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Original article

In-silico design and network pharmacological approach on schiff base derivatives with sulfonamide moieties for antimicrobial property

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ABSTRACT

Background: Antimicrobial resistance is a global public health and economic threat. Sulfonamides are structural analogues of para-amino benzoic acid, which act as competitive inhibitors of folic acid metabolism. Although resistance has limited their use as monotherapy, sulfonamide-containing conjugates and hybrids remain valuable. Schiff bases are versatile groups with broad-spectrum biological activities, including antibacterial and antifungal properties. **Objective:** To design and evaluate novel Schiff base derivatives incorporating sulfonamide moieties as potential antibacterial and antifungal agents using a comprehensive *in-silico* drug discovery approach. **Methods**: A series of sulfonamide-linked Schiff bases was designed using ACD/Labs ChemSketch 12.0. All compounds were filtered according to Lipinski's rule of five and physicochemical properties. Bioactivity scores were predicted using Molinspiration and PASS Online. ADMET profiles were assessed with admetSAR and ADMETlab2.0. Target fishing and network pharmacology analysis were performed using Swiss Target Prediction, MolsoftL.L.C, String, Gene card Venny 2.0, and Cytoscape. Molecular docking studies were carried out using Biovia Discovery Studio to evaluate binding affinity against relevant microbial targets. **Results:** This study has predicted the biological action of some of the proposed analogues, including the compound SB8 (4-{(Z)-[(4'-hydroxy[1,1'-biphenyl]-4-yl) methylidene] amino} benzene-1 sulfonamide), which exhibits antifungal activity and a high binding affinity for the target with a LibDock score of 93.17 and compound SB5 (4-{(E)-[(4-methyl-1H-imidazol-5-yl)methylidene]amino}benzene-1-sulfonamide) shows antibacterial activity and a binding affinity score of 71.72. **Conclusion:** The result showed that ligand SB5 and SB8 have high binding affinity (LibDock score: 71.72 and 71.18) to the target compared to other ligands for antibacterial activity, and ligand SB8 has high binding affinity (LibDock score: 93.17) to the target compared to other ligands for antifungal activity.

1. INTRODUCTION

Antimicrobial resistance becomes the top global health threat. As per WHO studies, antibacterial resistance becomes responsible for about 1.27 million deaths by the year 2024 (Bertagnolio et al.,2024). Resistance to antimicrobial agents makes infections complicated to treat and thereby complicates medical

procedures like surgery, cancer treatment, etc. The creation of new treatments based on biological targets is accomplished through the innovative and creative process of drug design. In general, rational drug design is another name for it. Perfect treatments are always needed since several diseases provide a continual threat to human existence. Using biological target information, the innovative process of creating new medications is called "drug designing." The creation of medicines with a high degree of chemotherapeutic index and focused action is the aim of "tailor-made compounds" or drug design(Niazi et al.,2023).

Researchers have focused on sulfonamide-based Schiff base derivatives that include the azomethine/amine (single bond, double bond, and triple bond) group and associated metal complexes for a variety of pharmacological and medicinal uses (Basarn et al.,2025). As sulfonamide was used widely, it caused the development of mutations in dihydropteroate synthase and caused overproduction of PABA. Schiff bases cause the degradation of cell walls and destroy the microorganisms. According to the SAR of sulfonamide change in the amino group, and adding other groups like an aryl aldehyde(Ar) increases the activity of the compound with less antimicrobial resistance (Berredjem et al.,2023).

The idea is to combine the biological activity and the drug action network in order to examine the connection between the sulfonamide moieties and the network's parameters. After that, the focus shifts from searching for a specific target to doing a thorough network analysis for finding the specific antimicrobial activity.

2. METHODS

The *in-silico* modelling of all compounds was performed by various software tools with the purpose of predicting the physicochemical properties. Molinspiration, PASS, admetSAR, ACD Lab ChemSketch, and other programs were used for *in-silico* studies. Molecular docking analysis was done by Biovia Discovery Studio.

With ACD Lab ChemSketch, novel structures were developed, which include chemical name and SMILES notation (Harutyunyan et al.,2021). The Lipinski rule of five was checked and determined using Molinspiration software (Barman et al.,2021). It helps to assess a chemical's drug likeness by checking its physical and chemical characteristics that are crucial for a drug's pharmacokinetics. PASS software helps to provide the list of probable biological activities by using the 2D structure of the compound with 2 probability values: Pa (probability to be active) and Pi (probability to be inactive) (Lagunin et al.,2000). Using admetSAR software, the ADMET profile of the drug was identified (Yang et al.,2019). The toxicity of candidate chemicals and unintended pharmacokinetics are the main reasons why a medication fails. ADMET 2.0 is used to determine the toxicity and unintended pharmacokinetics of the novel drugs prepared (Xiong et al.,2019).

Drug likeness profiling using Molsoft L.L.C was done to determine a set of properties that make a molecule likely to develop as a drug, such as absorption, distribution, metabolism, and excretion, but it's devoid of toxicity (UAP Fields,2012). The targets for the ligand molecule produced*, i.e., SB1-SB10,* are determined using Swiss target prediction (Gfeller et al., 2014). Gene card provides the targets that are responsible for the development of the disease (Safran et al., 2010). Venny 2.1.0 helps to indicate the common targets among the given target proteins (Safran et al.,2010). Protein- Protein interaction of both targets of ligand and disease was determined by using STRING software (Alzarea et al.,2022).

Correlation between pathways and targets of both ligand and disease is determined by using Cytoscape software (Saito et al.,2012). It helps to identify whether a drug helps to reduce the development of disease by interacting with the specific target. Docking analysis of the molecules for a specific target was identified by using Discovery Studio v.21 (Gao et al.,2011) by using the protein crystallographic profile obtained from RCSB-PDB (Rcsb, P.D.B, 2000). Docking studies are done on the Department of Computational Biology and Bioinformatics, University of Kerala, Karyavattom, India.

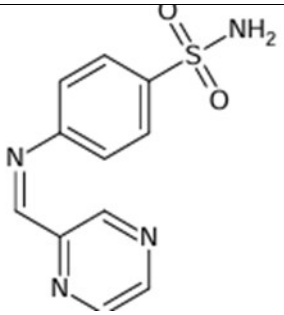
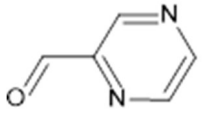
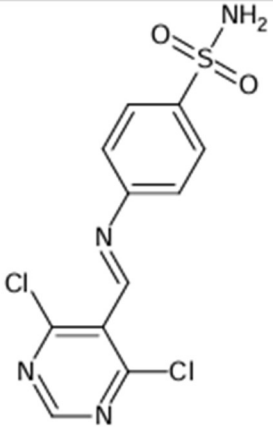
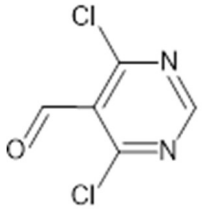
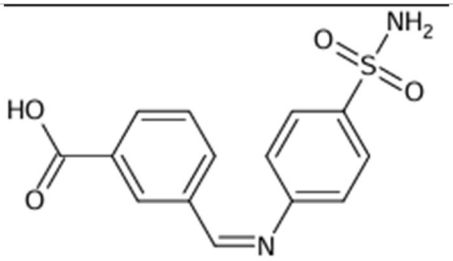
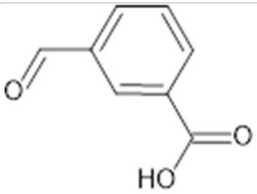
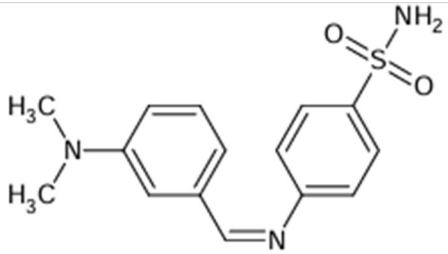
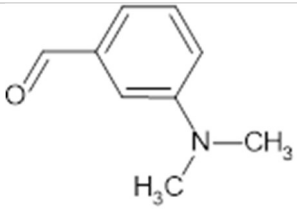
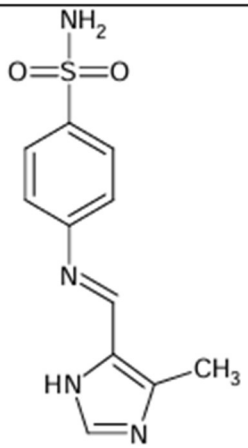
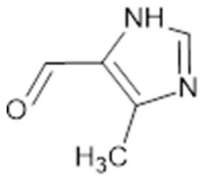
3. RESULTS AND DISCUSSIONS

In this study, many novel Schiff base derivatives of sulfonamide compounds were evaluated for their antibacterial and antifungal properties. Antimicrobial resistance has been increasing steadily due to the overuse and misprescription of antibiotics. Resistance of microbes to existing antibiotics leads to complications and risks in treating infections, and therefore, it contributes to mortality, which accounts for approximately 9% of global deaths. Antimicrobial resistance is considered a global health threat. (Otani et al., 2003, Zerrouki et al., 2024)

In-silico molecular modelling

The novel structures were designed using ACD Lab ChemSketch12.0, are shown in Table 1. The compounds' structures were drawn, and the Smiles notation was obtained. We have incorporated Ar by

Table 1: The novel compounds obtained from ACD Lab ChemSketch, along with their smiles notation

COMPOUND CODE	STRUCTURE	Ar molecule attached to sulfonamide
SB1		
SB2		
SB3		
SB4		
SB5		

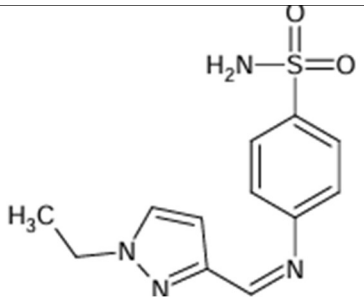
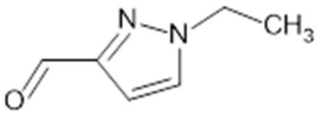
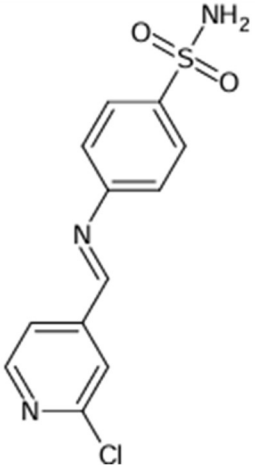
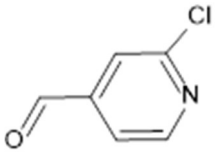
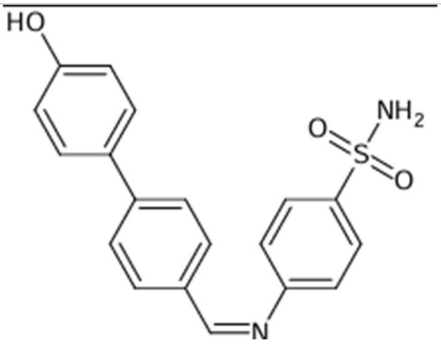
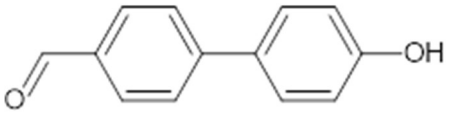
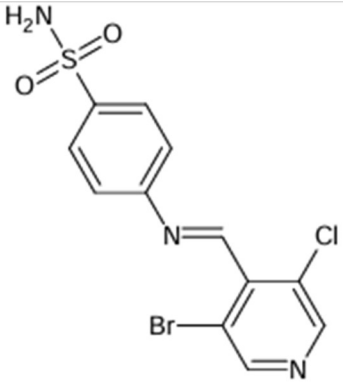
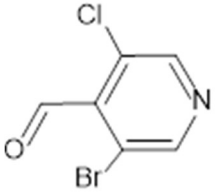
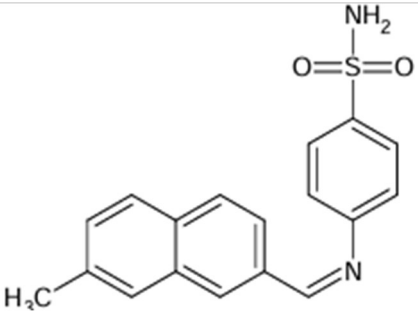
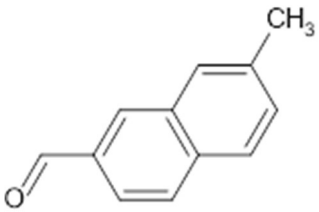
SB6		
SB7		
SB8		
SB9		
SB10		

Table 2: Details of Lipinski's Rule of Five

Compound	Milogp	MW	HBA	HBD	Violations	nrot B
SB1	0.7	262.29	6	2	0	3
SB2	1.99	331.18	6	2	0	3
SB3	2.05	304.33	6	3	0	4
SB4	2.24	303.39	5	2	0	4
SB5	0.61	264.31	6	3	0	3
SB6	1.23	278.34	6	2	0	4
SB7	1.9	295.75	5	2	0	3
SB8	3.48	352.42	5	3	0	4
SB9	2.65	374.65	5	2	0	3
SB10	3.77	324.4	4	2	0	3

Milog P: Molinspiration Log P(partition coefficient), MW: molecular weight, HBA: hydrogen bond acceptor, HBD: hydrogen bond donor, nrot B: no of rotatable bonds

Table 3: ADMET properties of novel molecules obtained from admetSAR software

Compound Code	ADME prediction					Toxicity prediction	
	HIA	Subcellular localization		Bio degradation	Cytochrome 450 3A4		
SB1	0.9723	Mitochondria	0.4558	NRB	Non-inhibitor	Non - AMES toxic	Non carcino gens
SB2	0.9789	Mitochondria	0.4764	NRB	Non-inhibitor	Non - AMES toxic	Non - carcino gens
SB3	0.7812	Mitochondria	0.5688	NRB	Non-inhibitor	Non - AMES toxic	Non - carcino gens
SB4	0.9770	Lysosomes	0.4995	NRB	Inhibitor	Non - AMES toxic	Non - carcino gens
SB5	0.9805	Lysosomes	0.5435	NRB	Non-inhibitor	Non - AMES toxic	Non - carcino gens
SB6	0.9880	Plasma membrane	0.3534	NRB	Non-inhibitor	Non - AMES toxic	Non - carcino gens
SB7	0.9801	Lysosomes	0.4334	NRB	Inhibitor	Non - AMES toxic	Non - carcino gens
SB8	0.9870	Mitochondria	0.6265	NRB	Non-inhibitor	Non - AMES toxic	Non - carcino gens
SB9	0.9819	Lysosomes	0.4747	NRB	Inhibitor	Non - AMES toxic	Non - carcino gens
SB10	0.9898	Lysosomes	0.5068	NRB	Inhibitor	Non - AMES toxic	Non - carcino gens

HIA: human intestinal absorption, NRB: not readily biodegradable, AMES: Bacterial reverse mutation test.

Table 4: Data computed from PASS software

COMPOUND CODE	Anti-bacterial Activity		Anti-fungal Activity	
	Pa	Pi	Pa	Pi
SB1	0.843	0.004	0.813	0.004
SB2	0.866	0.003	0.857	0.003
SB3	0.877	0.003	0.887	0.003
SB4	0.754	0.008	0.828	0.004
SB5	0.75	0.01	0.751	0.008
SB6	0.826	0.005	0.833	0.004
SB7	0.831	0.004	0.738	0.009
SB8	0.827	0.004	0.733	0.01
SB9	0.815	0.004	0.759	0.007
SB10	0.839	0.004	0.76	0.007

replacing the amino group of sulfonamides. The scheme of work was selected from the previous studies (Mondal et al.,2017; Khan et al.,2018). It shows that the condensation of Ar with sulfonamides in the presence of ethanol and glacial acetic acid, and refluxing it for about 5-6 hours, produces the Schiff base of sulfonamides.

In this study, we created about 25 ligand molecules. The prepared structures were energy minimized and optimized as per a study on antibacterial and antifungal properties of benzene sulfonamide derivatives, where they designed 8 molecules (Thangavelu et al.,2018).

Analysis of the Lipinski rule

Analysis of the Lipinski rule of five was carried out for the proposed analogues using Molinspiration software and is given in Table 2.

From the 25 structures, 10 compounds were selected which obeys Lipinski rule of five. As per the previous study (Thiri et al., 2017), the calculation of molecular properties of compounds like molecular weight, number of hydrogen bond acceptors, number of hydrogen bond receptors, and value of partition coefficient was determined. We found Pfizer rule violations of 0 for all molecules.

As per the studies of the National Institute of Health, an ideal range of Log P value for Blood Brain Barrier (BBB) penetrability is 1.5-2.5 (Krátký et al., 2017). A higher Log P value is necessary for the ability to penetrate the BBB, where an excessively higher Log P value can also hinder the entry of drugs into the BBB. Compounds SB8, SB9 & SB10, shows a higher Log P value when compared to other compounds.

ADMET properties

The ADMET software's information on absorption, distribution, metabolism, elimination, and toxicity properties was tabulated in Table 3.

As per the previous studies, subcellular localization to lysosomes or endosomes is essential for the antimicrobial activity while targeting antimicrobial agents. These lysosomes are involved in the complete waste management in the cell, which can help in the disruption of the survival mechanism of microbes (Mondal et al., 2017). Compounds such as SB4, SB5, SB7, SB9, and SB10 show subcellular localization in lysosomes. Subcellular localization to mitochondria helps in identifying novel antimicrobial agents and testing the target fungal pathogens through their unique machinery. Compounds other than SB7, SB9 & SB10 are non-inhibitors of CYP3A4, which can lead to reduced effectiveness or can reduce the duration of action of the drug in the body (Al- Masoudi et al., 2016).

The compounds SB1-SB10 are predicted to be non- AMES toxic and non -carcinogenic. The toxicity can only be predicted by means of toxicity studies.

Antimicrobial properties

Different biological activities were predicted using PASS software. The novel compounds selected show a Pa value above 0.7, which indicates that they have the probability to show higher activity. Table 4 shows the Pa and Pi values of the whole 10 compounds.

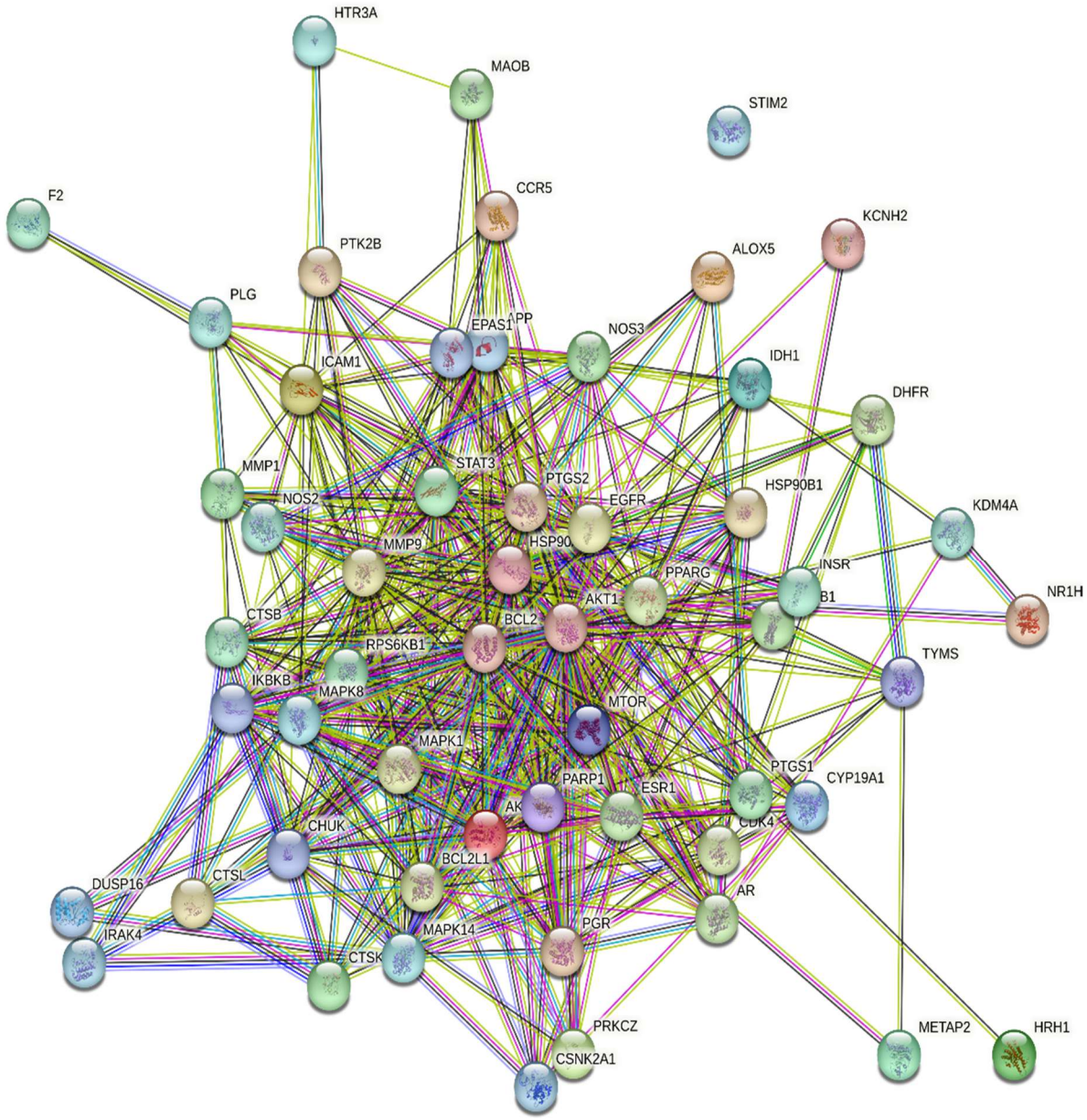


Figure 1: Protein - Protein interaction from String database

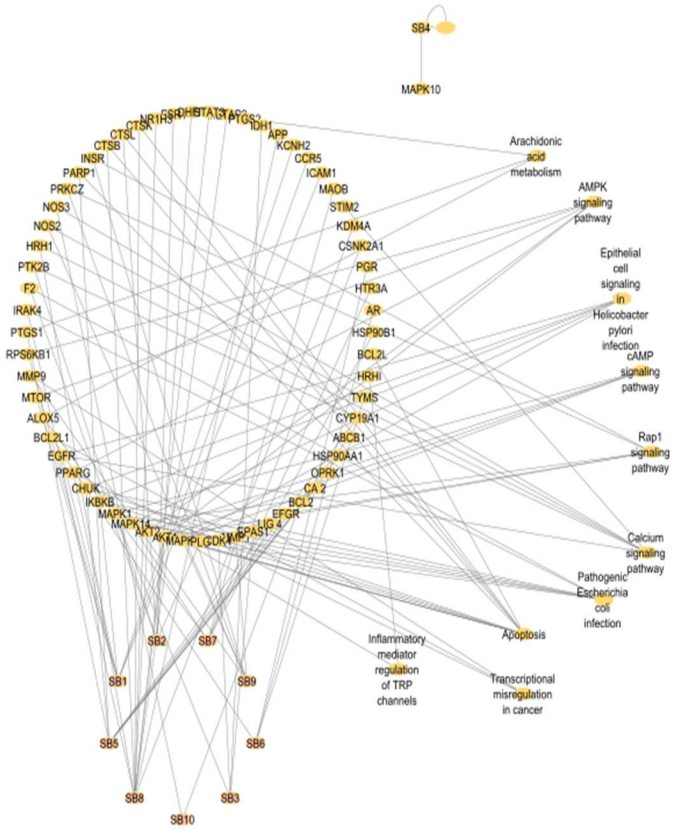


Figure 2: Cytoscape coorelation

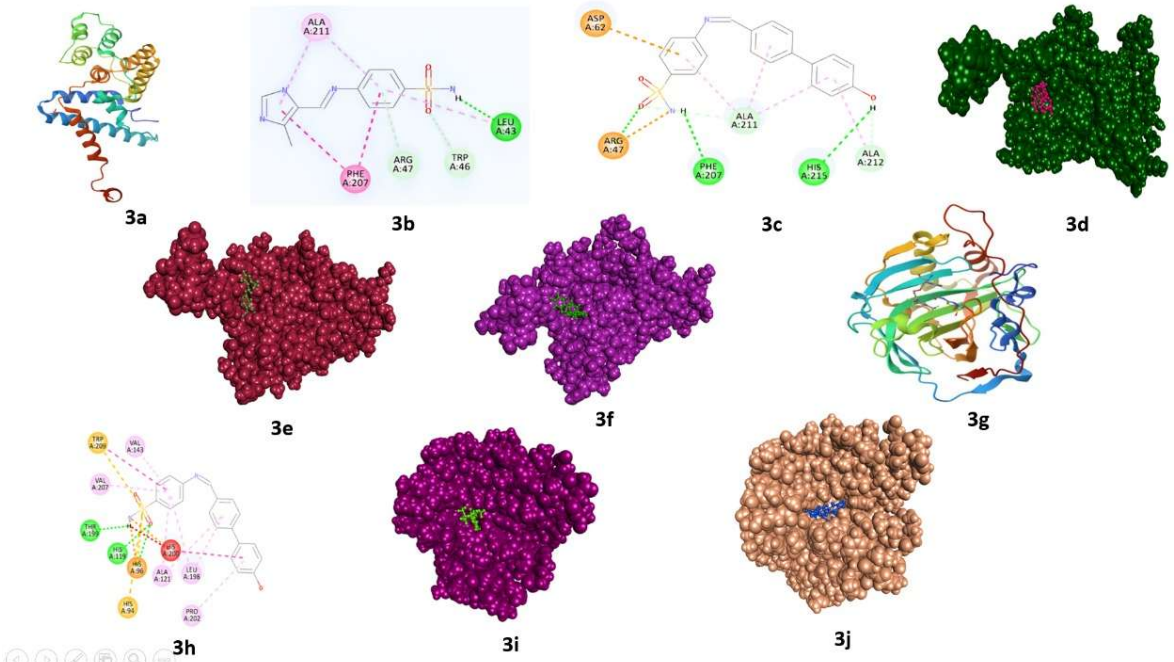


Figure 3: 3a: Crystallographic resolution of protein 4HTO, 3b: Interaction of SB5 with 4HTO, 3c: Interaction of SB8 with 4HTO, 3d: Docking image of ciprofloxacin with 4HTO, 3e: Docking image of SB5 with 4HTO, 3f: Docking image of SB8 with 4HTO, 3g: Crystallographic resolution of protein 3W6H, 3h: Interaction of SB8 with 3W6H, 3i: Docking image of Griseofulvin with 3W6H, 3j: Docking image of SB8 with 3W6H.

By comparing the data obtained from the previous study, all 10 compounds show a probability of activity value of > 0.7, which is better for the probability of higher activity in both antibacterial andantifungal activity (Shallangwa et al.,2015).

Drug likeness score

The drug likeness score obtained from the software Molsoft L.L.C were follows: SB1: 0.05, SB2: -0.09, SB3: -0.45, SB4: -1.06, SB5: -0.07, SB6: 0.30, SB7: -0.36, SB8: -0.60, SB9: -0.28, SB10: -1.32. Compound SB1-SB10 showed antimicrobial activity.

Target prediction and identification

Target proteins for each compound were predicted by means of Swiss target prediction software. In SB1-SB10 compounds,1103 ligand targets were obtained.

Disease targets for both antibacterial and antifungal were found by using Gene Cards. In this study, 765 disease targets were identified. From disease targets, protein-encoding genes of 415 were selected for the identification of common targets. A Venn diagram was drawn with the help of Venny 2.1.0 by using the disease targets and ligand targets. The Venn diagrams for compounds SB1- SB10 are drawn, and the common targets obtained are as follows: SB1: 16, SB2: 14, SB3: 15, SB4: 13, SB5: 12, SB6: 13, SB7:14, SB8:17, SB9: 13, SB10: 19.

Protein-Protein interaction and Molecular docking

The protein-protein interaction between the disease target and the ligand target was found by using the String Database. Figure 1 represents the protein – protein interaction network obtained from the String Database. It provides information about the global set of all protein interactions associated with antimicrobial diseases. Figure 2 represents a comparison and correlation between the pathway obtained from the string database and the protein – ligand targets by using Cytoscape. It understands how the proteins and the ligands, that are SB1 – SB10, interact. It is shown that every ligand interacts with more than 3 proteins associated with antibacterial disease and antifungal disease, except SB4.

Docking analysis of the selected targets with synthetic ligands was performed using the docking software Discovery Studio 2018. Before docking, the targets and ligands were reprocessed to optimize and minimize the structure and generate conformers, respectively. The three-dimensional structure of DNA ligase 4 (Figure 3a) from Homo sapiens was downloaded from the PDB database with PDB ID: 4HTO with a crystallographic resolution of 2.81 Å. The protein chain consists of one polypeptide chain A. The protein has a total of 240 amino acids with a molecular weight of 27.54 kDa. The PDB active site of molecules was selected as the binding site**.** Human DNA ligase is used as a selectivity control to ensure the newly synthesised moieties inhibit bacterial target without affecting the human DNA (Podos et.al., 2012).

149 poses of the selected ligands in the docked complexes were generated. The interacting molecular complexes among these having the top LibDock Score, the maximum number of hydrogen bonds, and active residues were selected. From the 10 ligands, 9 showed good interaction with DNA ligase 4 (Figure 3b-3f).

The docking score for the designed compounds for their antibacterial activity is as follows

Standard (Ciprofloxacin); (78.59)> SB5 (71.72) > SB8 (71.18) > SB2 (69.16) >SB9 (69.08) >SB10(66.12)> SB6 (58.41) >SB4 (56.52) > SB1 (54.17) >SB7 (0)

The three-dimensional structure of Carbonic anhydrase 1(Figure 3g**)** from Homo sapiens was downloaded from the PDB database with PDB ID: 3W6H with a crystallographic resolution of 2.96 Å. The protein chain consists of two polypeptide chain A and B. The protein has a total of 260 amino acids with a molecular weight of 58.73 kDa. 3W6H acts as a counter target in the development of antifungal agents(Kose et.al.,2016). The PDB active site of molecules was selected as the binding site (Figure 3h-3j).

1402 poses of the selected ligands in the docked complexes were generated. From the 10 ligands, 10 showed good interaction with Carbonic anhydrase 1.

The docking score for the designed compounds for their antifungal activity is as follows

SB8 (93.17) > SB2 (84.97) >SB9 (84.79) >SB7 (84.35) >SB5 (82.64) >Standard (Griseofulvin); (81.67) > SB10 (81.16) > SB3 (78.60) > SB6 (76.32)> SB4 (75.39)> SB1(67.97)

The result showed that ligand SB5 and SB8 have high binding affinity (LibDock score: 71.72 and 71.18) to the target compared to other ligands for antibacterial activity, and ligand SB8 has high binding affinity (LibDock score: 93.17) to the target compared to other ligands for antifungal activity.

As per the results obtained, the compound SB8 shows a higher docking score than that of the standard drug Griseofulvin [30]. Further pharmacological and toxicological conformational results can be obtained

by conducting *in vitro* and *in vivo* studies.

4. CONCLUSION

The prime objective of the present work was to design and evaluate the antimicrobial properties of the Schiff base of sulphonamides. This involves the preliminary *in silico* screening of various analogues to analyse their molecular descriptors using computational software. Derivatives with desired physicochemical properties and obeying the Lipinski rule of five were selected for molecular docking studies. The compounds that follow Lipinski rule are directed to a series of network pharmacology studies. This study has predicted the biological action of some of the proposed analogues, including the compound SB8(4-{(Z)-[(4'-hydroxy[1,1'-biphenyl]-4-yl)methylidene]amino}benzene-1sulfonamide), which exhibits antifungal activity and a high binding affinity for the target with a LibDock score of 93.17 and compound SB5 (4-{(E)-[(4-methyl-1H-imidazol-5-yl)methylidene]amino}benzene-1-sulfonamide) shows antibacterial activity and a binding affinity score of 71.72. Therefore, the *in-silico* studies indicate the relevance of the work, and these analogues can undergo more thorough pharmacological screening in order to develop new drug candidates.

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Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this manuscript.

REFERENCES

Al-Masoudi, W. A., Faaz, R. A., Al-Asadi, R. H., & Jabbar, H. S. (2016). Synthesis, antimicrobial activity and modelling studies of some new metal complexes of Schiff base derived from sulphonamide drug in vitro. *European Journal of Chemistry, 7*(1), 102-106. https://doi.org/10.5155/eurjchem.7.1.102-106.1374

Alzarea, S. I., Qasim, S., Uttra, A. M., Khan, Y. H., Aljoufi, F. A., Ahmed, S. R., ... & Malhi, T. H. (2022). Network Pharmacology and Molecular Docking Based Prediction of Mechanism of Pharmacological Attributes of Glutinol. *Processes*, *10*(8), 1492. https://doi.org/10.3390/pr10081492

Barman, K., Das, G., G. I., Kalita, J. M., & Dasgupta, P. Design and molecular docking of sulfonamide derivatives. *International Journal of Current Pharmaceutical Research*, *13*(4), 93-97. https://dx.doi.org/10.22159/ijcpr.2021v13i4.42752

Başaran, E., Çakmak, R., Türkmenoğlu, B., Akkoc, S., & Köprü, S. (2025). Synthesis of Sulfonamide-Based Schiff Bases as Potent Anticancer Agents: Spectral Analyses, Biological Activity, Molecular Docking, ADME, DFT, and Pharmacophore Modelling Studies. *Chemistry & Biodiversity*, *22*(2), e202402229. https://doi.org/10.1002/cbdv.202402229

Berredjem, M., Bouchareb, F., Djouad, S. E., Bouasla, R., Bahadi, R., Redjemia, R., ... & Dekir, A. (2023). Recent Progress in Synthesis of Sulfonamides and N-Acylsulfonamides, Biological Applications and Their Structure-Activity Relationship (SAR) Studies. *Chemistry Select*, *8*(35), e202301859. https://doi.org/10.1002/slct.202301859

Bertagnolio, S., Dobreva, Z., Centner, C. M., Olaru, I. D., Donà, D., Burzo, S., …& Van Weezenbeek, K., (2024). WHO global research priorities for antimicrobial resistance in human health. *The Lancet Microbe, 5*(11), 100902. https://doi.org/10.1016/S2666-5247(24)00134-4

Chohan, Z. H., & Shad, H. A. (2008). Structural elucidation and biological significance of 2-hydroxy-1-naphthaldehyde derived sulfonamides and their first row d-transition metal chelates. *Journal of Enzyme Inhibition and Medicinal Chemistry, 23*(3), 369-379. https://doi.org/10.1080/14756360701585692

Chohan, Z. H., & Shad, H. A. (2012). Metal-based new sulfonamides: Design, synthesis, antibacterial, antifungal, and cytotoxic properties. *Journal of Enzyme Inhibition and Medicinal Chemistry, 27*(3), 403-412. https://doi.org/10.3109/14756366.2011.593515

Fields, U. A. P. (2012). MolSoft ICM Quarterly.

Gahimbare, L., Muvunyi, C. M., Guessennd, N. A. K., Rutanga, J. P., Gashema, P., Fuller, W., ... & Yahaya, A. A. (2024). Antimicrobial resistance in the WHO African Region: A systematic literature review 2016–2020. *Antibiotics*, *13*(7), 659. https://doi: 10.3390/antibiotics13070659

Gao, Y. D., & Huang, J. F. (2011). An extension strategy of Discovery Studio 2.0 for non-bonded interaction energy automatic calculation at the residue level. *Zoological Research, 32*(3), 262-266. https://doi.org/10.3724/SP.J.1141.2011.03262

Gfeller, D., Grosdidier, A., Wirth, M., Daina, A., Michielin, O., & Zoete, V. (2014). SwissTargetPrediction: a web server for target prediction of bioactive small molecules. *Nucleic Acids Research*, *42*(W1), W32-W38. https://doi.org/10.1093/nar/gku293

Harutyunyan, A., Gukasyan, G. T., Grigoryan, A. S., & Stepanyan, H. M. (2021). Antibacterial and mao-inhibiting properties of new styryl derivatives of pyrimidines, quinazolines and bis-quinazolines. *Ajastan Kensabanakan Handes*, *73*(2), 26-30.

Khan, M. N., Khan, A. M., Ullah, H., Hussain, S., & Khattak, A. K. (2018). Synthesis and antibacterial activity of the sulfonamide based schiff base and its transition metal (II) complexes. *Pakistan Journal of Pharmaceutical Sciences,31*(1), 103-111.

Kose, L. P., Gulcin, İ., Yıldırım, A., Atmaca, U., Çelik, M., Alwasel, S. H., & Supuran, C. T. (2016). The human carbonic anhydrase isoenzymes I and II inhibitory effects of some hydroperoxides, alcohols, and acetates. *Journal of Enzyme Inhibition and Medicinal Chemistry*, *31*(6), 1248-1253. https://doi.org/10.3109/14756366.2015.1120723

Krátký, M., Dzurková, M., Janoušek, J., Konečná, K., Trejtnar, F., Stolaříková, J., & Vinšová, J. (2017). Sulfadiazine salicylaldehyde-based Schiff bases: Synthesis,

antimicrobial activity and cytotoxicity. *Molecules, 22*(9), 1573. https://doi.org/10.3390/molecules22091573

Lagunin, A., Stepanchikova, A., Filimonov, D., & Poroikov, V. (2000). PASS: prediction of activity spectra for biologically active substances. *Bioinformatics*, *16*(8), 747-748. https://doi.org/10.1093/bioinformatics/16.8.747

Mondal, S., Mandal, S. M., Mondal, T. K., & Sinha, C. (2017). Spectroscopic characterization, antimicrobial activity, DFT computation and docking studies of sulfonamide Schiff bases. *Journal of Molecular Structure, 1127*, 557-567. http://dx.doi.org/10.1016/j.molstruc.2016.08.011

Niazi, S. K., & Mariam, Z. (2023). Computer-aided drug design and drug discovery: a prospective analysis. *Pharmaceuticals*, *17*(1), 22. https://doi.org/10.3390/ph17010022

Otani, K. (2003). Cytochrome P450 3A4 and benzodiazepines. *Seishin Shinkeigaku Zasshi, 105*(5), 631-642.

Othman, R. M., Al-Masoudi, W. A., Hama, A. A., & Hussain, S. M. (2019). Antimicrobial activity and molecular modeling study of Schiff base derived from sulfamerazine. *Indian Journal of Forensic Medicine & Toxicology, 13*(4), 694-699.

Podos, S. D., Thanassi, J. A., & Pucci, M. J. (2012). Mechanistic assessment of DNA ligase as an antibacterial target in Staphylococcus aureus. *Antimicrobial Agents and Chemotherapy*, *56*(8), 4095-4102. https://doi.org/10.1128/AAC.00215-12

RCSB Protein Data Bank. (n.d.). RCSB.org. *https://www. rcsb. org/(visited on 09/15/2022)*.

Safran, M., Dalah, I., Alexander, J., Rosen, N., & Lancet, D. (2010). GeneCards Version 3:the human gene integrator. *Database*, *2010*. https://doi.org/10.1093/database/baq020

Saito, R., Smoot, M. E., Ono, K., Ruscheinski, J., Wang, P. L., Lotia, S., ... & Ideker, T. (2012). A travel guide to Cytoscape plugins. *Nature Methods*, *9*(11), 1069-1076. https://doi.org/10.1038/nmeth.2212

Shallangwa, G. A., Musa, H., & Ogbe, E. (2015). Design and synthesis of new series of one pot Schiff bases of 4-aminobenzenesulfon-amideas potent antibacterial and anti-fungal agents. *Journal of Progressive Research in Chemistry, 1*, 14-21.

Tahriri, M., Yousefi, M., Mehrani, K., Tabatabaee, M., & Ashkezari, M. D. (2017). Synthesis, characterization and antimicrobial activity of two novel sulfonamide Schiff base compounds. *Pharmaceutical Chemistry Journal, 51*(5), 425-428. https://doi.org/10.1007/s11094-017-1626-z

Thangavelu, P., & Thangavel, S. (2018). Design, synthesis, and docking of sulfadiazine Schiff base scaffold for their potential claim as Inha enoyl-(acyl-carrier-protein) reductase inhibitors. *Asian Journal of Pharmaceutical and Clinical Research, 11*(10), 233. http://dx.doi.org/10.22159/ajpcr.2018.v11i10.27179

Ul-Hassan, M., Chohan, Z. H., Scozzafava, A., & Supuran, C. T. (2004). Carbonic anhydrase inhibitors: Schiff's bases of aromatic and heterocyclic sulfonamides and their metal complexes. *Journal of Enzyme Inhibition and Medicinal Chemistry, 19*(3), 263-267. https://doi.org/10.1080/14756360410001689595

Xiong, G., Wu, Z., Yi, J., Fu, L., Yang, Z., Hsieh, C., ... & Cao, D. (2021). ADMETlab 2.0: an integrated online platform for accurate and comprehensive predictions of ADMET properties. *Nucleic acids research*, *49*(W1), W5-W14. https://doi.org/10.1093/nar/gkab255

Yang, H., Lou, C., Sun, L., Li, J., Cai, Y., Wang, Z., ... & Tang, Y. (2019). ADMETSAR 2.0: web-service for prediction and optimization of chemical ADMET properties. *Bioinformatics*, *35*(6), 1067-1069. https://doi.org/10.1093/bioinformatics/bty707

Zemede, Y. B., Nithyakalyani, D., & Kumar, S. A. (2015). Synthesis, characterization and antimicrobial properties of some transition metal complexes with NS-chelating Schiff base ligand incorporating thiophene and sulfonamide moieties. *Asian Journal of Chemistry*, 27(3), 941-948. http://dx.doi.org/10.14233/ajchem.2015.17627

Zerrouki, S., Bouchoucha, A., Djellouli, F., Bouzaheur, A., Si Larbi, K., & Bourouai, M. A. (2024). New Schiff base Derivatives Bearing Sulfonamide Moiety: Synthesis, In vitro Antimicrobial Activity, DFT Calculations, ADMET and Molecular Docking Study. *Iranian Journal of Chemistry and Chemical Engineering, 43*(1).204-224. https://doi.org/10.30492/ijcce.2023.1987960.5829

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