, Ar-CH), 7.64-7.61 (q, $J = 6.4\text{Hz}$, 1H, Ar-CH), 3.95-3.93 (t, $J = 4.8\text{ Hz}$, 2H, CH₂), 3.71-3.68 (t, $J = 4.4\text{ Hz}$, 2H, CH₂), 3.46 (s, 4H, 2CH₂), 1.43 (s, 9H, 3(CH₃)). ¹³C NMR (100 MHz, *DMSO-d*₆): 150.04, 155.34, 153.70, 148.18, 140.77, 129.65, 127.44, 120.74, 113.08, 79.31, 46.21, 42.14, 28.01. LC-MS (m/z): 97%, $[M-56]^+$: 310, $[M-54]^+$: 312. Anal. Calcd. C₁₇H₂₀ClN₃O₄ (365.81): C, 55.82; H, 5.51; N, 11.49%. Found C, 55.78; H, 5.49; N, 11.53%.

Procedure for synthesis of (5-chlorobenzo[d]oxazol-2-yl)(piperazin-1-yl)methanone hydrochloride (7)

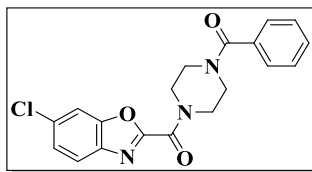


4M HCl in 50 mL of dioxane was added dropwise at 0 °C to agitate a solution of tert-butyl 4-(5-chlorobenzo[d]oxazole-2-carbonyl)piperazine-1-carboxylate (**6**, 16 g, 0.044 mol) in ethyl acetate (100 mL). After 16h of stirring the reaction mixture, TLC was used to track its development. After finishing, the solvent was removed using n-pentane and evaporated under low pressure, yielding the crude solid product (5-chlorobenzo[d]oxazol-2-yl)(piperazine-1-yl)methanone hydrochloride (**7**), off pink color (10.5 g, 90% yield).¹⁰³ mp : 110-112 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3367 (NH), 3071 (aromatic-CH), 2933 (aliphatic-CH), 1649 (C=O), 1587 (C-O), 1535 (C=N), 1138 (C-N). ¹H NMR (400MHz, *DMSO-d*₆): 9.26 (s, 2H, (NH.HCl salt)), 8.06 (d, J = 2 Hz, 1H, Ar-CH), 7.95-7.93 (d, J = 8.8Hz, 1H, Ar-CH), 7.65-7.62 (m, 1H, Ar-CH), 4.28 (m, 2H, CH₂), 3.92 (m, 2H, CH₂), 3.23 (s, 4H, 2CH₂). ¹³C NMR (100 MHz, *DMSO-d*₆): 155.64, 115.16, 148.18, 140.71, 129.73, 127.65, 120.79, 113.14, 43.38, 42.65, 42.21. LC-MS (m/z) = 100%, [M]⁺: 266, [M+2]⁺: 268. Anal. Calcd. C₁₂H₁₃Cl₂N₃O₂ (265.70): C, 47.70; H, 4.34; N, 13.91%. Found C, 47.68; H, 4.38; N, 13.88%.

General procedure for the synthesis of benzoxazole-piperizine hybrid compounds with amide linkage (9a-n)

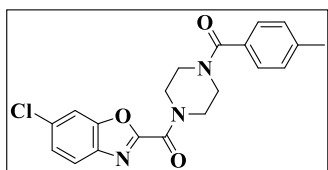
At 0 °C, HATU (1.5 eq) was added to a thoroughly mixed solution of the corresponding acid (**8a-n**) (1.0 eq) dissolved in DMF in a nitrogen environment. At room temperature, the mixture was agitated for half an hour. Then, at 0 °C in a nitrogen environment, {1-[(5-chlorobenzo[d]oxazol-2-yl)carbonyl]piperazine} [hydrochloride] (**7**) (1.5 eq) and DIPEA (3 eq) were added to the reaction mixture. After then, the reaction was let to continue for 16 more hours at room temperature.¹⁰² TLC was used to track the reaction's development. After finishing, the precipitates were obtained by pouring the reaction mixture into ice-cold water. Acetonitrile and 0.1% formic acid in water were used as the mobile phase in reverse-phase flash chromatography on C18 silica gel (15 μm particle size) to purify the crude precipitates. The relevant desirable products were obtained by vacuum-evaporating the accumulated eluent.

{4-[(Benzoyl)piperazin-1-yl]-6-chlorobenzo[d]oxazol-2-yl}methanone (9a)



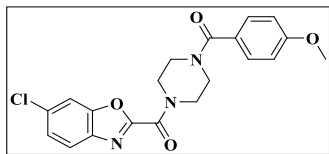
Compound **9a** was prepared from **8a** (0.1 g, 0.82 mmol), HATU (0.470 g, 1.23 mmol) in DMF (2 mL), DIPEA (0.45 mL, 0.317 g, 2.44 mmol), and compound **7** (0.371 g, 1.22 mmol). Off cream solid (0.250 g, 82% yield). mp: 172-175 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3082 (aromatic-CH), 2922 (aliphatic-CH), 1645 (C=O), 1619 (C=O), 1558 (C=N), 1118 (C-N), 1004 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.06 (s, 1H, Ar-CH), 7.94-7.92 (d, *J* = 8Hz, 2H), 7.64-7.61 (m, 1H, Ar-CH), 7.52-7.42 (m, 5H, Ar-CH (phenyl ring)), 4.04 (s, 2H), 3.77 (s, 4H), 3.50 (s, 2H). ^{13}C NMR (100 MHz, *DMSO-d*₆): 169.76, 156.52, 155.92, 148.70, 141.27, 136.00, 130.22, 128.94, 127.94, 127.55, 121.23, 113.57, 46.80, 42.70. LCMS (*m/z*): 99% [*M*]⁺:370, [*M*+2]⁺: 372. Anal. Calcd. C₁₉H₁₆ClN₃O₃ (369.81): C, 61.71; H, 4.36; N, 11.36%. Found C, 61.65; H, 4.40; N, 11.31%.

(6-chlorobenzo[d]oxazol-2-yl)(4-(4-methylbenzoyl)piperazin-1-yl)methanone (9b)



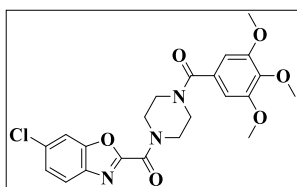
Compound **9b** was prepared from **8b** (0.1 g, 0.73 mmol), HATU (0.418 g, 1.1 mmol) in DMF (2 mL), DIPEA (0.38 mL, 0.284 g, 2.20 mmol) and **7** (0.332 g, 1.10 mmol). Off cream solid (0.220 g, 78% yield). mp: 135-138 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3080 (aromatic-CH), 2926 (aliphatic-CH), 1645 (C=O), 1617 (C=O), 1556 (C=N), 1121 (C-N), 1004 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.03 (s, 1H, Ar-CH), 7.90-7.88 (d, *J* = 8Hz, 1H, Ar-CH), 7.62-7.59 (m, 1H, Ar-CH), 7.36-7.34 (d, *J* = 8Hz, 2H, 2Ar-CH), 7.28-7.26 (d, *J* = 8Hz, 2H, 2Ar-CH), 4.01 (s, 2H, CH₂), 3.75 (s, 4H, 2CH₂), 3.60 (s, 2H, CH₂), 2.34 (s, 3H, CH₃). ^{13}C NMR (100 MHz, *DMSO-d*₆): 169.90, 156.52, 155.93, 141.27, 139.97, 133.03, 130.17, 129.41, 127.95, 127.72, 121.23, 113.57, 46.84, 42.78, 21.40. LC-MS (*m/z*): 98%, [*M*]⁺: 384, [*M*+1]⁺: 386. Anal. Calcd. C₂₀H₁₈ClN₃O₃ (383.83): C, 62.58; H, 4.73; N, 10.95 %. Found C, 62.60; H, 4.70; N, 10.97%.

(6-chlorobenzo[d]oxazol-2-yl)(4-(4-methoxybenzoyl)piperazin-1-yl)methanone
(9c)



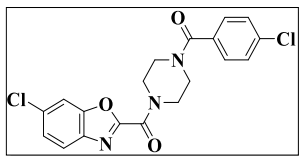
Compound **9c** was prepared from **8c** (0.1 g, 0.65 mmol), HATU (0.372 g, 0.98 mmol) in DMF (2 mL), DIPEA (0.34 mL, 0.253 g, 1.95 mmol) and **7** (0.298 g, 0.98 mmol). Off-cream solid (0.220 g, 83% yield). mp: 127-130 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3080 (aromatic-CH), 2920 (aliphatic-CH), 1640 (C=O), 1606 (C=O), 1543 (C=N), 1151 (C-N), 1000 (C-O). ^1H NMR (400MHz, $\text{DMSO}-d_6$): δ ppm 8.06 (s, 1H, Ar-CH), 7.94-7.92 (d, J = 8Hz, 1H, Ar-CH), 7.64-7.61 (m, 1H, Ar-CH), 7.46-7.42 (d, J = 16Hz, 2H, 2Ar-CH), 7.03-7.00 (d, J = 12Hz, 2H, 2Ar-CH), 4.03 (s, 2H, CH_2), 3.81 (s, 3H, OCH_3), 3.77 (s, 2H, CH_2), 3.63 (s, 4H, 2 CH_2). ^{13}C NMR (100 MHz, $\text{DMSO}-d_6$): 169.72, 160.89, 156.54, 155.93, 148.71, 141.29, 130.17, 129.71, 127.94, 121.24, 114.19, 113.58, 55.78, 46.86, 42.80. LC-MS (m/z): 97%, $[\text{M}]^+$: 400, $[\text{M}+1]^+$: 402. Anal. Calcd. $\text{C}_{20}\text{H}_{18}\text{ClN}_3\text{O}_4$ (399.83): C, 60.08; H, 4.54; N, 10.51%. Found C, 60.11; H, 4.51; N, 10.53%.

(6-chlorobenzo[d]oxazol-2-yl)(4-(3,4,5-trimethoxybenzoyl)piperazin-1-yl)methanone (9d)



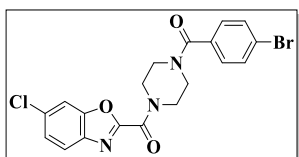
Compound **9d** was prepared from **8d** (0.1 g, 0.47 mmol), HATU (0.268 g, 0.70 mmol) in DMF (2 mL), DIPEA (0.24 mL, 0.182 g, 1.41 mmol) and **7** (0.213 g, 0.70 mmol). Off cream solid (0.180 g, 83% yield). mp: 127-130 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3093 (aromatic-CH), 2942 (aliphatic-CH), 1654 (C=O), 1612 (C=O), 1552 (C=N), 1123 (C-N), 1012 (C-O). ^1H NMR (400MHz, $\text{DMSO}-d_6$): δ ppm 8.06 (s, 1H, Ar-CH), 7.96-7.92 (m, 1H, Ar-CH), 7.64-7.61 (m, 1H, Ar-CH), 7.75 (s, 2H, 2Ar-CH), 4.04 (s, 2H, CH_2), 3.81-3.79 (m, 11H, 3(OCH_3) CH_2), 3.70 (s, 4H, 2 CH_2). ^{13}C NMR (100 MHz, $\text{DMSO}-d_6$): 169.41, 156.50, 155.93, 153.27, 148.68, 141.25, 138.83, 131.33, 130.15, 127.94, 121.22, 113.59, 105.02, 60.51, 56.51, 46.86, 42.70. LC-MS (m/z): 98%, $[\text{M}]^+$: 460, $[\text{M}+1]^+$: 462. Anal. Calcd. $\text{C}_{22}\text{H}_{22}\text{ClN}_3\text{O}_6$ (459.88): C, 57.46; H, 4.82; N, 9.14%. Found C, 57.42; H, 4.79; N, 9.16%.

(6-chlorobenzo[d]oxazol-2-yl)(4-(4-chlorobenzoyl)piperazin-1-yl)methanone (9e)



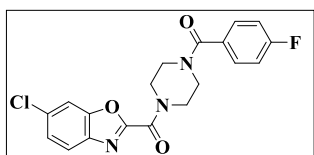
Compound **9e** was prepared from **8e** (0.1 g, 0.63 mmol), HATU (0.361 g, 0.95 mmol) in DMF (2 mL), DIPEA (0.33 mL, 0.245 g, 1.90 mmol) and **7** (0.289 g, 0.95 mmol). Brown solid (0.230 g, 89% yield). mp: 168-170 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3080 (aromatic-CH), 2935 (aliphatic-CH), 1660 (C=O), 1638 (C=O), 1559 (C=N), 1151 (C-N), 1004 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.06 (s, 1H), 7.94-7.92 (d, J = 8Hz, 1H), 7.64-7.61 (d, J = 12Hz, 1H), 7.56-7.49 (q, J = 8.4 Hz, 4H), 4.04 (s, 2H), 3.77 (s, 4H), 3.49 (s, 2H). ^{13}C NMR (100 MHz, *DMSO-d*₆): 168.73, 156.51, 155.91, 148.71, 141.28, 134.93, 134.79, 130.18, 129.61, 129.05, 127.96, 121.23, 113.58, 46.77, 42.71. LC-MS (m/z): 100%, $[\text{M}]^+$: 404, $[\text{M}+1]^+$: 406. Anal. Calcd. $\text{C}_{19}\text{H}_{15}\text{Cl}_2\text{N}_3\text{O}_3$ (404.25): C, 56.45; H, 3.74; N, 10.39%. Found C, 56.42; H, 3.70; N, 10.43%.

(4-(4-bromobenzoyl)piperazin-1-yl)(6-chlorobenzo[d]oxazol-2-yl)methanone (9f)



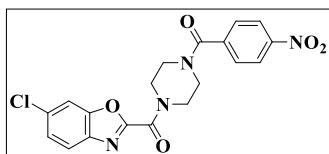
Compound **9f** was prepared from **8f** (0.1 g, 0.49 mmol), HATU (0.281 g, 0.74 mmol) in DMF (2 mL), DIPEA (0.25 mL, 0.191 g, 1.48 mmol) and **7** (0.225 g, 0.74 mmol). Off white solid (0.190 g, 85% yield). mp: 172-175 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3082 (aromatic-CH), 2918 (aliphatic-CH), 1653 (C=O), 1634 (C=N), 1533 (C=C), 1146 (C-N), 1002 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.06 (s, 1H, Ar-CH), 7.94-7.92 (d, J = 8Hz, 1H, Ar-CH), 7.69-7.61 (m, 3H, 3Ar-CH), 7.44-7.42 (d, J = 8Hz, 2H, 2Ar-CH), 4.05 (s, 2H, CH₂), 3.76 (s, 4H, 2CH₂), 3.51-3.46 (m, 2H, CH₂). ^{13}C NMR (100 MHz, *DMSO-d*₆): 168.74, 156.47, 155.87, 148.67, 141.25, 135.12, 131.95, 130.15, 129.81, 127.95, 123.63, 121.23, 113.59, 46.96, 42.54. LC-MS (m/z): 98%, $[\text{M}]^+$: 448, $[\text{M}+1]^+$: 450. Anal. Calcd. $\text{C}_{19}\text{H}_{15}\text{BrClN}_3\text{O}_3$ (448.70): C, 50.86; H, 3.37; N, 9.37%. Found C, 50.83; H, 3.40; N, 9.41%.

(6-chlorobenzo[d]oxazol-2-yl)(4-(4-fluorobenzoyl)piperazin-1-yl)methanone (9g)



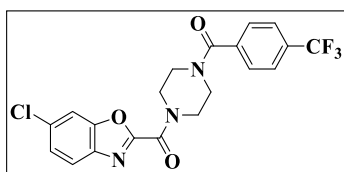
Compound **9g** was prepared from **8g** (0.1 g, 0.71 mmol), HATU (0.406 g, 1.07 mmol) in DMF (2 mL), DIPEA (0.37 mL, 0.276 g, 2.14 mmol) and **7** (0.323 g, 1.07 mmol). Off cream solid (0.250 g, 90% yield). mp: 199-202 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3080 (aromatic-CH), 2920 (aliphatic-CH), 1645 (C=O), 1621 (C=O), 1558 (C=N), 1120 (C-N), 1002 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.02 (s, 1H, Ar-CH), 7.90-7.88 (d, *J* = 8Hz, 1H, Ar-CH), 7.62-7.59 (m, 1H, Ar-CH), 7.55-7.51 (t, *J* = 8Hz, 2H, 2CH₂), 7.31-7.27 (t, *J* = 8Hz, 2H, 2Ar-CH), 4.02 (s, 2H, CH₂), 3.85-3.60 (m, 6H, 3CH₂). ^{13}C NMR (100 MHz, *DMSO-d*₆): 168.89, 164.40, 161.94, 156.52, 155.92, 148.71, 141.28, 132.39, 130.27, 130.18, 127.95, 121.23, 116.02, 115.81, 113.57, 46.78, 42.71. LC-MS (*m/z*): 99%, [*M*]⁺: 388, [*M*+2]⁺: 390. Anal. Calcd. C₁₉H₁₅ClFN₃O₃ (387.80): C, 58.85; H, 3.90; N, 10.84%. Found C, 58.89; H, 3.88; N, 10.86%.

(6-chlorobenzo[d]oxazol-2-yl)(4-(4-nitrobenzoyl)piperazin-1-yl)methanone (9h)



Compound **9h** was prepared from **8h** (0.1 g, 0.59 mmol), HATU (0.338 g, 0.89 mmol) in DMF (2 mL), DIPEA (0.31 mL, 0.231 g, 1.79 mmol) and **7** (0.269 g, 0.89 mmol). Off cream solid (0.220 g, 88% yield). mp: 230-233 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3058 (aromatic-CH), 2957 (aliphatic-CH), 1645 (C=O), 1623 (C=O), 1526 (C=N), 1161 (C-N), 1004 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.32 (s, 1H, Ar-CH), 8.09-8.00 (d, *J* = 8Hz, 1H, Ar-CH), 7.98 (s, 1H, Ar-CH), 7.76-7.74 (d, *J* = 7.6Hz, 2H, 2Ar-CH), 7.63 (s, 1H, Ar-CH), 4.12-4.00 (m, 2H, CH₂), 3.85-3.70 (m, 4H, 2CH₂), 3.43 (s, 2H, CH₂). ^{13}C NMR (100 MHz, *DMSO-d*₆): 167.88, 162.28, 156.46, 155.90, 148.69, 148.40, 142.31, 141.25, 130.17, 128.93, 127.98, 124.28, 121.24, 113.58, 46.86, 42.79. LC-MS (*m/z*): 100%, [*M*]⁺: 415, [*M*+2]⁺: 417. Anal. Calcd. C₁₉H₁₅ClN₄O₅ (414.80): C, 55.02; H, 3.65; N, 13.51%. Found C, 55.06; H, 3.68; N, 13.53%.

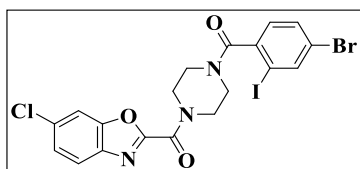
(6-chlorobenzo[d]oxazol-2-yl)(4-(4-(trifluoromethyl)benzoyl)piperazin-1-yl)methanone (9i)



Compound **9i** was prepared from **8i** (0.1 g, 0.52 mmol), HATU (0.300 g, 0.79 mmol) in DMF (2 mL), DIPEA (0.27 mL, 0.204 g, 1.58 mmol) and **7** (0.238 g, 0.79 mmol). Off

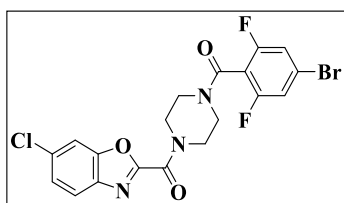
white solid (0.180 g, 78% yield). mp: 167-171 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3015 (aromatic-CH), 2924 (aliphatic-CH), 1643 (C=O), 1617 (C=O), 1558 (C=N), 1121 (C-N), 1002 (C-O). ^1H NMR (400MHz, $\text{DMSO}-d_6$): δ ppm 8.15-7.95 (m, 1H, Ar-CH), 7.94-7.92 (d, $J = 8\text{Hz}$, 1H, Ar-CH), 7.85 (s, 2H, 2Ar-CH), 7.71-7.69 (d, $J = 8\text{Hz}$, 2H, 2Ar-CH), 7.64-7.62 (d, $J = 8\text{Hz}$, 1H, Ar-CH), 4.15-3.95 (m, 2H, CH_2), 3.88-3.65 (m, 4H, 2 CH_2), 3.45 (s, 2H, CH_2). ^{13}C NMR (100 MHz, $\text{DMSO}-d_6$): 168.37, 156.46, 155.88, 148.67, 141.24, 140.12, 130.15, 128.38, 127.96, 126.01, 121.21, 113.59, 46.94, 42.36. LC-MS (m/z): 97%, $[\text{M}]^+$: 438, $[\text{M}+2]^+$: 440. Anal. Calcd. $\text{C}_{20}\text{H}_{15}\text{ClF}_3\text{N}_3\text{O}_3$ (437.80): C, 54.87; H, 3.45; N, 9.60%. Found C, 54.91; H, 3.49; N, 9.64%.

(4-(4-bromo-2-iodobenzoyl)piperazin-1-yl)(6-chlorobenzo[d]oxazol-2-yl)methanone (9j)



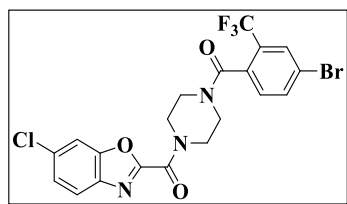
Compound **9j** was prepared from **8j** (0.1 g, 0.30 mmol), HATU (0.174 g, 0.46 mmol) in DMF (2 mL), DIPEA (0.16 mL, 0.119 g, 0.92 mmol), **7** (0.138 g, 0.46 mmol). Off cream solid (0.125 g, 71% yield). mp: 187-191 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3073 (aromatic-CH), 2924 (aliphatic-CH), 1654 (C=O), 1602 (C=O), 1545 (C=N), 1155 (C-N), 1002 (C-O). ^1H NMR (400MHz, $\text{DMSO}-d_6$): δ ppm 8.16-8.01 (m, 2H, 2Ar-CH), 7.96-7.92 (t, $J = 8\text{Hz}$, 1H, Ar-CH), 7.75-7.70 (m, 1H, Ar-CH), 7.66-7.61 (m, 1H, Ar-CH), 7.33-7.29 (m, 1H, Ar-CH), 4.12-4.03 (m, 2H, CH_2), 3.88-3.69 (m, 4H, 2 CH_2), 3.34-3.25 (m, 2H, CH_2). ^{13}C NMR (100 MHz, $\text{DMSO}-d_6$): 168.28, 156.42, 155.90, 148.69, 148.66, 141.48, 141.26, 141.21, 140.87, 140.81, 132.00, 130.17, 129.25, 127.98, 122.90, 121.30, 121.15, 113.59, 95.06, 48.88, 42.37. LC-MS (m/z): 96%, $[\text{M}]^+$: 574, $[\text{M}+2]^+$: 576. Anal. Calcd. $\text{C}_{19}\text{H}_{14}\text{BrClIN}_3\text{O}_3$ (574.60): C, 39.72; H, 2.46; N, 7.31%. Found C, 39.75; H, 2.48; N, 7.34%.

(4-(4-bromo-2,6-difluorobenzoyl)piperazin-1-yl)(6-chlorobenzo[d]oxazol-2-yl)methanone (9k)



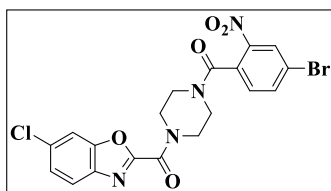
Compound **9k** was prepared from **8k** (0.1 g, 0.42 mmol), HATU (0.239 g, 0.63 mmol) in DMF (2 mL), DIPEA (0.21 mL, 0.162 g, 1.26 mmol) and **7** (0.190 g, 0.63 mmol). Cream solid (0.150 g, 73% yield), mp: 160-164 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3080 (aromatic-CH), 2920 (aliphatic-CH), 1638 (C=O), 1615 (C=O), 1541 (C=N), 1157 (C-N), 1004 (C-O). ^1H NMR (400MHz, $\text{DMSO}-d_6$): δ ppm 8.11-8.02 (m, 1H, Ar-CH), 7.96-7.92 (m, 1H, Ar-CH), 7.72-7.61 (m, 3H, 3Ar-CH), 4.14-4.10 (t, $J = 8\text{Hz}$, 1H, CH), 4.00-3.97 (m, 1H, CH), 3.81-3.76 (m, 3H, CH₂, CH), 3.70-3.67 (m, 1H, CH), 3.50-3.46 (m, 2H, CH₂). ^{13}C NMR (100 MHz, $\text{DMSO}-d_6$): 159.40, 159.31, 158.55, 156.90, 156.81, 155.92, 155.36, 155.29, 148.18, 140.79, 179.72, 127.57, 123.26, 120.85, 120.69, 116.36, 116.11, 113.14, 112.70, 46.24, 41.72. LC-MS (m/z): 94%, $[\text{M}]^+$: 484, $[\text{M}+2]^+$: 486. Anal. Calcd. $\text{C}_{19}\text{H}_{13}\text{BrClF}_2\text{N}_3\text{O}_3$ (484.68): C, 47.08; H, 2.70; N, 8.67%. Found C, 47.10; H, 2.72; N, 8.64%.

(4-(4-bromo-2-(trifluoromethyl)benzoyl)piperazin-1-yl)(6-chlorobenzo[d]oxazol-2-yl)methanone (9l)



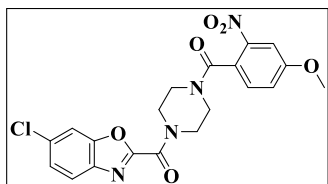
Compound **9l** was prepared from **8l** (0.1 g, 0.37 mmol), HATU (0.209 g, 0.55 mmol) in DMF (2 mL), DIPEA (0.19 mL, 0.142 g, 1.10 mmol) and **7** (0.168 g, 0.55 mmol). Off orange solid (0.160 g, 83% yield). mp: 129-132 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3075 (aromatic-CH), 2920 (aliphatic-CH), 1641 (C=O), 1593 (C=O), 1565 (C=N), 1131 (C-N), 1006 (C-O). ^1H NMR (400MHz, $\text{DMSO}-d_6$): δ ppm 8.11-8.08 (m, 1H, Ar-CH), 8.06-7.99 (m, 2H, 2Ar-CH), 7.96-7.91 (m, 1H, Ar-CH), 7.65-7.58 (m, 1H, Ar-CH), 7.57-7.55 (m, 1H, Ar-CH), 4.09 (m, 1H, CH), 4.00-3.73 (m, 3H, CH₂, CH), 3.72-3.55 (m, 2H, CH₂), 3.30-3.15 (m, 2H, CH₂). ^{13}C NMR (100 MHz, $\text{DMSO}-d_6$): 196.83, 165.96, 156.42, 155.83, 148.68, 141.25, 136.49, 134.04, 130.21, 129.88, 127.98, 124.58, 123.07, 123.00, 121.86, 121.29, 121.12, 113.58, 46.67, 41.98. LC-MS (m/z): 99%, $[\text{M}]^+$: 516, $[\text{M}+2]^+$: 518. Anal. Calcd. $\text{C}_{20}\text{H}_{14}\text{BrClF}_3\text{N}_3\text{O}_3$ (516.70): C, 46.49; H, 2.73; N, 8.13%. Found C, 46.52; H, 2.76; N, 8.17%.

(4-(4-bromo-2-nitrobenzoyl)piperazin-1-yl)(6-chlorobenzo[d]oxazol-2-yl)methanone (9m)



Compound **9m** was prepared from **8m** (0.1 g, 0.40 mmol), HATU (0.209 g, 0.60 mmol) in DMF (2 mL), DIPEA (0.21 mL, 0.157 g, 1.22 mmol) and **7** (0.181 g, 0.60 mmol). Off cream solid (0.190 g, 94% yield). mp: 147-150 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3082 (aromatic-CH), 2924 (aliphatic-CH), 1653 (C=O), 1627 (C=O), 1530 (C=N), 1157 (C-N), 1000 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.45-8.42 (m, 1H, Ar-CH), 8.14-7.99 (m, 2H, 2Ar-CH), 7.96-7.91 (m, 1H, Ar-CH), 7.65-7.58 (m, 2H, 2Ar-CH), 4.12 (s, 1H, CH), 3.96 (s, 1H, CH), 3.87-3.68 (m, 4H, 2CH₂), 3.46-3.44 (m, 2H, CH₂). ^{13}C NMR (100MHz, *DMSO-d*₆): 165.32, 156.46, 155.92, 155.82, 148.66, 146.60, 141.22, 138.16, 131.51, 130.33, 130.17, 128.00, 123.01, 121.30, 121.12, 113.59, 46.80, 42.13. LC-MS (*m/z*): 98%, [*M*]⁺: 493, [*M*+2]⁺: 495. Anal. Calcd. C₁₉H₁₄BrClN₄O₅ (493.70): C, 46.22; H, 2.86; N, 11.35%. Found C, 46.25; H, 2.90; N, 11.38%.

(6-chlorobenzo[d]oxazol-2-yl)(4-(4-methoxy-2-nitrobenzoyl)piperazin-1-yl)methanone (9n)



Compound **9n** was prepared from **8n** (0.1 g, 0.51 mmol), HATU (0.289 g, 0.76 mmol) in DMF (2 mL), DIPEA (0.26 mL, 0.196 g, 1.52 mmol) and **7** (0.230 g, 0.76 mmol). Off cream solid (0.215 g, 95% yield). mp: 197-200 °C. IR (KBr) $\nu_{\text{max}}/\text{cm}^{-1}$: 3089 (aromatic-CH), 2924 (aliphatic-CH), 1660 (C=O), 1630 (C=O), 1565 (C=N), 1142 (C-N), 1000 (C-O). ^1H NMR (400MHz, *DMSO-d*₆): δ ppm 8.11-7.96 (m, 1H, Ar-CH), 7.94-7.91 (m, 2H, 2Ar-CH), 7.96-7.91 (m, 1H, Ar-CH), 7.72-7.69 (m, 1H, Ar-CH), 7.65-7.58 (m, 1H, Ar-CH), 7.55-7.52 (m, 1H, Ar-CH), 7.48-7.42 (m, 1H, Ar-CH), 4.11 (s, 1H, CH), 3.96-3.90 (m, 4H, CH₃, CH), 3.83 (s, 1H, CH), 3.80-3.75 (m, 2H, CH₂), 3.69 (s, 1H, CH), 3.39-3.37 (m, 2H, CH₂). ^{13}C NMR (100 MHz, *DMSO-d*₆): 166.18, 160.38, 156.48, 148.71, 147.26, 141.29, 130.18, 129.76, 127.98, 124.59, 121.30, 121.14, 121.04, 113.58, 110.20, 56.72, 46.82, 42.16. LC-MS (*m/z*): 96%, [*M*]⁺: 445, [*M*+2]⁺:

447. Anal. Calcd. $C_{20}H_{17}ClN_4O_6$ (444.83): C, 54.00; H, 3.85; N, 12.60%. Found C, 53.96; H, 3.87; N, 12.64%.

2.8.2 Protocol of Antimicrobial Activity

Along with strains of two gram-positive (*Bacillus subtilis* and *Staphylococcus aureus*) and two gram-negative (*Pseudomonas aeruginosa* and *Escherichia coli*) bacteria, the antibacterial and antifungal activity was tested against the common fungal pathogens *Aspergillus niger* and *Candida albicans*. The inhibition zone (mm) of nutrient agar with the composition (g/L): Sodium chloride, 5.0; Beef extract, 10.0; Peptone, 10.0 was tested using the antibacterial and antifungal standards Chloramphenicol (30 µg/disc), Gentamicin (10 µg/disc), and Nystatin (10 µg/disc), respectively. The medium was brought to a pH of 7.2 prior to sterilization.¹⁰⁹ The experimental results showed that the investigated chemicals strongly inhibited all bacterial strains, with an inhibition zone ranging from 10 to 36 mm and an inhibition zone ranging from 11 to 30 mm for fungal species. In comparison to reference medications, the synthesized molecule exhibited a greater and more moderate activity. The antibacterial activity of the investigated chemical was assessed using a molecule's 10 µg/disc attentiveness in DMSO.

2.8.3 Protocol of Molecular Docking Study

E. Coli DNA gyrase B (PDB: 4DUH) high-resolution crystal structures were obtained from the PDB database (<https://www.rcsb.org/>). In order to ensure that the docking investigation was unaffected by extraneous entities, the protein receptors were prepared for molecular docking by removing water molecules and associated ligands using Discovery Studio Visualizer (v21.1.0). Empirical force fields were then used to minimize energy and create lower-energy protein conformations.¹¹² Using AutoDock (v4.2) virtual screening software, molecular docking analysis was performed, treating the chemicals as ligand molecules and the 4DUH protein as the macromolecules. For 4DUH, a cubic grid box measuring $72.77 \times 47.35 \times 62.99$ was constructed. Eight separate docking runs were performed on each compound, and conformations were grouped according to an RMSD of less than 2.0 \AA .¹¹³ The lowest free binding energy (in kcal/mol) was used to determine each compound's optional binding configuration. Discovery Studio Visualizer (v21.1.0) was used to evaluate molecular interactions and offer comprehensive information about the binding profiles.

2.8.4 Protocol of Molecular Dynamic Simulation

Using Desmond software from Schrodinger LLC, a 100-nanosecond MDS was carried out.¹¹⁴ Protein-ligand docking was performed before starting MDS to ascertain how the molecule would stay positioned inside the protein's active site. By simulating atomic motions over time using Newton's classical equations of motion, MDS offers comprehensive insights into the dynamics of ligand-binding in a physiological setting.¹¹⁵ Using Maestro's Protein Preparation Wizard, the ligand-receptor complex was pre-processed, encompassing energy minimization, optimization, and, if necessary, resolving any missing residues. The System Builder tool was then used to prepare the system. The models were relaxed before the simulation was conducted, and trajectories were captured for in-depth examination at 100 ps intervals.

2.8.5 Protocol of ADMET Study

The Swiss Institute of Bioinformatics (SIB) developed SwissADME, a free web application that forecasts small compounds' Absorption, Distribution, Metabolism, and Excretion (ADME) characteristics. It is frequently employed to evaluate pharmacokinetics and other drug-like properties.¹¹⁴

2.9 Conclusion

Using ¹H NMR, ¹³C NMR, LC-MS, and IR spectrum analysis, a new series of hybrid molecules comprising benzoxazole derivatives with substituted piperazine moieties was created and examined. The bactericidal qualities of each produced molecule were assessed. Excellent antibacterial activity against both gram-positive and gram-negative infections was demonstrated by the majority of the recently produced drugs. Compounds **9f** and **9b**, which had the highest docking scores of -7.8 kcal/mol and -7.7 kcal/mol, respectively, showed the most promising findings in antibacterial activity among the synthesized compounds. With a docking score of -7.5 kcal/mol, compounds **9c**, **9i**, and **9n** demonstrated modest antibacterial activity. Furthermore, compound **9f**'s antibacterial efficacy may be due to its inhibition of *E. coli* DNA gyrase, according to molecular docking and molecular dynamics simulations. With the exception of compounds **9k** and **9l**, which had molecular weights more than 500, all produced compounds adhered to Lipinski's rule of five. Interestingly, the lipophilicity ratings of

all benzoxazole derivatives ranged from 1.94 to 4.31. Using SwissADME, the computational analysis was carried out.

2.10 Representative spectral data

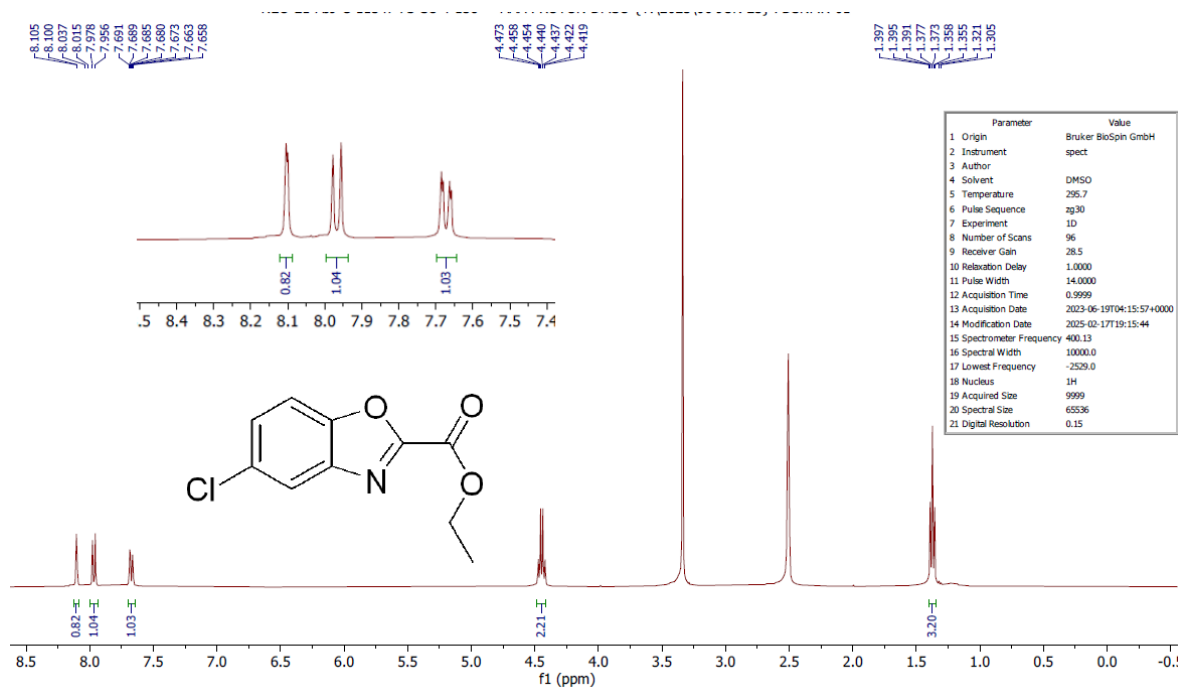
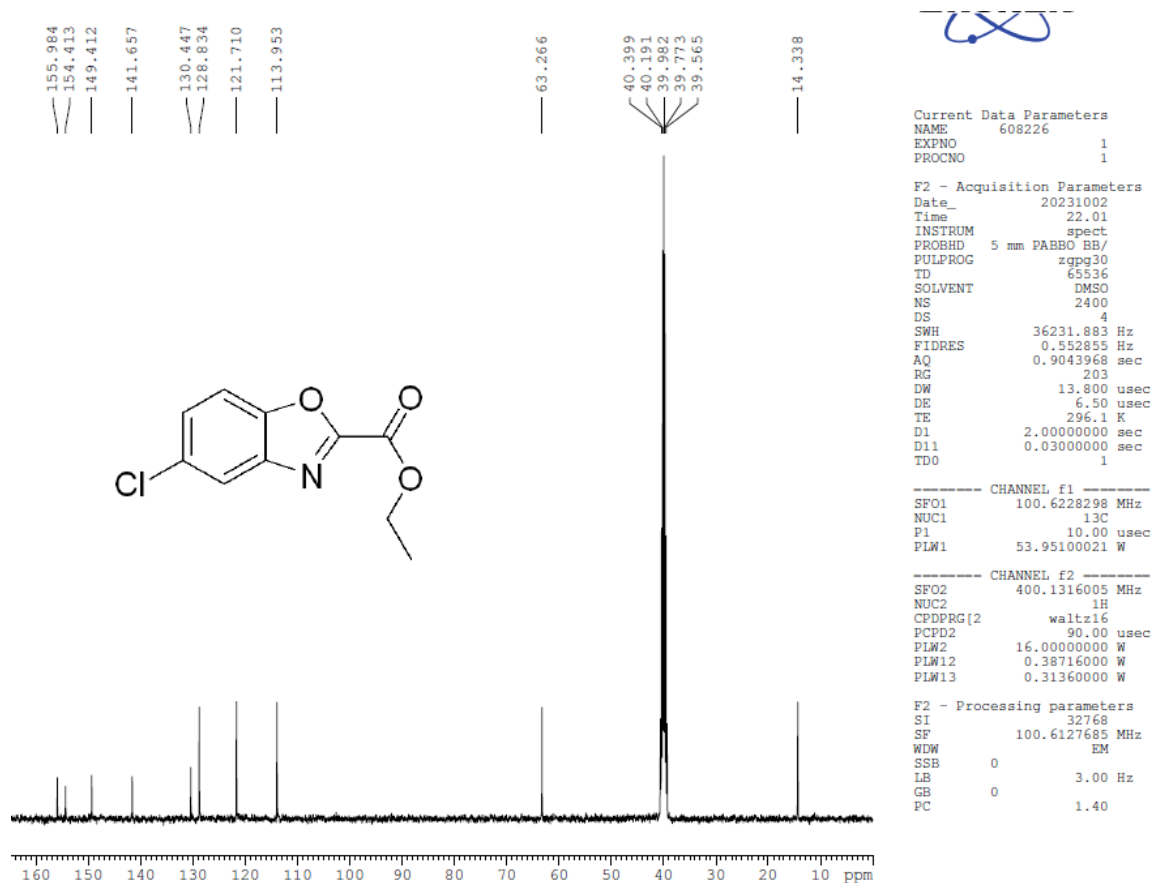
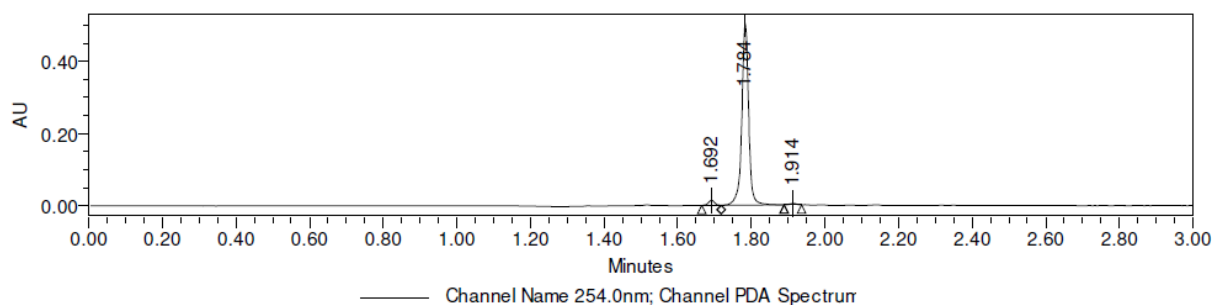
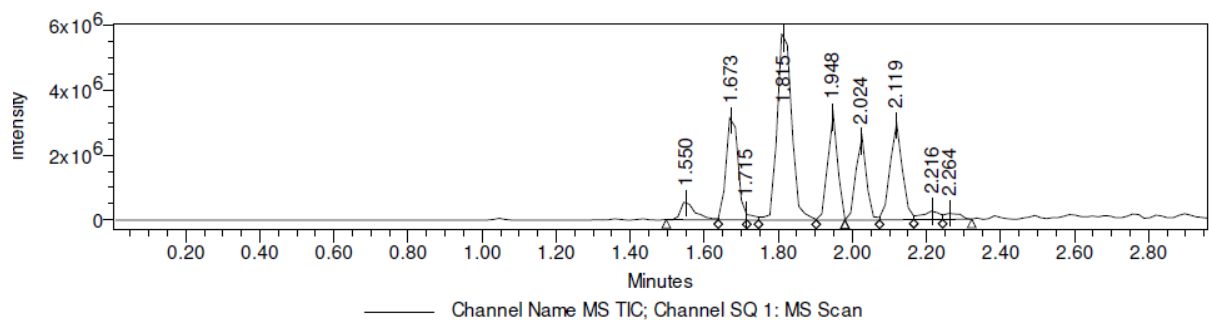


Figure 19: ¹H NMR of compound 4.



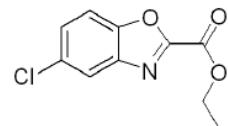
Sample Name:		
Sample Type:	Unknown	Acquired By: LCMS_03
Vial:	2:A,7	Sample Set Name: 17062023_UCH_177
Injection #:	1	Acq. Method Set: PDS_METHOD_C
Injection Volume:	1.00 ul	Processing Method: PDS_METHOD_C_03,
Run Time:	3.0 Minutes	Channel Name: 220.0nm, MS TIC, 254.0nm
Project Name	LCMS-03_JUN-2023_17062023	Proc. Chnl. Descr.: SQ 3: MS Scan MS TIC, PDA
Date Acquired:	17-06-2023 20:32:43 IST	
Date Processed:	17-06-2023 21:00:28 IST, 17-06-2023 21:00:42 IST, 17-06-2023 21:01:20 IST, 17-06-2023	





Channel: PDA Spectrum

	Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV*sec)	% Area	Channel	Channel Name
1	1.530		6952	18860	2.92	PDA Spectrum	220.0nm
2	1.638		9813	20665	3.20	PDA Spectrum	220.0nm
3	1.692		13492	15268	2.27	PDA Spectrum	254.0nm
4	1.693		14839	23365	3.62	PDA Spectrum	220.0nm
5	1.784		388989	527273	81.66	PDA Spectrum	220.0nm
6	1.784		504167	653443	97.09	PDA Spectrum	254.0nm
7	1.823		9194	21778	3.37	PDA Spectrum	220.0nm
8	1.914		3951	4344	0.65	PDA Spectrum	254.0nm
9	1.915		12386	20095	3.11	PDA Spectrum	220.0nm
10	1.940		6006	7228	1.12	PDA Spectrum	220.0nm
11	1.987		4411	6456	1.00	PDA Spectrum	220.0nm



Chemical Formula: $C_{10}H_8ClNO_3$
Molecular Weight: 225.63

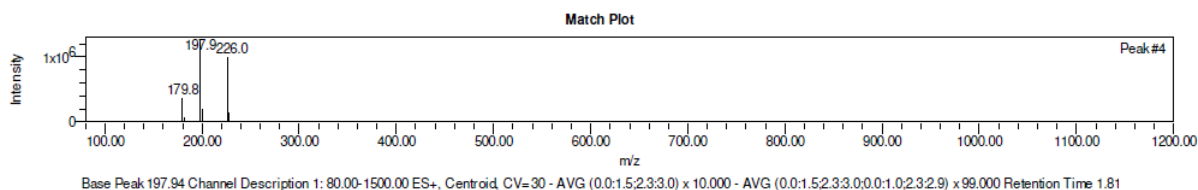


Figure 21: LC-MS of compound 4.

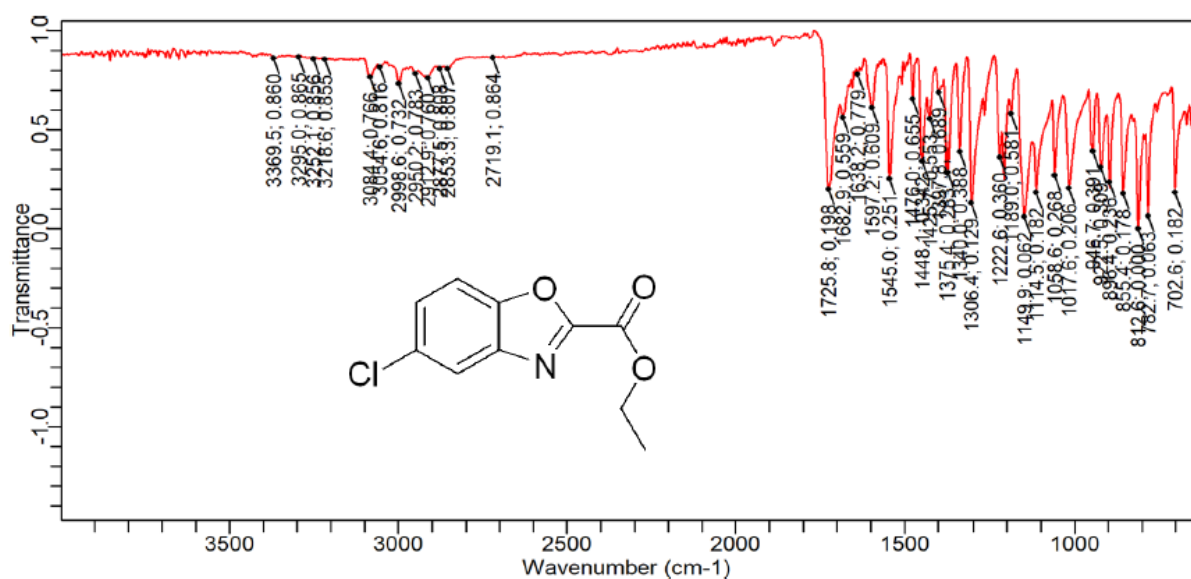


Figure 22: IR of compound 4.

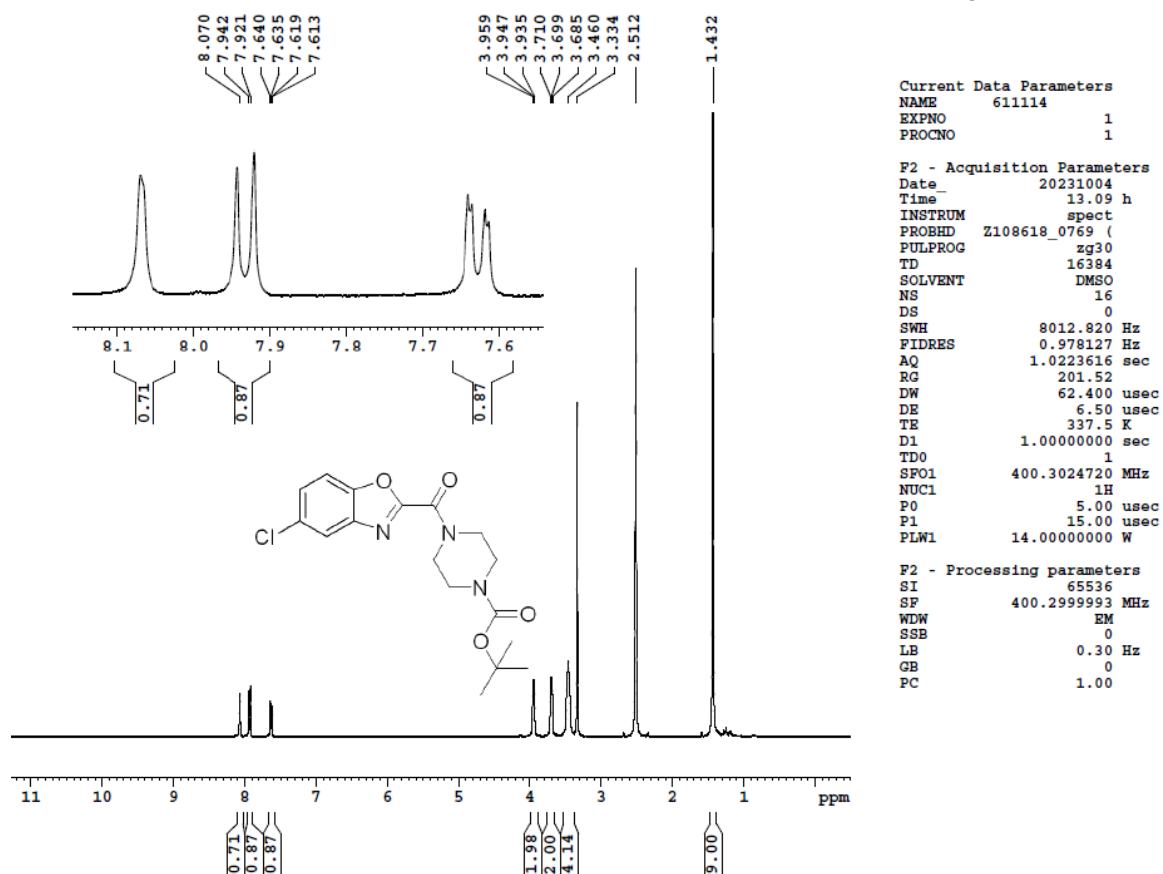


Figure 23: ^1H NMR of compound 6.

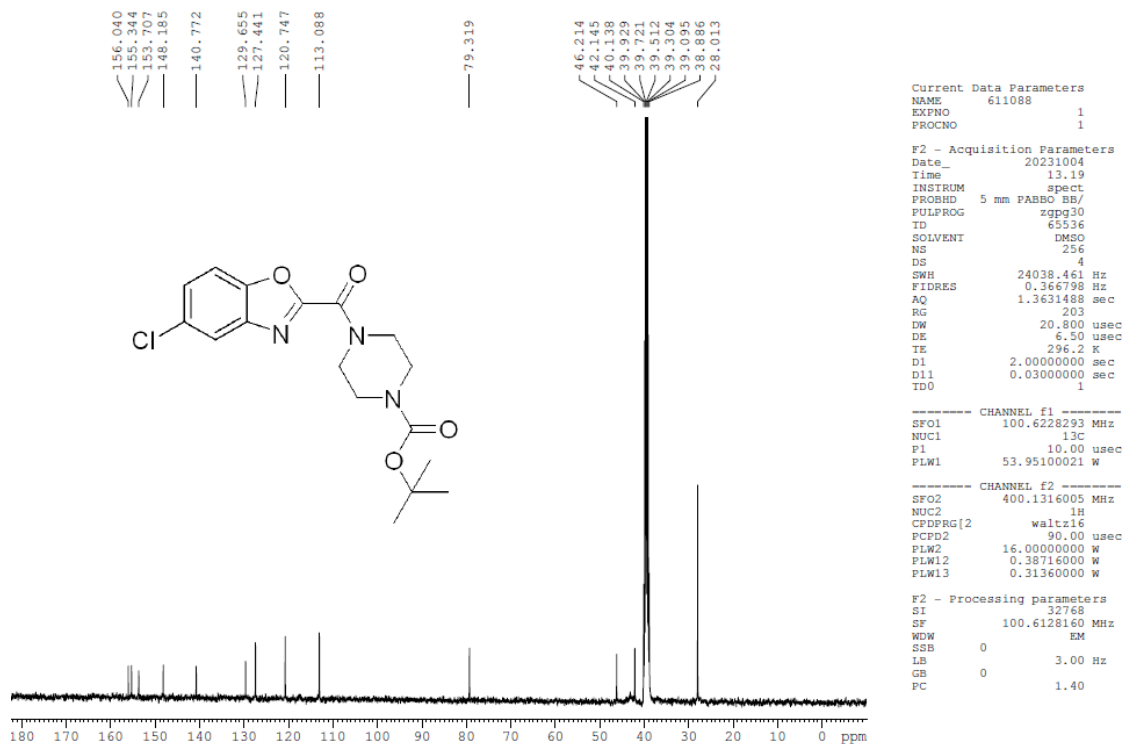
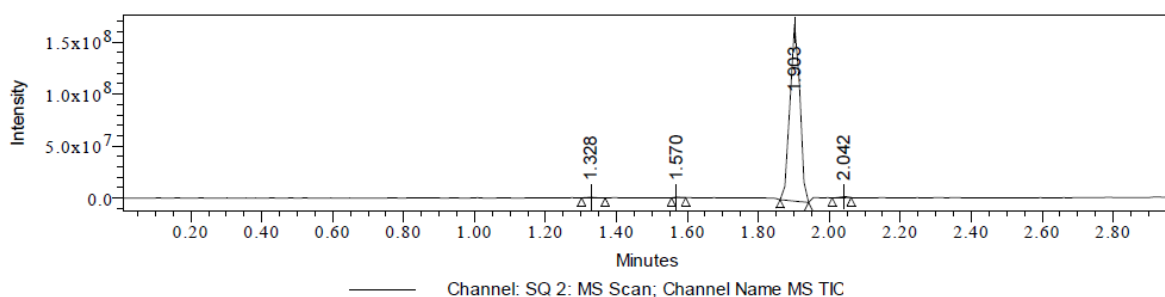
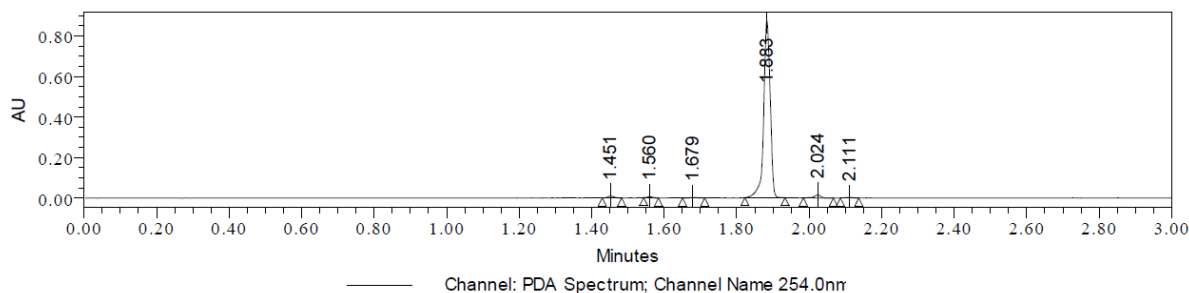


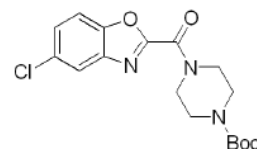
Figure 24: ^{13}C NMR of compound 6.

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Vial: 1:A,3
Injection #: 1
Injection Volume: 1.00 ul
Run Time: 3.0 Minutes
Project Name LCMS-02_JUNE-2023_25062023
Date Acquired: 25-06-2023 12:52:24 IST
Date Processed: 25-06-2023 13:31:16 IST, 25-06-2023 13:31:25 IST, 25-06-2023 13:31:41 IST, 25-06-2023
Acquired By: LCMS-02
Sample Set Name: 25062023_UCH 128_1ST
Acq. Method Set: METHOD C3
Processing Method: LCMS METHOD J2_02,
Channel Name: 230.0nm, MS TIC, 254.0nm,
Proc. Chnl. Descr.: PDA 290.0 nm Blank Subtracted



Channel: PDA Spectrum

	Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV*sec)	% Area	Channel	Channel Name
1	1.346		6008	6137	0.67	PDA Spectrum	230.0nm
2	1.451		9389	8850	0.96	PDA Spectrum	230.0nm
3	1.451		8310	9756	0.86	PDA Spectrum	254.0nm
4	1.452		5159	5344	0.59	PDA Spectrum	290.0nm
5	1.560		5115	5759	0.51	PDA Spectrum	254.0nm
6	1.560		8803	16314	1.77	PDA Spectrum	230.0nm
7	1.621		4750	5424	0.59	PDA Spectrum	230.0nm
8	1.679		1834	2175	0.19	PDA Spectrum	254.0nm
9	1.883		704495	889086	98.69	PDA Spectrum	290.0nm
10	1.883		677011	856952	93.15	PDA Spectrum	230.0nm
11	1.883		873020	1093607	96.62	PDA Spectrum	254.0nm
12	2.022		6529	6492	0.72	PDA Spectrum	290.0nm
13	2.024		14671	17313	1.53	PDA Spectrum	254.0nm
14	2.025		21690	26307	2.86	PDA Spectrum	230.0nm
15	2.111		2316	3280	0.29	PDA Spectrum	254.0nm



Chemical Formula: $C_{17}H_{20}ClN_3O_4$
Molecular Weight: 365.81

M-56 mass observed

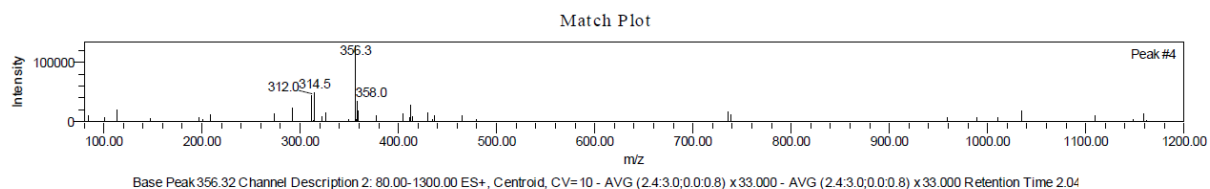


Figure 25: LC-MS of compound 6.

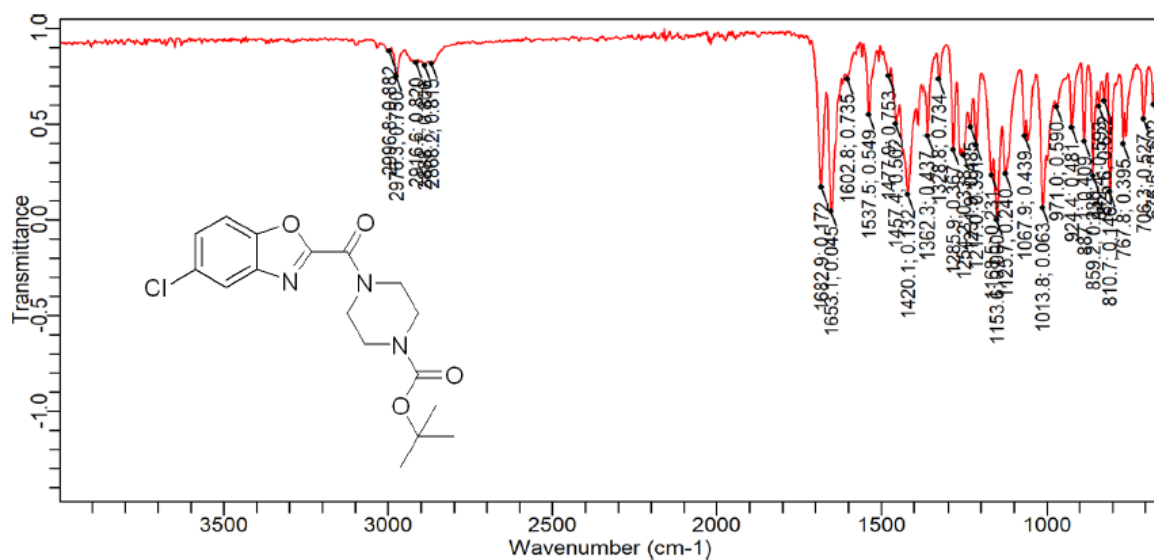


Figure 26: IR of compound 6.

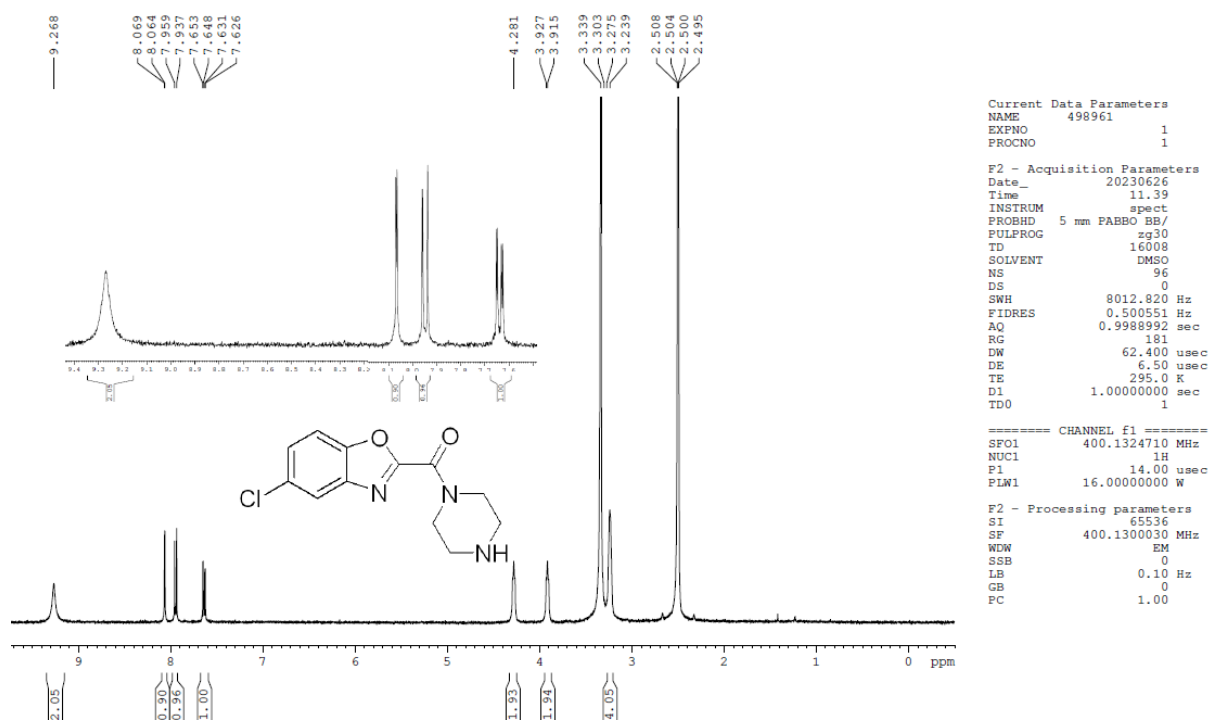


Figure 27: ¹H NMR of compound 7.

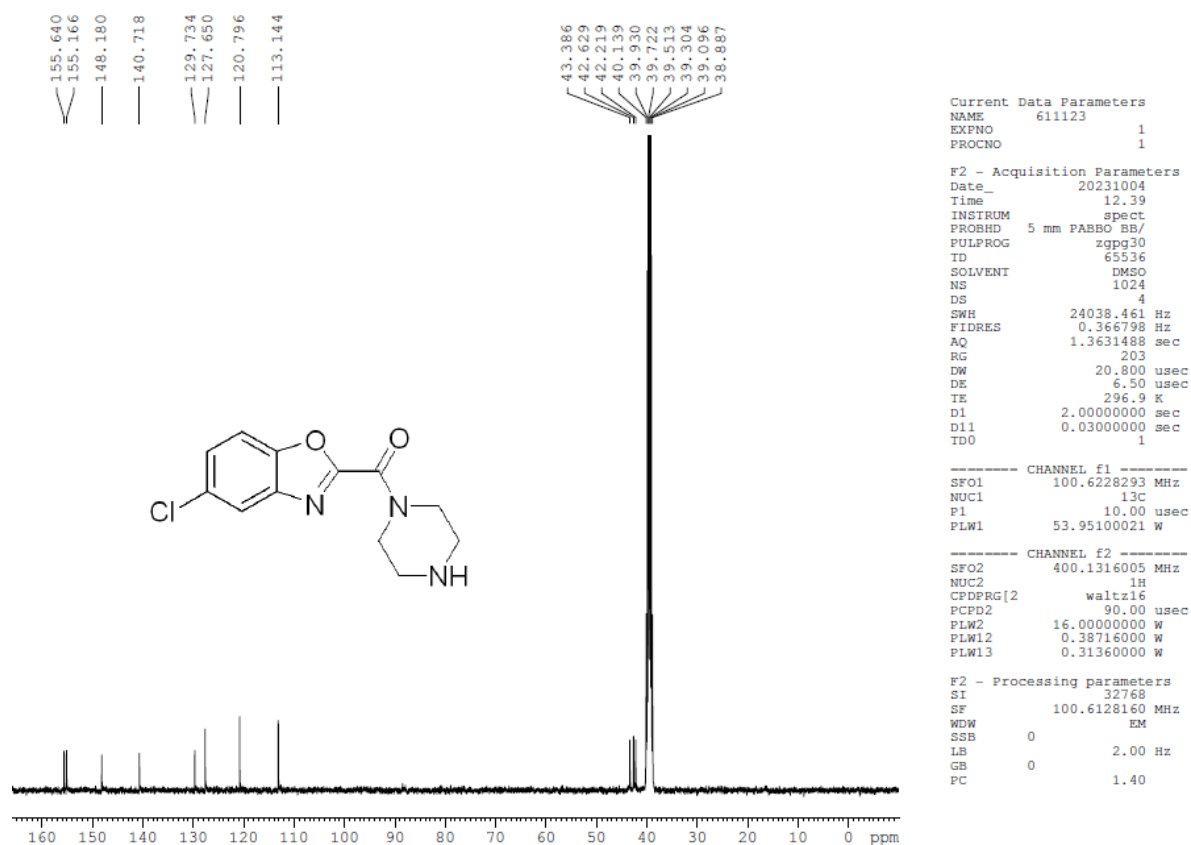
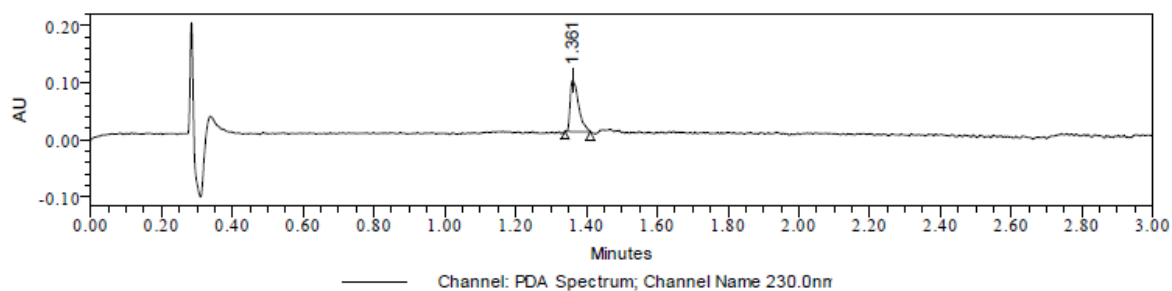


Figure 28: ^{13}C NMR of compound 7.

Sample Name:	Amine intermediate	Acquired By:	LCMS-02
Sample Type:	Unknown	Sample Set Name:	30062023 UCH 183 2nd
Vial:	2:D,7	Acq. Method Set:	METHOD C3
Injection #:	1	Processing Method:	METHOD_C3, METHOD_C3_02
Injection Volume:	0.70 ul	Channel Name:	230.0nm, MS TIC, 290.0nm
Run Time:	3.0 Minutes	Proc. Chnl. Descr.:	PDA 290.0 nm Blank Subtracted
Project Name	LCMS-02_JUNE-2023_30062023		
Date Acquired:	30-06-2023 21:26:11 IST		
Date Processed:	01-07-2023 01:33:21 IST, 01-07-2023 01:33:29 IST, 01-07-2023 01:33:40 IST		



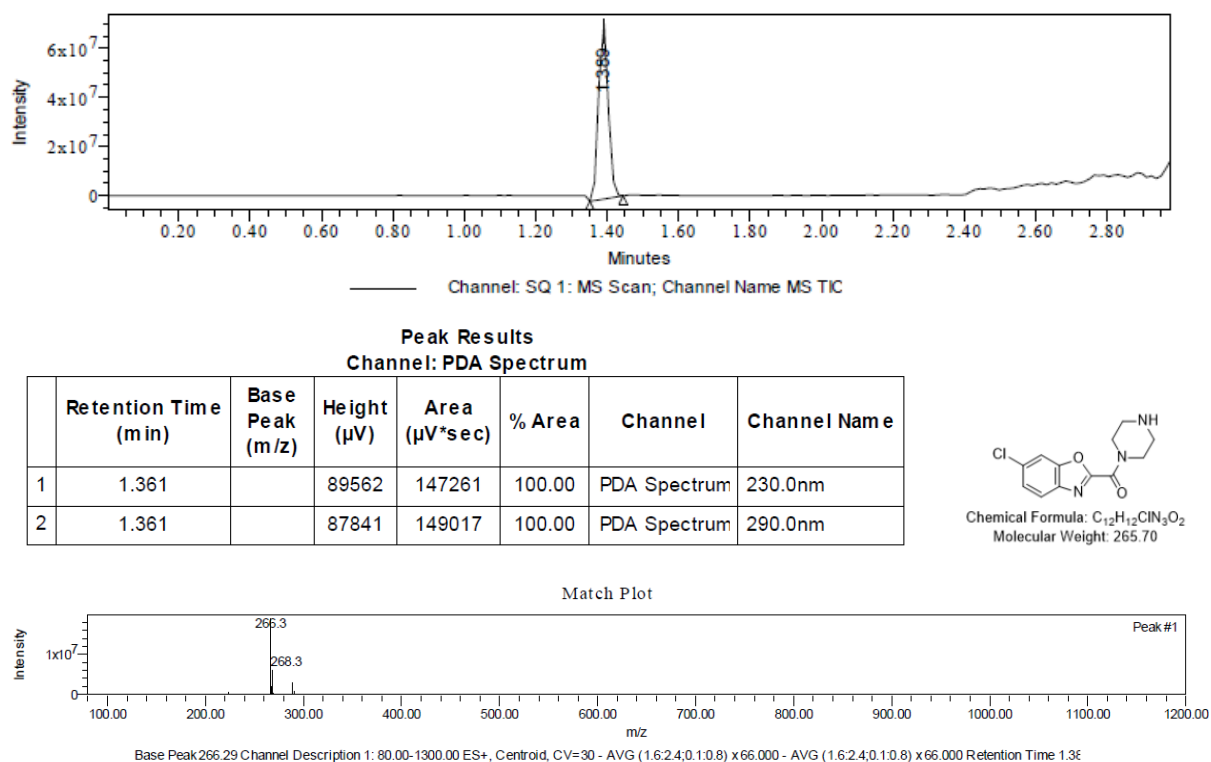


Figure 29: LC-MS of compound 7.

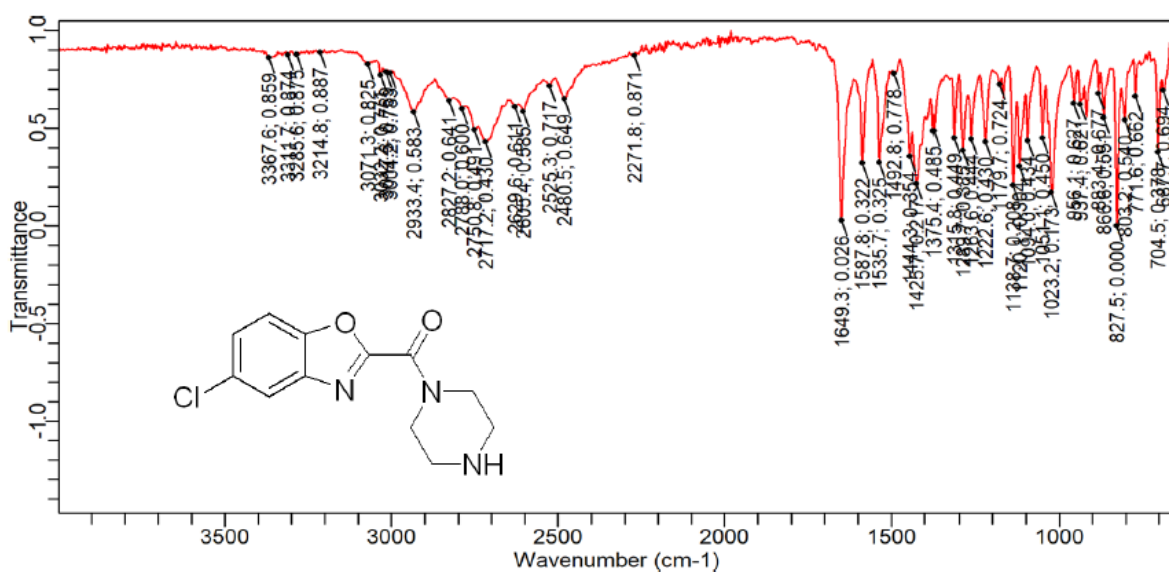


Figure 30: IR of compound 7.

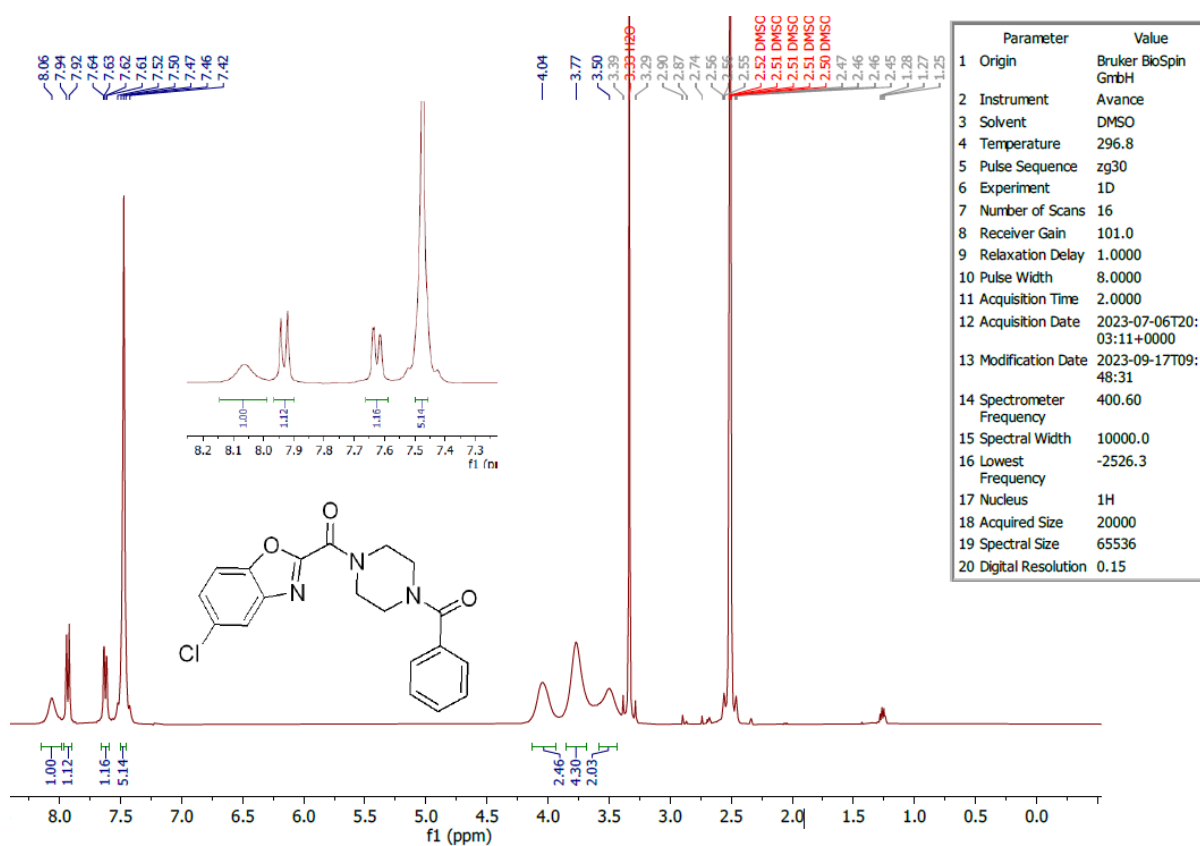


Figure 31: ¹H NMR of compound 9a.

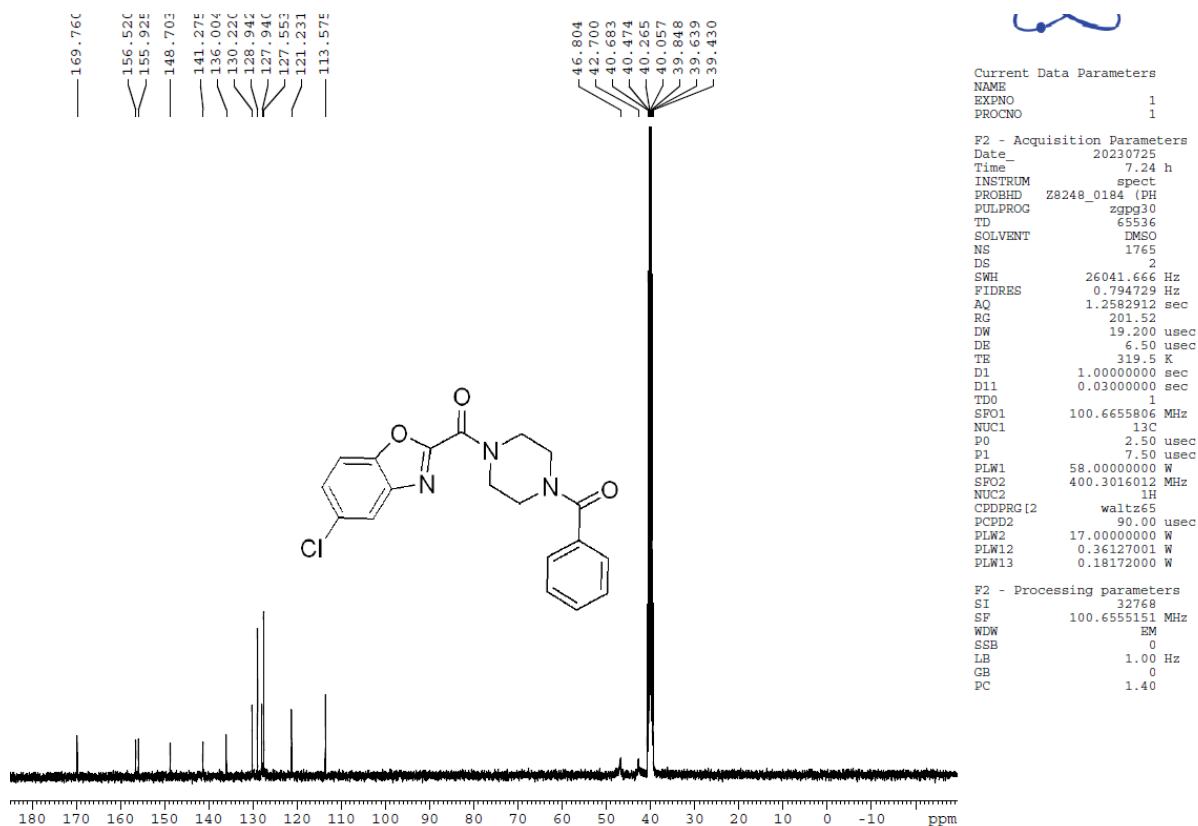
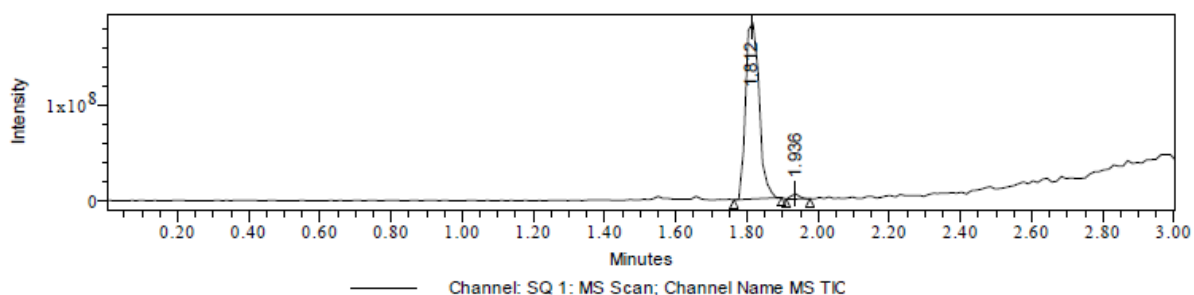
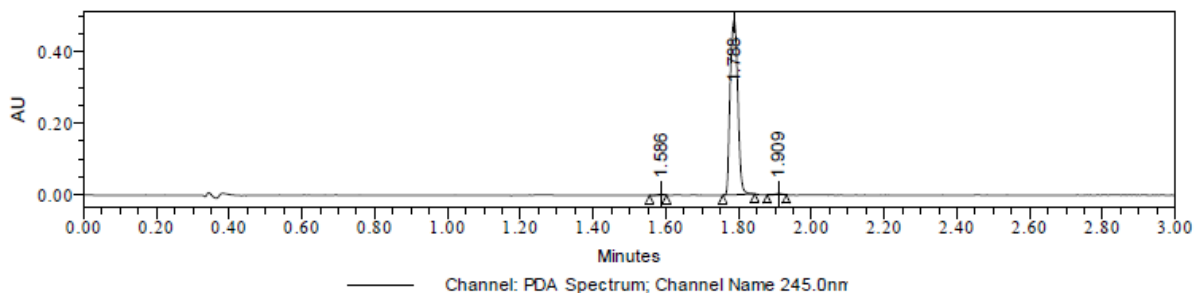


Figure 32: ¹³C NMR of compound 9a.

Sample Name:	Compound-9a	Acquired By:	LCMS-02
Sample Type:	Unknown	Sample Set Name:	040722023 UCH 183 3RD
Vial:	1:C,6	Acq. Method Set:	METHOD C3
Injection #:	1	Processing Method:	METHOD_C3_01, METHOD_C3
Injection Volume:	0.70 ul	Channel Name:	245.0nm, MS TIC
Run Time:	3.0 Minutes	Proc. Chnl. Descr.:	PDA 245.0 nm Blank Subtracted
Project Name	LCMS-02_JULY-2023_04072023		
Date Acquired:	04-07-2023 23:18:02 IST		
Date Processed:	05-07-2023 01:01:09 IST, 05-07-2023 01:01:35 IST		



Peak Results
Channel: PDA Spectrum

	Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV*sec)	% Area	Channel	Channel Name
1	1.586		2358	2805	0.39	PDA Spectrum	245.0nm
2	1.788		486026	707344	98.97	PDA Spectrum	245.0nm
3	1.909		3335	4579	0.64	PDA Spectrum	245.0nm

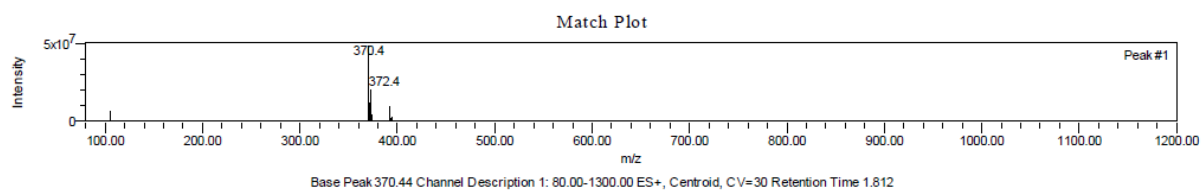
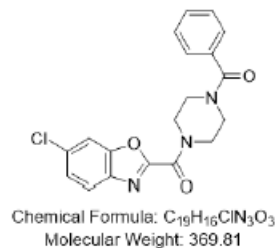


Figure 33: LC-MS of compound 9a.

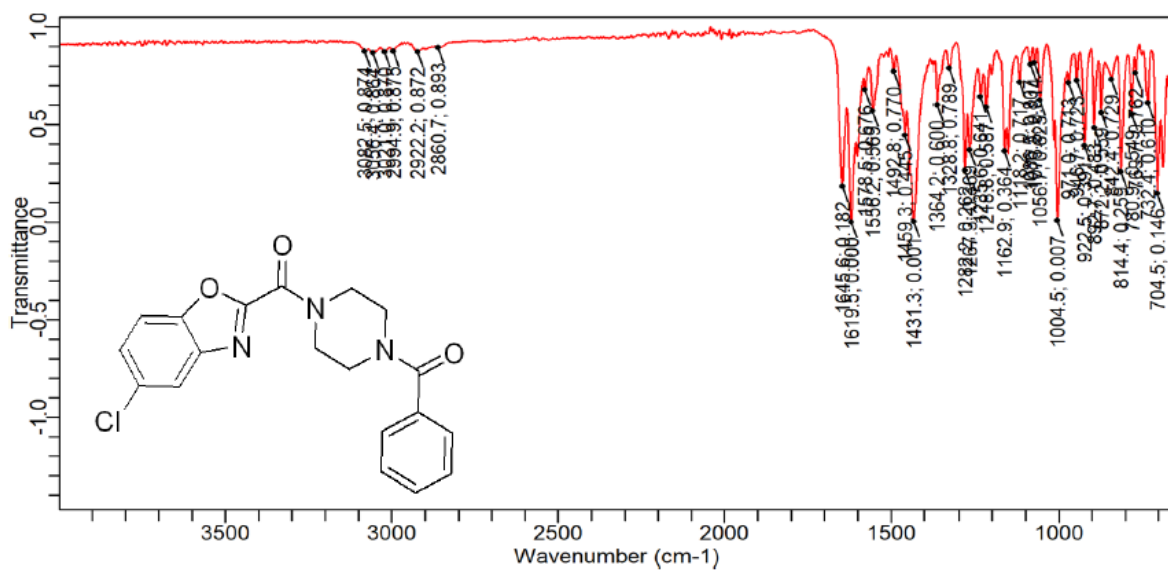


Figure 34: IR of compound 9a.

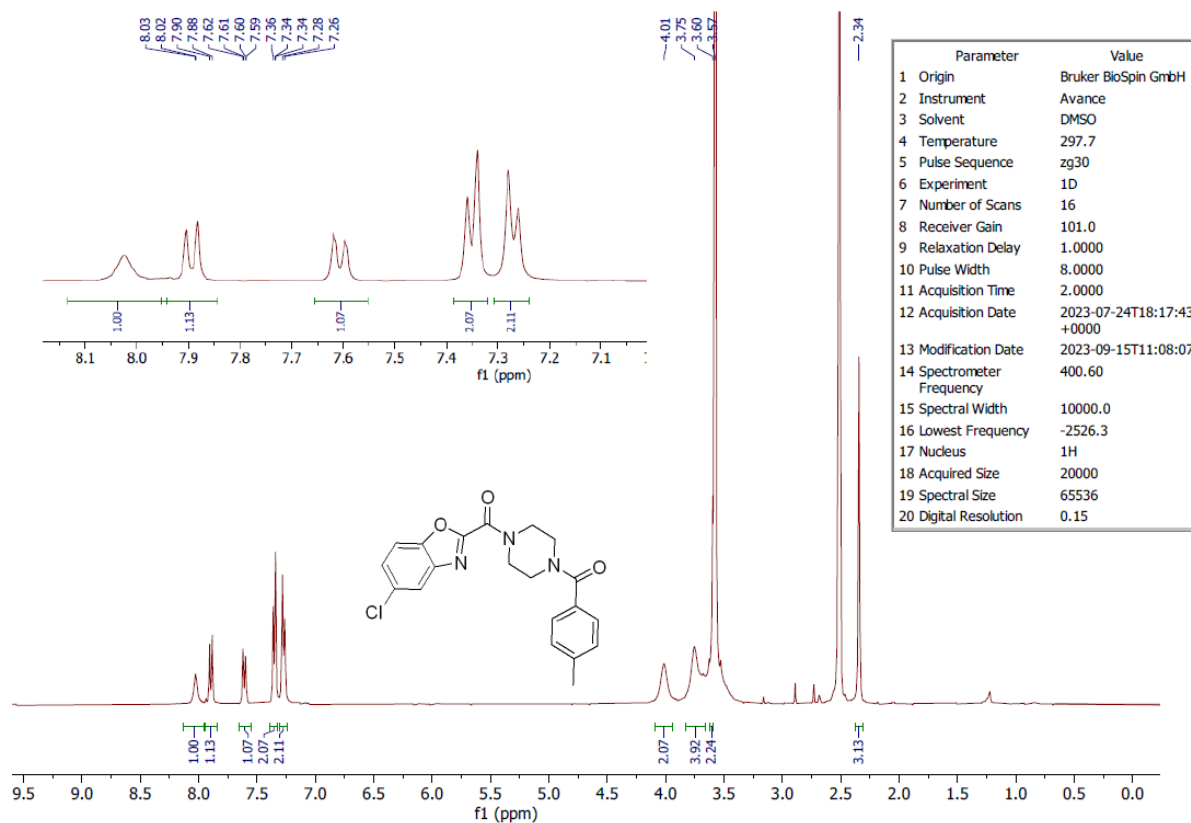


Figure 35: ¹H NMR of compound 9b.

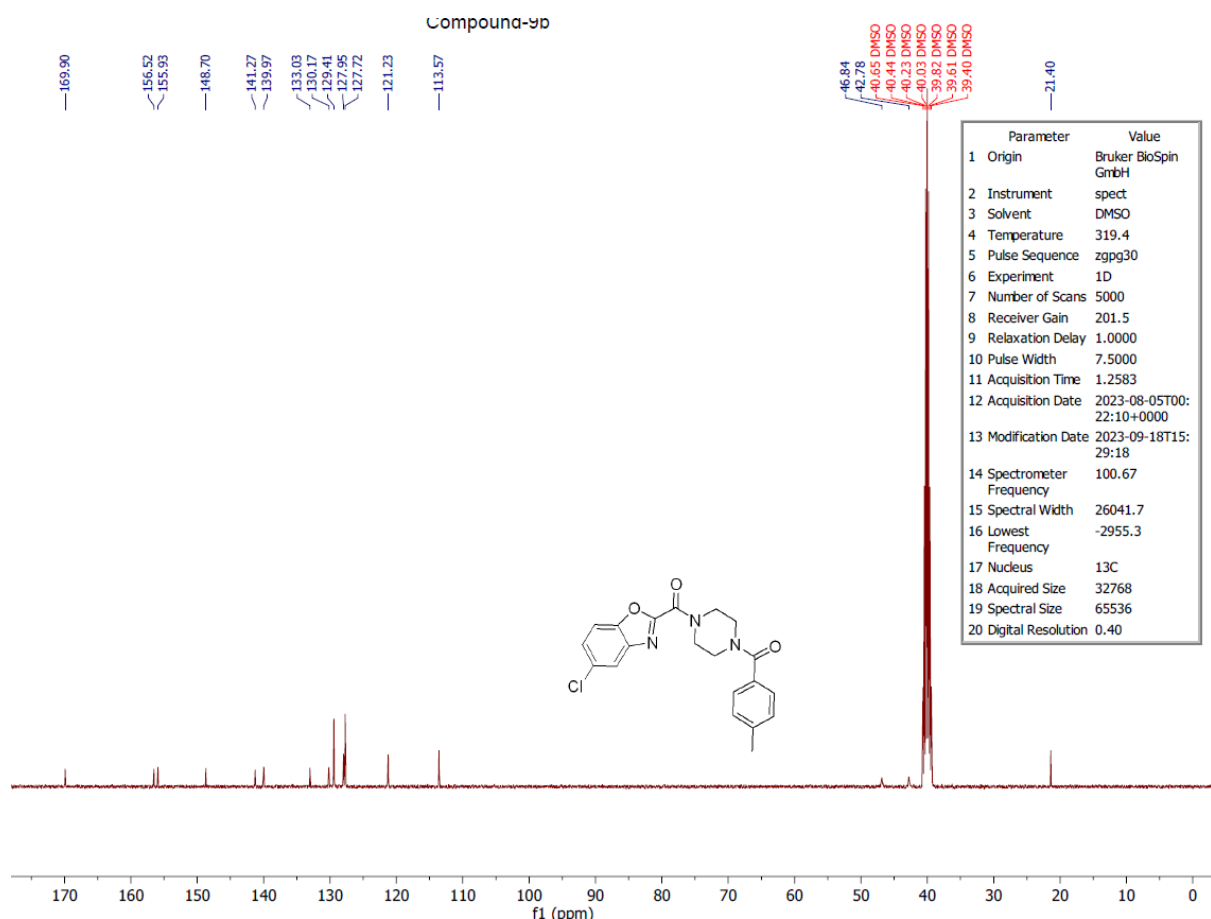
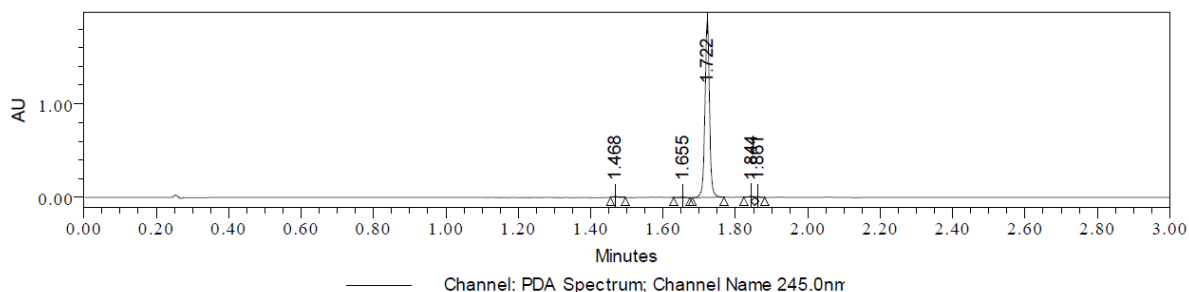
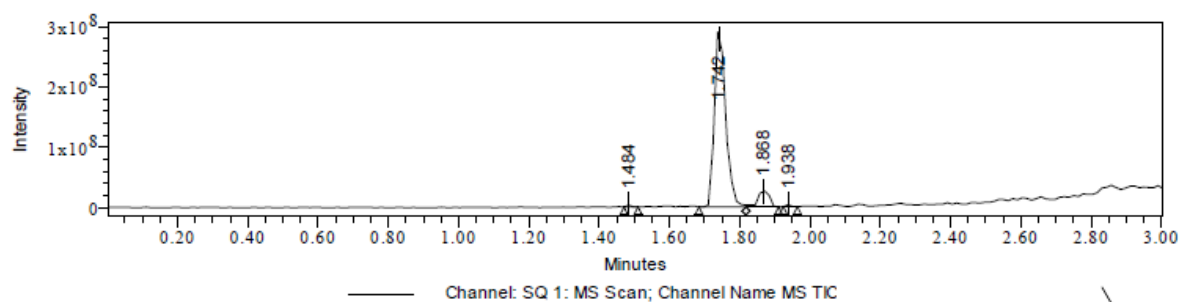


Figure 36: ^{13}C NMR of compound 9b.

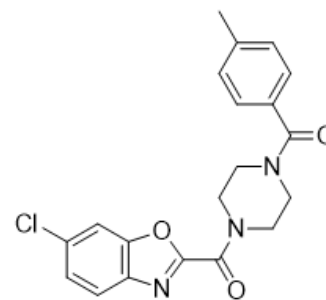
Sample Name:	Compound-9b	Acquired By:	LCMS-02
Sample Type:	Unknown	Sample Set Name:	11072023_UCH 183_NIGHT
Vial:	1:B,5	Acq. Method Set:	METHOD C3
Injection #:	1	Processing Method:	METHOD_C3 01, METHOD_C3
Injection Volume:	1.00 ul	Channel Name:	245.0nm, MS TIC, 210.0nm
Run Time:	3.0 Minutes	Proc. Chnl. Descr.:	PDA 245.0 nm Blank Subtracted
Project Name	LCMS-02_JULY-2023_11072023		
Date Acquired:	12-07-2023 00:01:57 IST		
Date Processed:	12-07-2023 03:13:37 IST, 12-07-2023 03:13:48 IST, 12-07-2023 03:14:05 IST		





Peak Results
Channel: PDA Spectrum

	Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV'sec)	% Area	Channel	Channel Name
1	1.468		10817	9200	0.54	PDA Spectrum	245.0nm
2	1.655		6773	7349	0.44	PDA Spectrum	245.0nm
3	1.721		819922	1126859	100.00	PDA Spectrum	210.0nm
4	1.722		1886890	1653346	97.94	PDA Spectrum	245.0nm
5	1.844		11524	10227	0.61	PDA Spectrum	245.0nm
6	1.861		9218	8038	0.48	PDA Spectrum	245.0nm



Chemical Formula: $C_{20}H_{18}ClN_3O_3$
Molecular Weight: 383.83

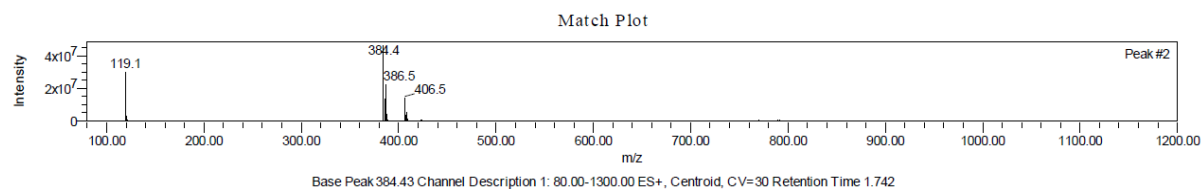


Figure 37: LC-MS of compound 9b.

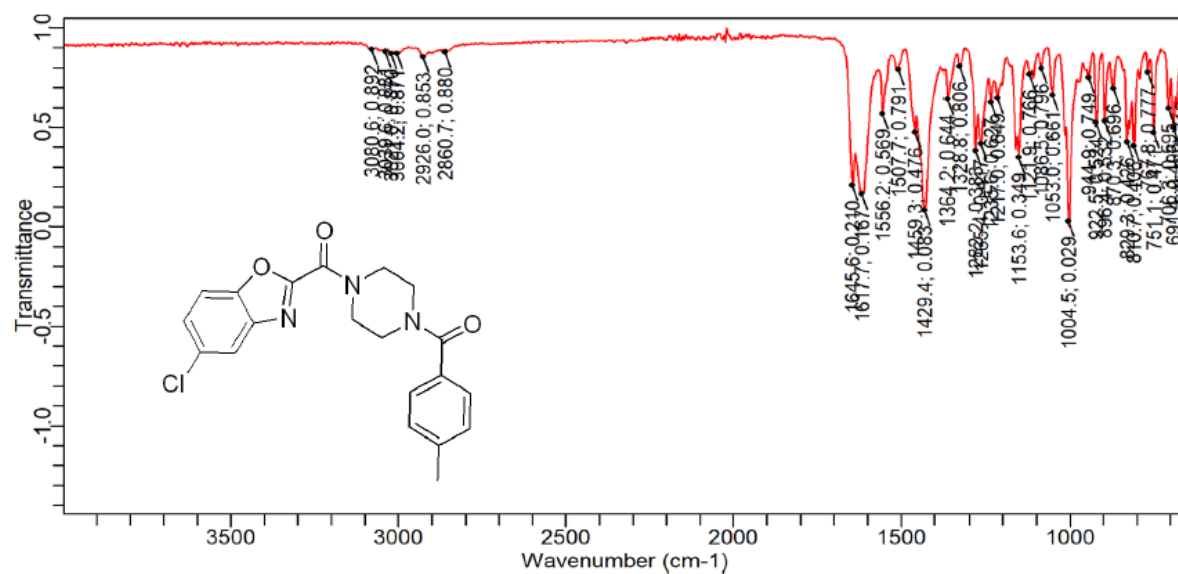


Figure 38: IR of compound 9b.

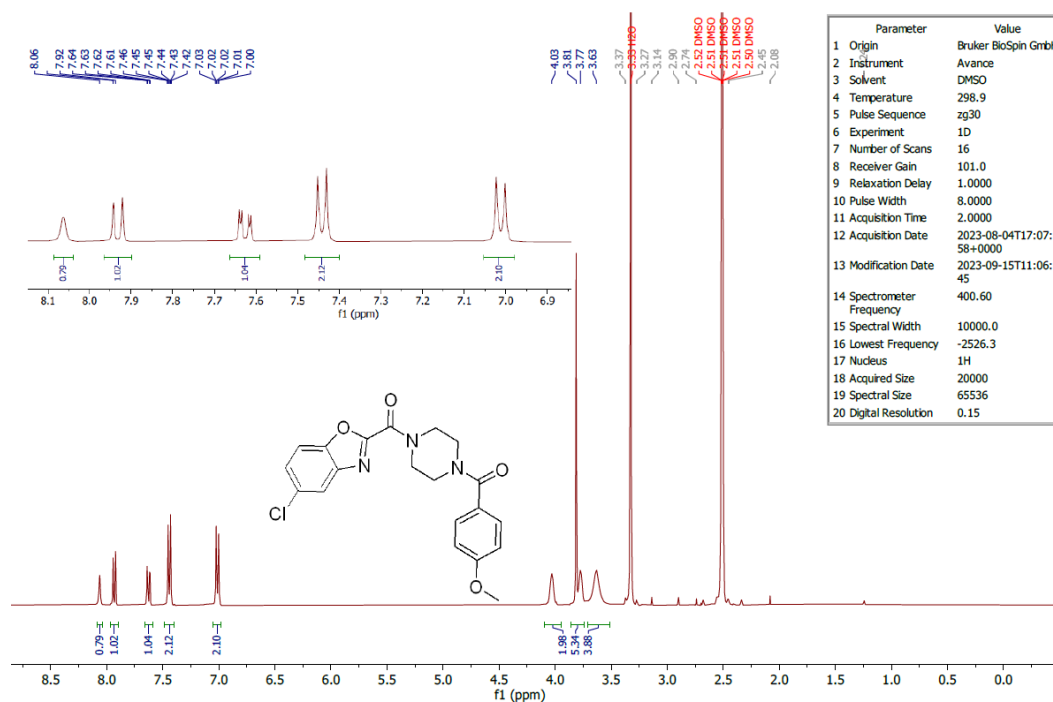


Figure 39: ¹H NMR of compound 9c.

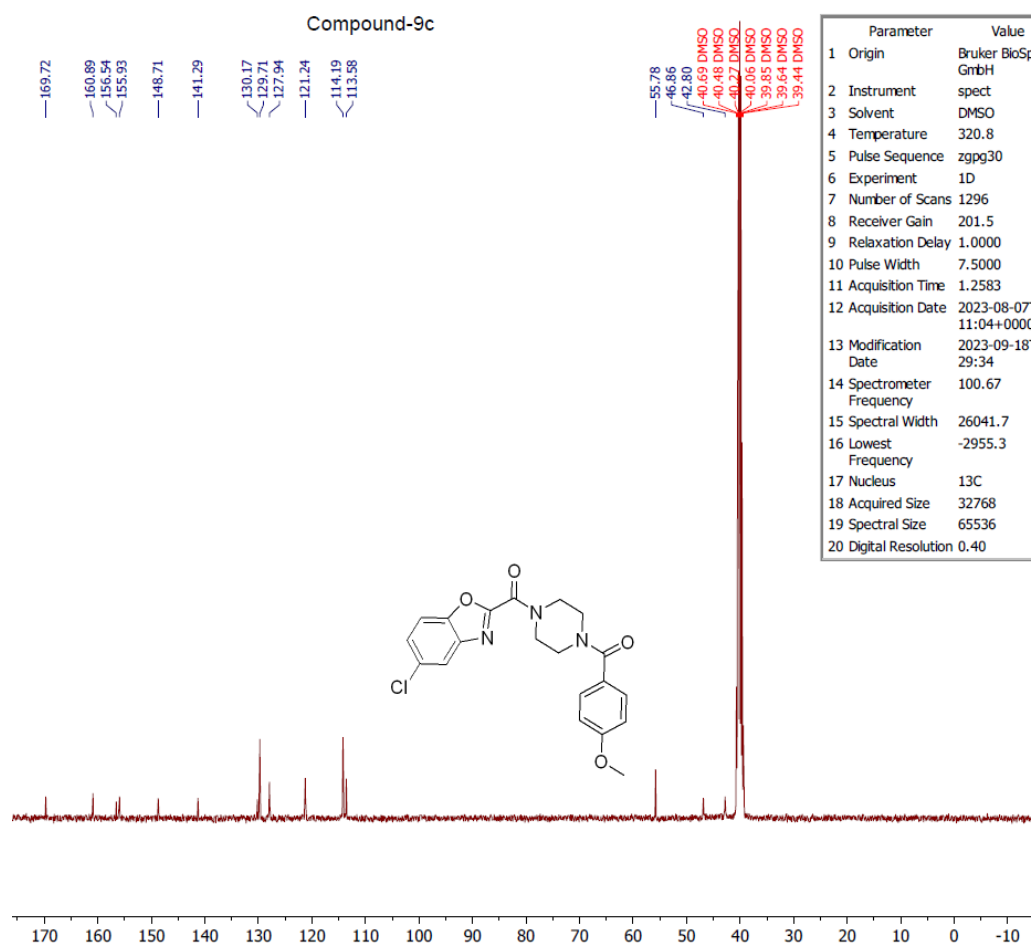
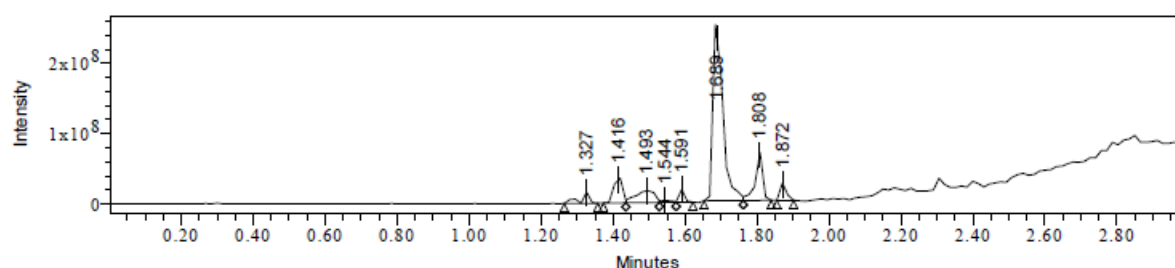
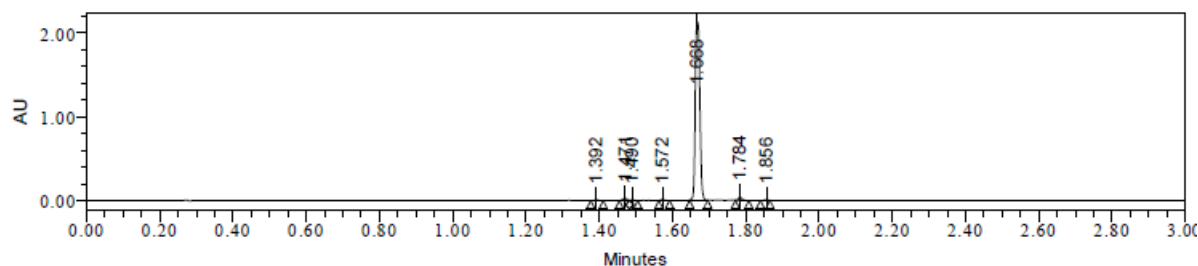


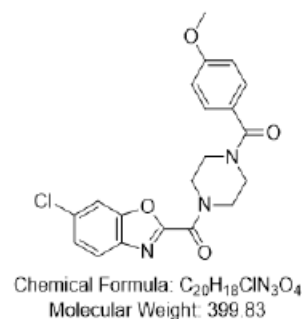
Figure 40: ¹³C NMR of compound 9c.

Sample Name: Compound-9c
Sample Type: Unknown
Vial: 1:C,5
Injection #: 1
Injection Volume: 1.00 ul
Run Time: 3.0 Minutes
Project Name LCMS-02_MAR-2024_04032023
Date Acquired: 04-03-2024 10:30:55 IST
Date Processed: 04-03-2024 10:56:55 IST, 04-03-2024 10:57:07 IST, 04-03-2024 10:57:18 IST
Acquired By: LCMS-02
Sample Set Name: 04032024 uch 210 1st
Acq. Method Set: METHOD_C3
Processing Method: METHOD_C3 01, METHOD_C3
Channel Name: MS TIC, 250.0nm
Proc. Chnl. Descr.: SQ 3: MS Scan MS TIC, PDA



Peak Results
Channel: PDA Spectrum

	Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV*sec)	% Area	Channel	Channel Name
1	1.392		10944	5866	0.31	PDA Spectrum	250.0nm
2	1.471		28495	21448	1.13	PDA Spectrum	250.0nm
3	1.490		8445	5171	0.27	PDA Spectrum	250.0nm
4	1.572		11190	6491	0.34	PDA Spectrum	250.0nm
5	1.668		2128571	1831501	96.34	PDA Spectrum	250.0nm
6	1.784		38474	25494	1.34	PDA Spectrum	250.0nm
7	1.856		8262	5056	0.27	PDA Spectrum	250.0nm



Match Plot

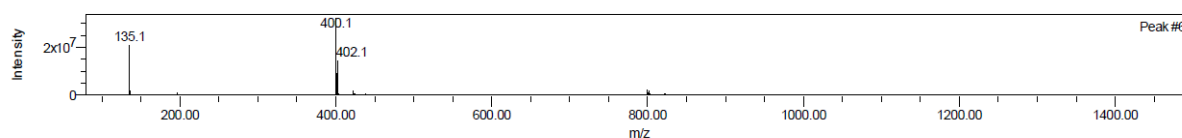


Figure 41: LC-MS of compound 9c.

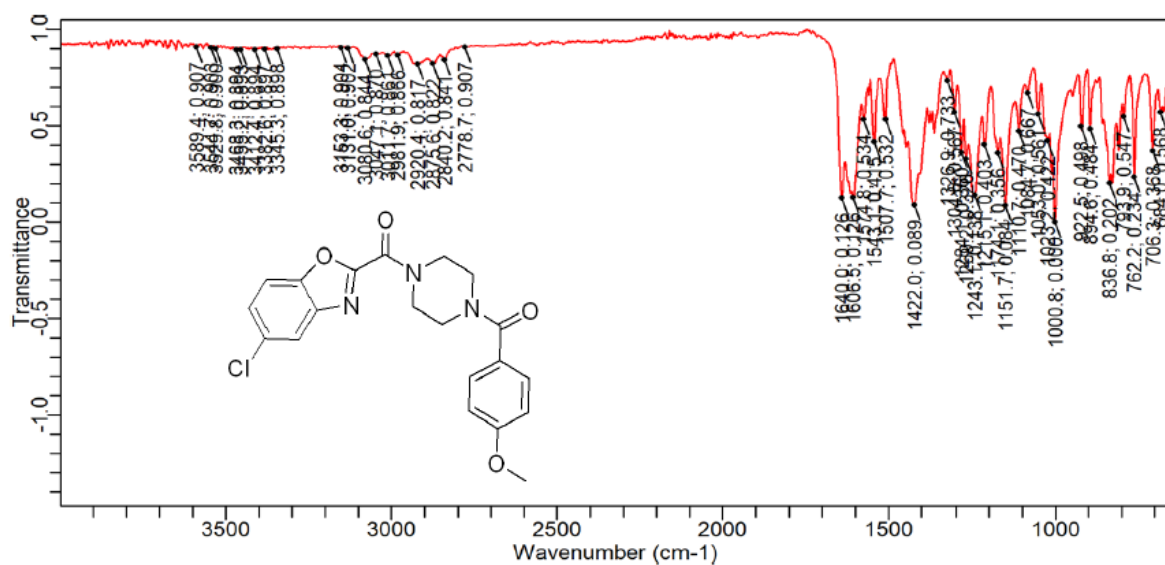


Figure 42: IR of compound 9c.

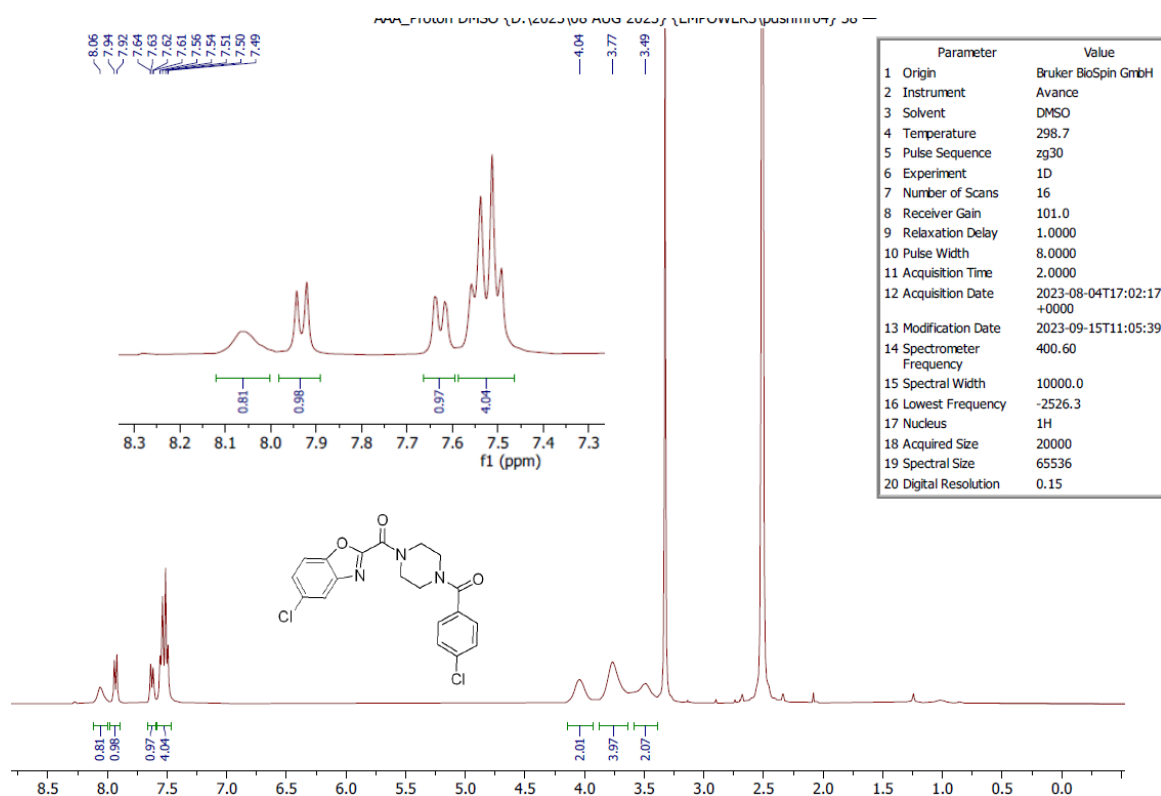


Figure 43: ¹H NMR of compound 9e.

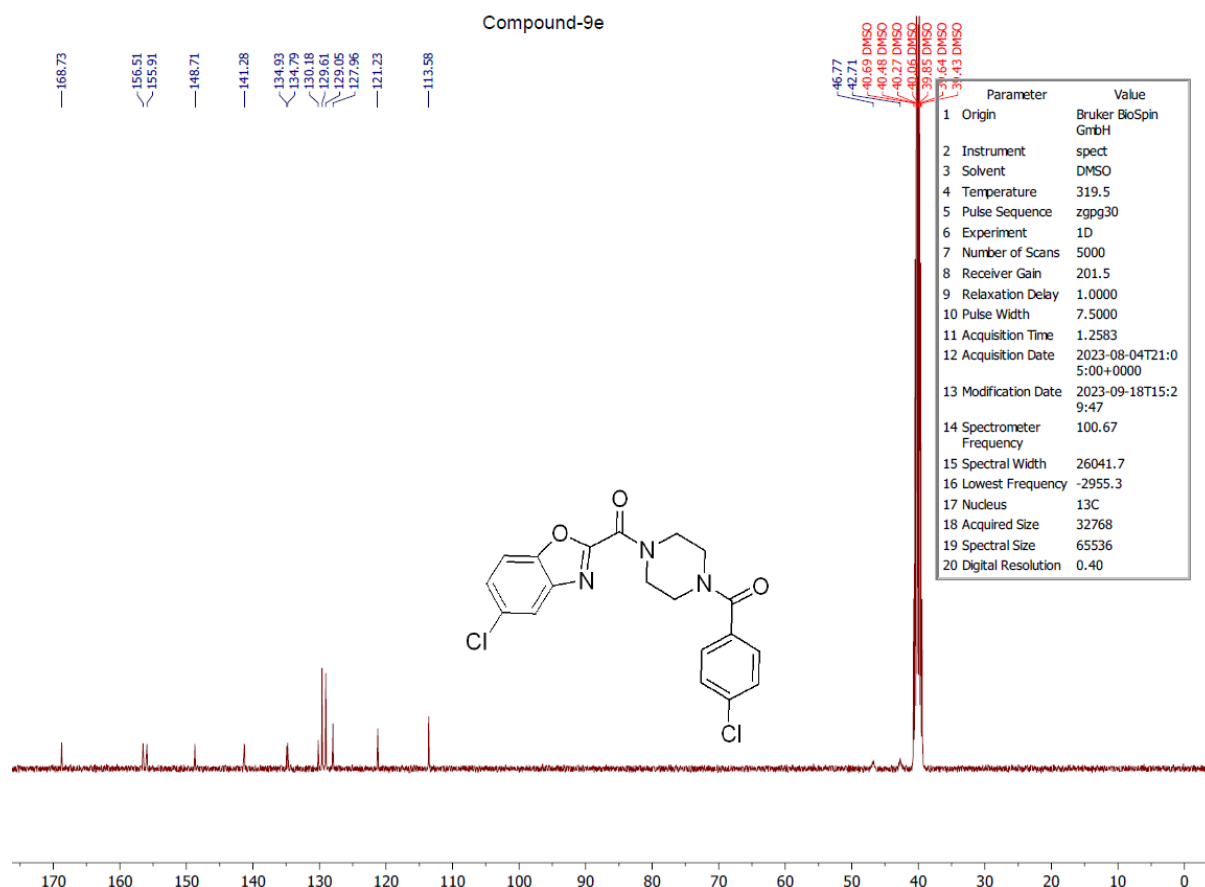
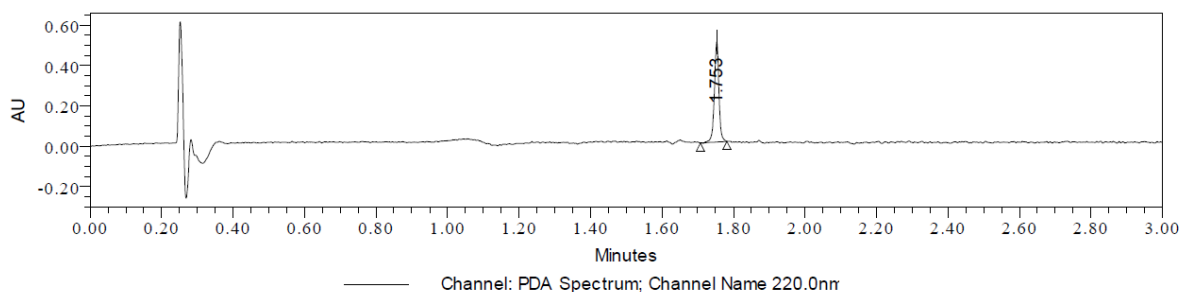
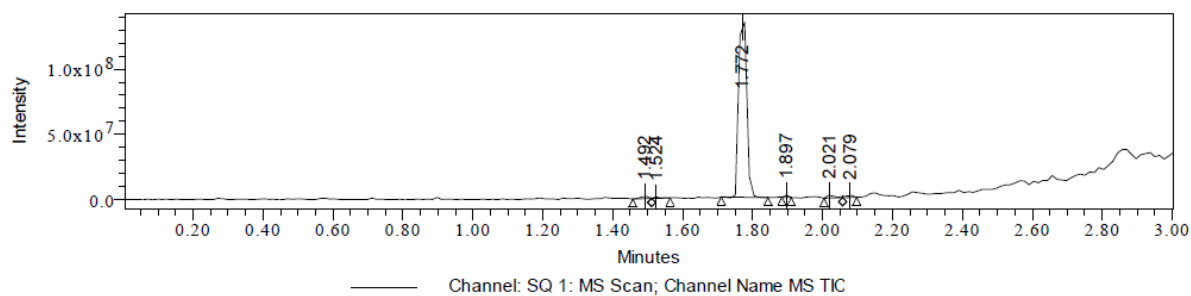


Figure 44: ¹³C NMR of compound 9e.

Sample Name:	Compound-9e	Acquired By:	LCMS-02
Sample Type:	Unknown	Sample Set Name:	11072023_UCH 183_NIGHT
Vial:	1:B,4	Acq. Method Set:	METHOD_C3
Injection #:	1	Processing Method:	METHOD_C3 01, METHOD_C3
Injection Volume:	1.00 ul	Channel Name:	220.0nm, MS TIC, 265.0nm
Run Time:	3.0 Minutes	Proc. Chnl. Descr.:	PDA 265.0 nm Blank Subtracted
Project Name	LCMS-02_JULY-2023_11072023		
Date Acquired:	11-07-2023 23:57:53 IST		
Date Processed:	12-07-2023 03:06:41 IST, 12-07-2023 03:07:02 IST, 12-07-2023 03:07:18 IST		





Peak Results
Channel: PDA Spectrum

	Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV·sec)	% Area	Channel	Channel Name
1	1.469		2183	1874	0.64	PDA Spectrum	265.0nm
2	1.652		2150	2324	0.80	PDA Spectrum	265.0nm
3	1.753		331369	283289	97.44	PDA Spectrum	265.0nm
4	1.753		496740	441578	100.00	PDA Spectrum	220.0nm
5	1.876		2866	2624	0.90	PDA Spectrum	265.0nm
6	1.902		997	618	0.21	PDA Spectrum	265.0nm

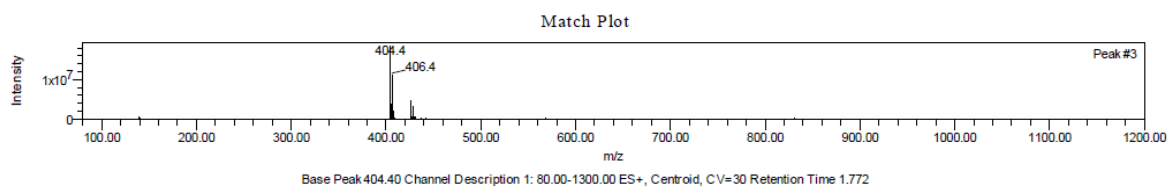
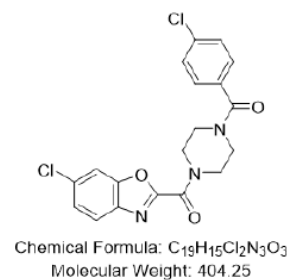


Figure 45: LC-MS of compound 9e.

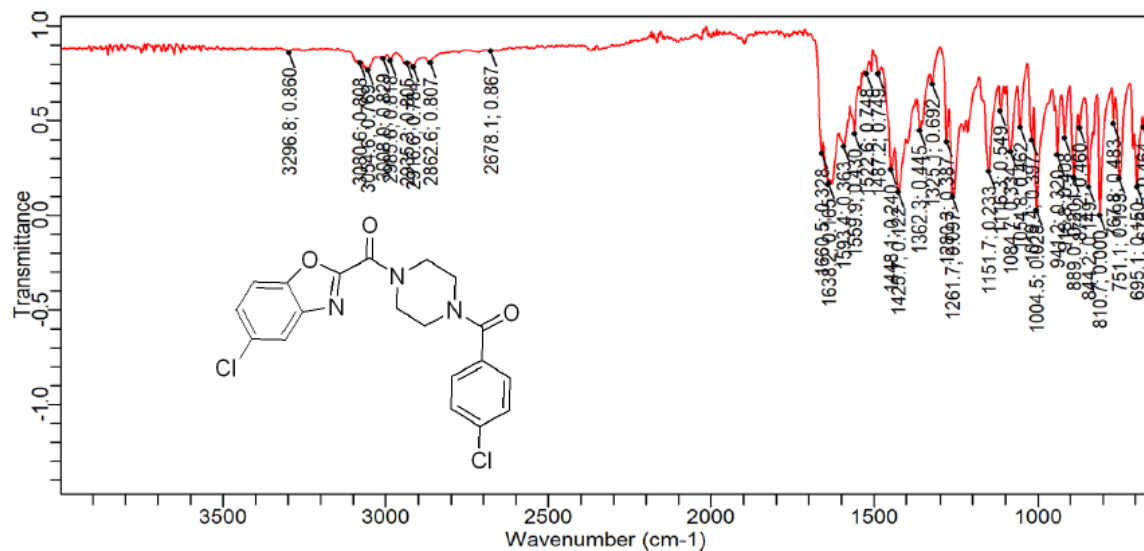


Figure 46: IR of compound 9e.

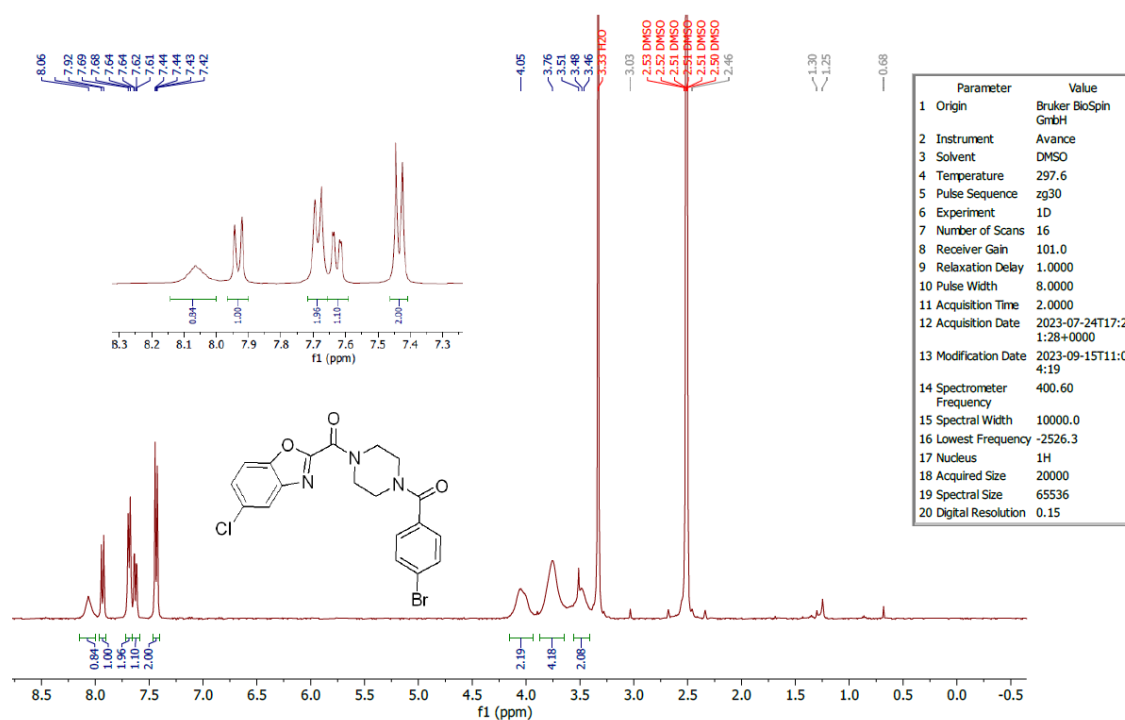


Figure 47: ¹H NMR of compound 9f.

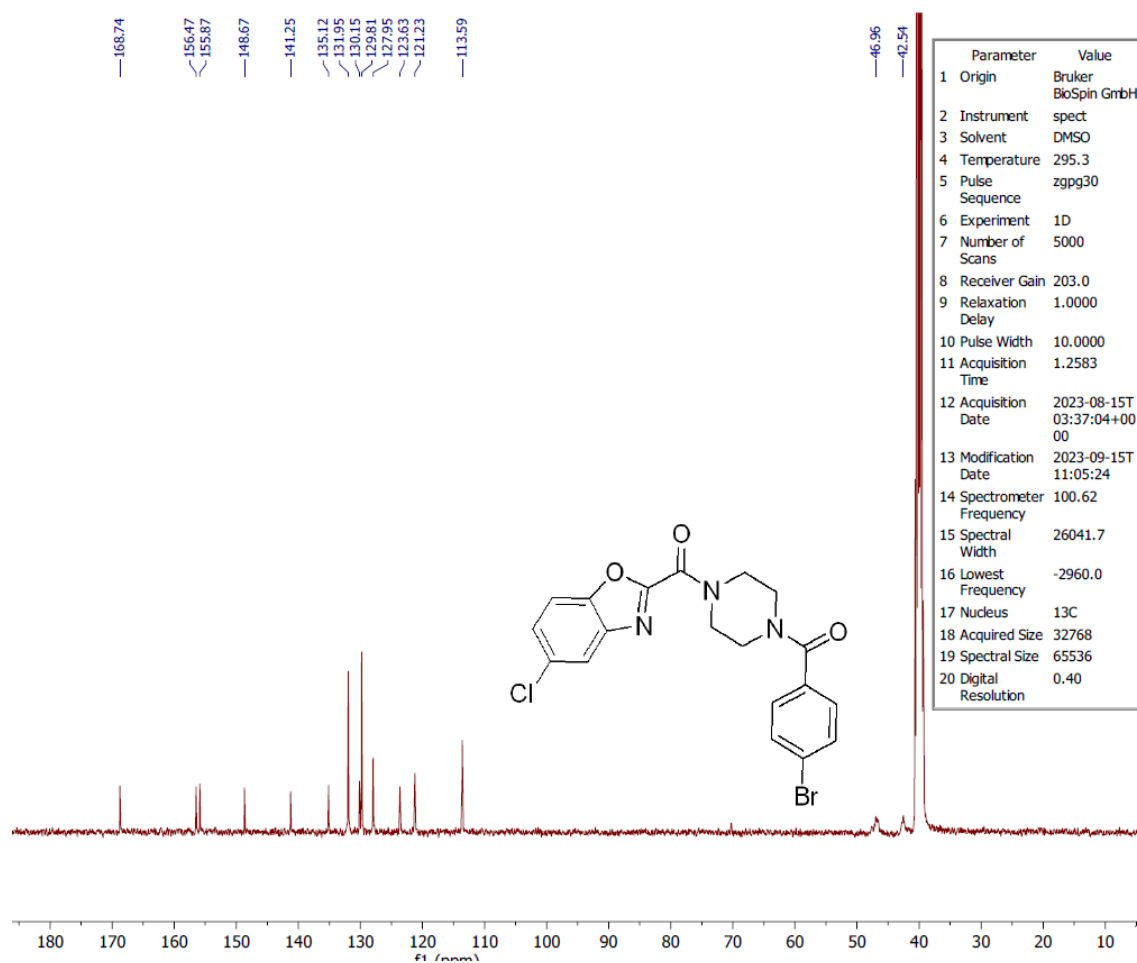
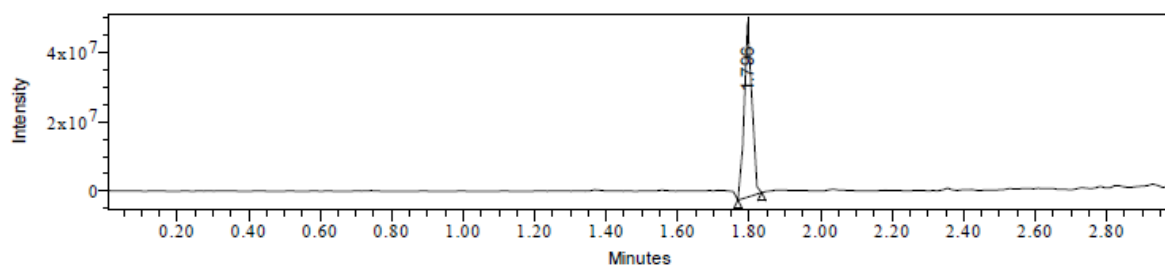
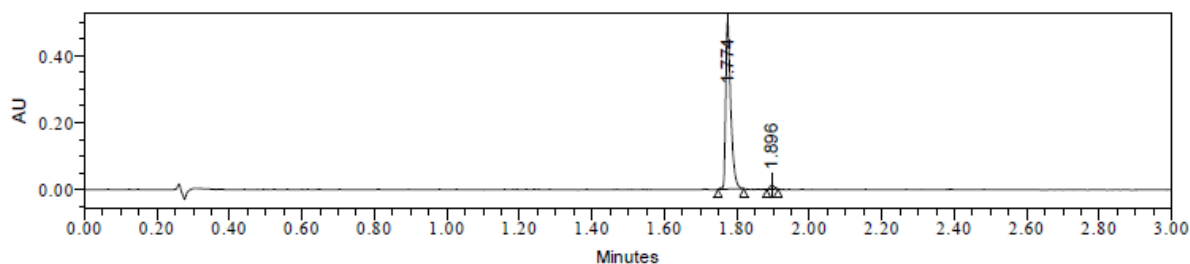


Figure 48: ¹³C NMR of compound 9f.

Sample Name:	Compound-9f		Acquired By:	LCMS-02
Sample Type:	Unknown		Sample Set Name:	20072023 UCH 189 3RD
Vial:	2:A,5		Acq. Method Set:	METHOD C3
Injection #:	1		Processing Method:	METHOD_C3_01, METHOD_C3
Injection Volume:	0.60 ul		Channel Name:	235.0nm, MS TIC
Run Time:	3.0 Minutes		Proc. Chnl. Descr.:	SQ 2: MS Scan MS TIC, Smoothed
Project Name LCMS-02_JULY-2023_20072023				
Date Acquired:	20-07-2023 23:42:00 IST			
Date Processed:	21-07-2023 01:02:47 IST, 21-07-2023 01:03:09 IST			

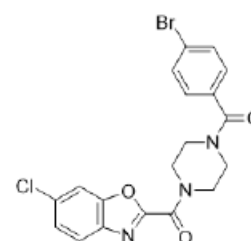


Peak Results
Channel: PDA Spectrum

Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV*sec)	% Area	Channel	Channel Name
1	1.774	500246	485643	97.90	PDA Spectrum	235.0nm
2	1.896	12003	10424	2.10	PDA Spectrum	235.0nm

Peak Results
Channel: SQ 2: MS Scan

Scan 179: MS Scan							
Retention Time (min)	Base Peak (m/z)	Height (μV)	Area (μV*sec)	% Area	Channel	Channel Name	
1	1.796	450.39	50708331	74856768	100.00	SQ 2: MS Scan	MS TIC



Chemical Formula: C₁₉H₁₅BrClN₃O₃
Molecular Weight: 448.70

Match Plot

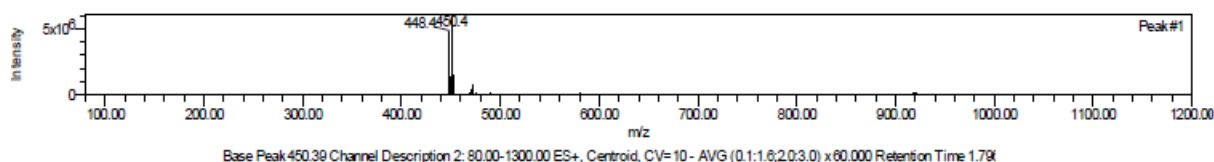


Figure 49: LC-MS of compound 9f.

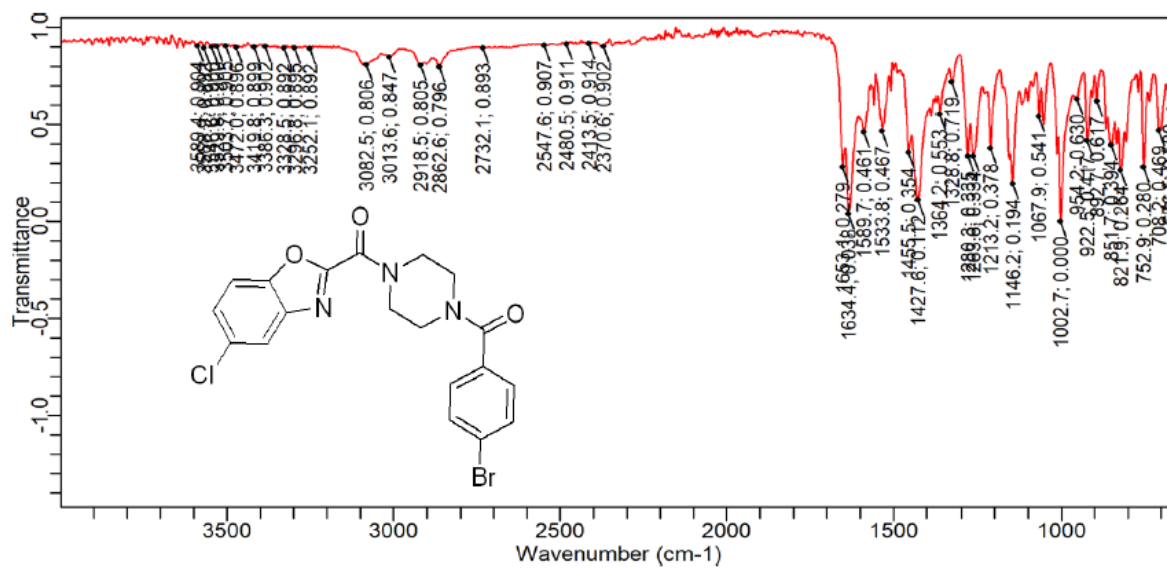


Figure 50: IR of compound 9f.