Original Article

Molecular Docking Studies of Novel Furan-azetidinone Hybrids as Potential Inhibitors of *Escherichia coli*

Judy Jays[1,*], Shamanna Mohan[2], Janardhanan Saravanan[2]

[1]Faculty of Pharmacy, M.S. Ramaiah University of applied sciences, M.S.R.I.T. Post, Bangalore, Karnataka, INDIA.
[2]PES College of Pharmacy, Hanumanthnagar, Bangalore, Karnataka, INDIA.

ABSTRACT

Escherichia coli is the predominant gram negative bacteria responsible for a variety of hospital-acquired infections and urinary tract infections. As the bacterial strains are rapidly acquiring resistance to the available antibiotics, there is a need to discover novel antibacterial agents with different scaffolds. In this study, sixteen novel furan derivatives containing the azetidinone moiety were designed and synthesized to arrive at potentially effective antibacterial agents. *In silico* antibacterial activity was carried out to identify the specificity of the furan derivatives for the antibacterial targets. Molecular docking studies were conducted on four antibacterial targets of *E. coli*; Dihydrofolate reductase, DNA gyrase, Enoyl reductase and methionine aminopeptidase. Energy minimization of title compounds was carried out and they were docked on to the active site of the enzymes. Ligands were ranked according to their docking scores and their binding energy with the enzyme. The results obtained for the molecular docking of the title compounds with enoyl reductase of *E. coli* is quite promising. The study suggests that compounds 4E and 4D are potential inhibitors of enoyl reductase and specifically bind to the enzyme.

Key words: Furan, Azetidinone, *E. coli*, Docking, Anti-bacterial activity.

INTRODUCTION

Escherichia coli is the predominant gram negative bacteria accountable for a variety of hospital-acquired infections, urinary tract infections and enterocolitis. *Escherichia coli* is also the frequent cause of life-threatening bloodstream infections.[1] The emergence of several resistant *E. coli* strains has resulted in a grave health problem.[2] Shockingly, most of these multidrug-resistant strains are picked up in the community.[3,4] As the bacterial strains are rapidly acquiring resistance to the available antibiotics, there is a need to discover novel antibacterial agents with different scaffolds. Many synthetic compounds containing furan nucleus possess various pharmacological activities such as antibacterial, antifungal, antiviral, antidepressant, anti-inflammatory, anti-ulcer, diuretic and antihypertensive activities.[5,6] Azetidinones possess antimicrobial, antifungal, antibacterial, antiviral, anticonvulsant, antioxidant, antimycobacterial and anthelmintic activities.[7,8] In this perspective, sixteen novel azetidinone-furan hybrids were synthesized with the objective of discovering more potent antibacterial which may be effective against *E. coli*.[9]

Virtual screening has been established as a very effective approach for discovery of ligand hits and for assisting lead optimization in structure-based drug discovery. Molecular docking studies of a set of compounds into structures of the target receptor helps to identify prospective lead optimization candidates and hence fewer compounds need to be experimentally screened. Besides identifying small molecules likely to bind well to a protein target, docking methods are used to explain the binding of the synthesized compounds with the target pro-

Submission Date: 29-01-2019;
Revision Date: 24-04-2019;
Accepted Date: 01-06-2019

DOI: 10.5530/ijper.53.3s.102

Correspondence:
Prof. Judy Jays,
Faculty of Pharmacy,
M.S. Ramaiah University of Applied Sciences, M.S.R.I.T. Post, Bangalore- 560054, Karnataka, INDIA.
Phone: +91 9845898654
E-mail: judyjays4@gmail.com

www.ijper.org

teins to acquire knowledge for structural optimization. All the synthesized furan- azetidinone hybrid compounds (Table 1) were docked onto the active site of the crystal structure of the specific enzymes using "Glide." The specificity of interaction of the furan-azetidinone hybrids were studied on four antibacterial targets of *E. coli*; Dihydrofolate reductase (PDB ID: 1RX7); DNA gyrase (PDB ID: 5MMO); Enoyl reductase (PDB ID: 1C14); methionine aminopeptidase (PDB ID: 4Z7M).

Dihydrofolate reductase catalyzes the reduction of dihydrofolate to tetrahydrofolate which is essential for the synthesis of important metabolites like thymidylate, a building block of DNA. Moreover, as the bacterial DHFR is different from the human enzyme, it has been recognized as a drug target for selectively inhibiting DNA synthesis in bacteria.[10-12]

Enoyl acyl carrier protein reductase (FabI) was identified as a novel antibacterial target.[13,14] This enzyme catalyzes the final reaction in bacterial fatty acid synthesis. It has recently been shown that FabI2a catalyzes this reaction in *Staphylococcus aureus* and *Escherichia coli*. Eukaryotes produce fatty acids via a FAS I system, where the lipids are synthesized using a multifunctional enzyme complex in which all of the catalytic domains reside on one or two polypeptide chains. The ACP is an integral part of this complex. In contrast, prokaryotes utilize the FAS II system where the enzymes which catalyze the individual steps are found on separate polypeptide chains and the ACP is a discreet protein. Therefore, there is considerable potential for selective inhibition of bacterial fatty acid biosynthesis.

Methionine aminopeptidase (MetAP) catalyzes the hydrolytic cleavage of the N-terminal methionine from newly synthesized polypeptides. For proteins with small, uncharged penultimate N-terminal residues, a methionine aminopeptidase can cleave the methionine residue. The number of genes encoding for a methionine aminopeptidase varies between organisms. In *E. coli*, there is only one known MetAP, a 29,333 Da coded for a gene. In humans, there are two genes encoding MetAP, MetAP1 and MetAP2. MetAP1 codes for a 42 kDa enzyme, while MetAP2 codes for a 67 kDa enzyme. Due to the difference in the substrate specificities of bacterial MetAP1, human MetAP1 and human MetAP2, the enzyme is a good target for antibacterial agents.[15,16]

DNA gyrase is an enzyme within the class of topoisomerase (Type II topoisomerase) that relieves strain while double-stranded DNA is being unwound by helicase. This causes negative supercoiling of the DNA. This process occurs in prokaryotes (particularly, in bacteria), whose single circular DNA is cut by DNA gyrase and the two ends are then twisted around each other to form supercoils. Bacterial DNA gyrase is the target of many antibiotics, including nalidixic acid, novobiocin and ciprofloxacin.[15-17] Novel Bacterial Topoisomerase Inhibitors (NBTIs) represent a new class of broad-spectrum antibacterial agents targeting bacterial Gyrase.[17-19]

MATERIALS AND METHODS

Molecular Modeling and Scoring[20-23]

Molecular modeling was carried out using GLIDE (Grid–based Ligand Docking with energetics) 2.0, running on Intel® Core TM i3-2130 CPU@ 3.40GHz processor using Linux professional workstation.

Preparation of ligands

The 3D structures of the furan derivatives (Table 1) were generated from the corresponding 2D structures with the software. The ligands were prepared using the "LigPrep" module.[20] A set of confirmations is generated for each ligand. By means of the standard bond lengths and bond angles, the geometry optimization was carried out with the help of standard OPLS_2005 force field. Finally the energy minimization was carried out and optimized confirmations are taken up for docking.

Preparation of protein

The crystal structures of the target proteins were downloaded from the Protein Data Bank (PDB) extracted from the Brookhaven Protein Database and taken for docking studies. The structures of the proteins were selected based on their resolution, R: enoyl reductase in complex with NAD and triclosan with Resolution, 2 Å (PDB ID 1C14); dihydrofolate reductase complexed with folate (PDB ID 1RX7) having Resolution 2.3 Å; DNA Gyrase (PDB ID 5MMO), in complex with [3-(3-ethyl-ureido)-5-(pyridin-4-yl)-isoquinolin-8-yl-methyl]-carbamic acid prop-2-ynyl ester, Resolution 1.8 Å; Methionine Aminopeptidase, complexed with N-2-[(3,5-difluorophenyl)acetyl]-N-[(3S,7R)-1-methyl-2-oxo-7-phenyl-2,3,4,7-tetrahydro-1H-azepin-3-yl]-L-alaninamid, Resolution 1.43 Å (PDB ID 4Z7M). "Protein preparation wizard"[21] was used to prepare the protein. Co-crystalized ligand and water molecules were removed, H-atoms were added, disulphide bonds were created and side chains were fixed during protein preparation. The structure was then subjected to an energy refinement and energy minimization procedure.

Receptor Grid generation

The optimized protein with co-crystallized ligand was taken to generate a 3D grid at the active site of the

target protein as per the standard protocol of glide manual. The co-crystallized ligand molecule is removed and the prepared ligand is docked in its place. Receptor grid generation allows outlining the position and size of active site of the protein for ligand docking.

Docking protocol

GLIDE module of Maestro was used to study the docking of the furan derivatives on the target proteins.[21-23] Glide was run on flexible docking mode where the protein is rigid and the ligand is flexible. The binding of the ligands were estimated using a variety of scoring functions that have been compiled into a single Glidescore (GScore).[24] As an empirical scoring function it is comprised of terms that account for the physics of the binding process encompassing a lipophilic-lipophilic term, hydrogen bond terms, a rotatable bond penalty and contributions from protein-ligand coulomb-vdW energies. Additionally, GlideScore includes terms to account for hydrophobic enclosure, which is the displacement of water molecules by a ligand from areas with many proximal lipophilic protein atoms. Primarily beneficial to binding is the formation of one or more protein-ligand hydrogen bonds within the regions of hydrophobic enclosure.

Glide uses the Emodel[25] scoring function to select between protein-ligand complexes of a given ligand and the GlideScore function to rank-order compounds to separate compounds that bind strongly (actives) from those that don't (inactives). The Emodel scoring function is primarily defined by the protein-ligand coulomb-vdW energy with a small contribution from GlideScore.

RESULTS AND DISCUSSION

Molecular docking of the title compounds with four potential targets of *E. coli* was performed. Glide combines a powerful sampling protocol with a value of a custom scoring function designed to identify ligand poses. Individual poses were examined to identify the binding interactions at the active site of respective protein and the ligands were evaluated in terms of Glide score and Emodel. The docked poses were ranked according to their docking scores. The ranking of the compounds was based on their binding energy with the enzyme. If the binging energy is less, the compound is more active.

Although docking simulations was carried out in both SP and XP modes of Glide,[26] the XP results are discussed. The chief purpose of XP mode is to weed out false positives and provide a better correlation between good poses and good scores. XP scoring function includes additional terms over the SP scoring function and provides a more complete treatment of some of the SP terms like scoring of H-bonds, detection of buried polar groups, etc.

Docking of title compounds with enoyl reductase of *E. coli*

The docking results of the ligands with enoyl reductase is given in Table 2. XP mode has given significant results with good glide scores and Emodel. Compound 4e with Glide Score -9.195, Emodel -73.407 was found with the highest score. The phenyl groups of 4e have formed pi-pi stacking interactions with PHE 94 and TYR 146 at the active site of the protein (Figure 1). The compound 4d with GScore -9.039 and Emodel -60.997 has also exhibited similar interaction with TYR 146. Most of the analogues have good GScores and show common binding interactions with PHE 94 and TYR 146 at the active site. The study suggests that pi-pi stacking interaction with PHE 94 and TYR 146 at the active site might be essential for enoyl reductase inhibition.

Docking of title compounds with DHFR of *E. col.*

The docking results of the ligands are given in Table 3. The XP mode has not given noteworthy results with the target protein. Compound 4c with Glide Score -5.454, Emodel -68.698 was found with highest score. The ligand is forming pi-pi stacking with PHE-31 and pi-cation interactions with ARG-52 at the active site (Figure 2). Interestingly, all the compounds except 4b and 4o form pi-cation interaction with ARG-52, implying

Table 1: Structures of the novel furan derivatives

Compound Code	R
4a	H
4b	2-ethyl
4c	4-ethyl
4d	4-chloro
4e	2,4-dichloro
4f	2-nitro
4g	4-nitro
4h	4-methoxy
4i	3-methoxy
4j	3-nitro
4k	3-chloro
4l	4-dimethyl amino
4m	3,4-dimethoxy
4n	3,4,5-trimethoxy
4o	2,6-dichloro
4p	Furfuryl

that it might be essential for DHFR inhibition. Nevertheless, GScore was found to be less indicating that the compound has not docked well into the protein pocket.

Docking of title compounds with methionine aminopeptidase of *E.coli*

The compounds have shown significant results for methionine aminopeptidase at it's active site. The docking results are given in Table 4. Compound 4h with XP Glide Score -7.606 and Emodel -66.888 was found with highest score among the derivatives. It has formed H-bond with HIE 79. It also displayed pi-pi stacking interactions with HIE 79 and TRP 221 (Figure 3). Most of the compounds have exhibited similar binding interactions with HIE 79 and TRP 221 at the active site indicating that these interactions may be essential for inhibition of the enzyme.

Docking of title compounds with DNA Gyrase of *E. coli*

The docking results are given in Table 5. The XP docking indicated that the ligands have not shown any significant results with DNA gyrase at its' active site. Compound 4f with Glide Score -4.803 and Emodel -61.315 was found with highest score among the derivatives. Although some compounds including 4f have displayed binding interactions with ARG 76 (pi-pi stacking) at the active site (Figure 4), poor Gscores indicate that the compounds have not docked well at the active site of the protein. The SP mode has given a better Glide

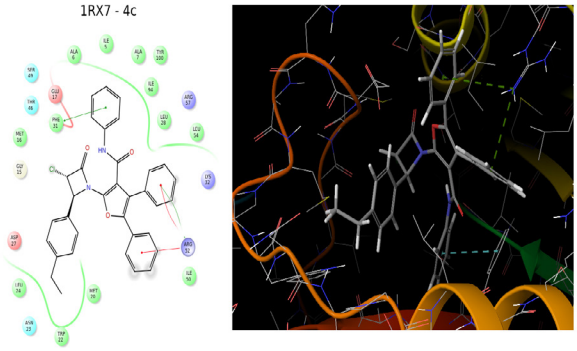


Figure 1: XP Docked pose of Compound 4e with enoyl reductase of *E. coli* (PDB ID: 1C14)

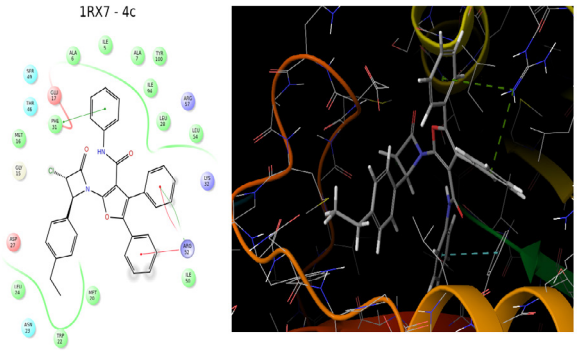


Figure 2: XP Docked pose of Compound 4c with DHFR of *E. coli* (PDB ID: 1RX7).

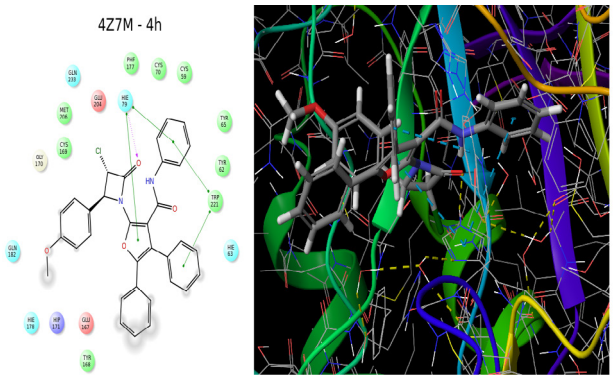


Figure 3: XP Docked pose of Compound 4h with methionine amiopepetidase (PDB ID: 4Z7M).

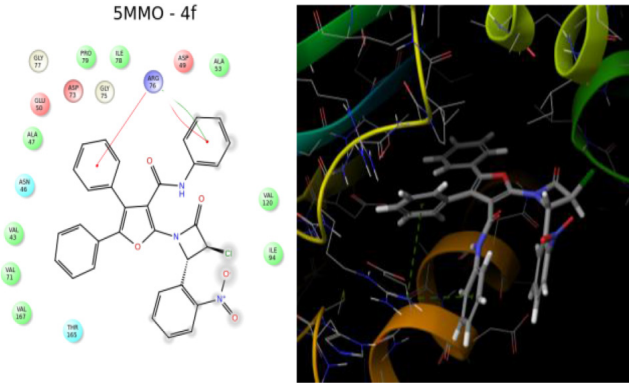


Figure 4: XP Docked pose of Compound 4f with DNA gyrase of *E. coli* (PDB ID: 5MMO).

Table 2: Molecular docking results of furan derivatives with protein 1C14 (enoyl reductase).

Compound Code	R	SP mode		XP mode		
		GScore	Emodel	GScore	Emodel	Interactions at active site
4e	2,4-dichloro	-8.955	-58.381	-9.195	-73.407	Tyr 146, Phe 94
Ciprofloxacin		-7.089	-53.006	-5.674	-49.544	Lys 163
Amoxacillin		-8.116	-75.563	-5.946	-56.025	Ala 196, Ala 95, Ile 192

Table 3: Molecular docking results of furan derivatives with protein IRX7 (DHFR).

Compound Code	R	SP mode		XP mode		
		GScore	Emodel	GScore	Emodel	Interactions at active site
4c	4-ethyl	-5.63	-64.336	-5.454	-68.698	Arg 52, Phe 31,
Trimethoprim		-6.187	-58.783	-7.385	-47.186	Asp 27, Glu 17, Trp 22, Leu 24
Ciprofloxacin		-6.039	-54.914	-7.19	-49.362	Asp 27
Amoxacillin		-6.738	-69.113	-6.739	-62.275	Ala 7, Asp 27, Glu 17, Trp 22

Table 4: Molecular docking of furan derivatives with protein 4Z7M (methionine aminopeptidase).

Compound Code	R	SP mode		XP mode		
		GScore	Emodel	GScore	Emodel	Interactions at active site
4h	4-methoxy	-6.988	-66.549	-7.606	-66.888	Hie 79, Trp 221
Ciprofloxacin		-5.578	-45.862	-6.895	-46.460	Asp 108, Ash 97, Glu 204, Hie 79
Amoxacillin		-4.113	-44.427	-6.828	-45.694	Asp 108, Ash 97, Glu 204, Hie 79, Hie 178, Phe 177,Cys 169

Table 5: Molecular docking results of furan derivatives with protein 5MMO (DNA gyrase).

Compound Code	R	SP mode		XP mode		
		GScore	Emodel	GScore	Emodel	Interactions at active site
4f	2-nitro	-5.48	-57.595	-4.803	-61.315	Arg 76
Ciprofloxacin		-5.416	-52.257	-4.235	-37.939	Val 43, Asp 73
Amoxacillin		-5.374	-52.296	-6.321	-48.115	Glu 50, Asp 73, Asn 46

Score -5.48, although that could be due to false positives.

CONCLUSION

Molecular docking studies were executed for all the novel furan derivatives on four antibacterial target proteins of *E. coli*. Energy minimization of title compounds was carried out, the proteins were optimized and minimized, a 3-dimensional grid was generated at the active site and molecular docking was carried out using the SP and XP docking modes of Glide module. The ligands were docked into the active site of the respective proteins. The molecules were ranked according to the results of the docking simulations- their docking scores (GScore) and their binding energy with the enzyme (Emodel). Usually good ligand affinity for the receptor may be expected for low Glide score. If the binding energy is less, compound is more active. The result obtained from molecular docking of title compounds with enoyl reductase of *E. coli* is quite promising. Compound 4e (2, 4 –dichloro derivative) showed the best inhibition of the enzyme. Hence it is predicted to have good antibacterial activity. The study executed by Glide postulates that all the ligands fit well into the binding pocket of the enzyme. Conformational examination of the various docked complexes also shows that residues TYR 146 and PHE 94 play an important role in the receptor's activity. From the docked poses, we may deduce that for successful docking, pi-pi stacking interactions between the ligand and the receptor are very important. The *in silico* predictions suggest that title compounds could be potential anti-bacterial drugs showing specificity in inhibiting the enoyl reductase enzyme of *E. coli*.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ACKNOWLEDGEMENT

Authors are thankful to "Pharmacological Modelling and Simulation Center" Ramaiah University of Applied sciences, for providing the facilities.

ABBREVIATIONS

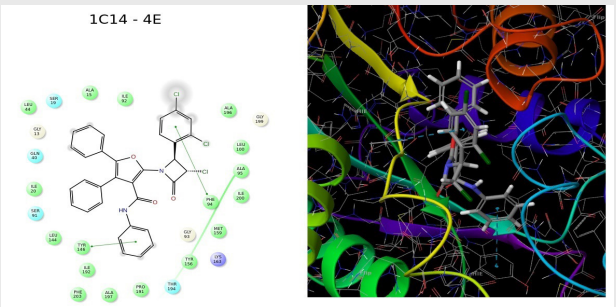
DHFR: Dihydrofolate reductase; **MetAP:** Methionine aminopeptidase; **DNA:** Deoxy ribonucleic acid; **SP:** standard Precision; **XP:** Extra precision; **PHE:** Phenylalanine; **TYR:** Tyrosine; **LYS:** Lysine; **ALA:** Alanine; **ILE:** Isoleucine; **ARG:** Arginine; **ASP:** Aspartic acid;

GLU: Gluatamine; **HIE:** Histidine; **TRP:** Tryptophan; **CYS:** Cysteine; **VAL:** Valine.

REFERENCES

1. Kennedy KJ, Roberts JL, Collinson PJ. *Escherichia coli* bacteraemia in Canberra: incidence and clinical features. Med J Aust. 2008;188(4):209-13.
2. Peter C. Resistant *Escherichia coli*-we are what we eat. Clin Infect Dis. 2009;49(2):202-4.
3. Laupland KB, Church DL, Vidakovich J, Mucenski M, Pitout JD. Community-onset extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli*: Importance of international travel. J Infect. 2008;57(6):441-8.
4. Saenz Y, Brinas L, Dominguez E, Ruiz J, Zarazaga M, Vila J, *et al*. Mechanisms of Resistance in Multiple-Antibiotic-Resistant *Escherichia coli* Strains of Human, Animal and Food Origins. Antimicrob Agents Chemother. 2004;10(10):3996-4001.
5. Banerjee R, Kumar HKS, Banerjee M. Medicinal significance of furan derivatives: A review. Int J Rev Life Sci. 2012;2(1):7-16.
6. Meotti FC, Silva DO, Santos ARS, Zeni G, Rocha JBT, Nogueira CW. Thiophenes and furans derivatives: A new class of potential pharmacological agents. Environ Toxicol Pharmacol. 2003;15(1):37-44.
7. Southgate R. The synthesis of natural β-lactam antibiotics. Contemp Org Synth. 1994;1(6):417-31.
8. Singh GS. β-Lactams in the New Millennium. Part-I: Monobactams and carbapenems. Mini Rev Med Chem. 2004;4(1):69-92.
9. Jays J, Mohan S, Saravanan J. Synthesis, characterization and antimicrobial screening of some novel furan-azetidinone hybrid compounds. Int J Pharma Bio Sci. 2018;9(1):79-87.
10. Sawaya MR, Kraut J. Loop and Subdomain Movements in the Mechanism of *Escherichia coli* Dihydrofolate Reductase: Crystallographic Evidence. Biochemistry. 1997;36(3):586-603.
11. Li X, Hilgers M, Cunningham M, Chen Z, Trzoss M, Zhang J. Structure-based design of new DHFR-based antibacterial agents: 7-aryl-2, 4-diaminoquinazolines. Bioorganic and Medicinal Chemistry Letters. 2011;21(18):5171-76.
12. Srinivasan B, Toddast-Navaei S, Skolnick J. Ligand binding studies, preliminary structure-activity relationship and detailed mechanistic characterization of 1-phenyl-6,6-dimethy-1,3,5-triazine-2,4-diamine derivatives as inhibitors of *Escherichia coli* dihyfrofolate reductase. European Journal of Medicinal Chemistry. 2015;103(10):600-14.
13. Heerding DA, Chan G, WolfJr WED, Fosberry AP, Ajanson C, Djaworski D, *et al*. 1,4-Disubstituted imidazoles are potential antibacterial agents functioning as inhibitors of enoyl acyl carrier protein reductase (FabI). Bioorg Med Chem Lett. 2001;11(16):2061-65.
14. Ling LL. Identification and characterization of inhibitors of bacterial enoyl-acyl carrier protein reductase. Antimicrob Agents Chemother. 2004;48(5):1541-7.
15. Rose JA, Lahiri SD, McKinney DC, Albert R, Morningstar M, Shapiro AB, *et al*. Novel broad-spectrum inhibitors of bacterial methionine aminopeptidase. Bioorg Med Chem Lett. 2015;25(16):3301-6.
16. Xiao Q, Zhang F, Nacev BA, Liu JO, Pei D. Protein N-terminal processing: substrate specificity of *Escherichia coli* and human methionine aminopeptidases. Biochemistry. 2010;49(26):5588-99.
17. Reece RJ, Maxwell A. DNA gyrase: Structure and function. Crit Rev Biochem Mol Biol. 1991;26(3):335-75.
18. Tse-Dinh YC. Targeting bacterial topoisomerases: How to counter mechanisms of resistance. Future Med Chem. 2016;8(10):1085-100.
19. Charrier C, Salisbury AM, Savage VJ, Duffy T, Moyo E, Chaffer-Malam N, *et al*. Novel Bacterial Topoisomerase Inhibitors with Potent Broad-Spectrum Activity against Drug-Resistant Bacteria. Antimicrob Agents Chemother. 2017;61(5):513-9.
20. Schrödinger: LigPrep software, version 2.5. New York NY LLC. 2011.
21. Beginning with Maestro. Schrödinger software release. LLC New York NY. 2015.
22. Schrödinger: Maestro, version 11. New York NY LLC. 2011.
23. Glide, version 6.7, User Manual. Schrödinger. LLC New York NY. 2015.
24. Friesner RA, Banks JL, Murphy RB, Halgren TA, Klicic JJ, Mainz DT, *et al*. Glide: A new approach for rapid, accurate docking and scoring. 1. Method and assessment of docking accuracy. J Med Chem. 2004;47(7):1739-49.
25. Halgren TA, Murph RB, Friesner RA, Beard HS, Frye LL, Pollard WT, *et al*. Glide: A new approach for rapid, accurate docking and scoring. 2. Enrichment factors in database screening. J Med Chem. 2004;47(7):1750-59.
26. Friesner RA, Murph RB, Repasky MP, Frye LL, Greenwood JR, Halgren TA, *et al*. Extra precision glide: docking and scoring incorporating a model of hydrophobic enclosure for protein-ligand complexes. J Med Chem. 2006;49(21):6177-96.

PICTORIAL ABSTRACT



2D and 3D docked pose of compound 4E with enoyl reductase of *E. coli*

SUMMARY

In silico molecular docking studies were carried out on a series of synthesized novel furan- azetidinone hydrids to identify potential inhibitors of *E. coli*. Many efforts at discovering new antimicrobials have been concentrated on biosynthetic enzymes. Hence four essential enzymes of *E. coli* were selected from the literature. Using the GLIDE module of Schrodinger, molecular docking studies were conducted on four antibacterial targets of *E. coli*; Dihydrofolate reductase, DNA gyrase, enoyl reductase and methionine aminopeptidase. The ligands were docked on to the active site of the enzymes. Ligands were ranked according to their docking scores and their binding energy with the enzyme. Docked poses were examined to study the interactions at the active site of the receptors. The results obtained for the molecular docking of the title compounds with enoyl reductase of *E. coli* is quite promising. The study suggests that compounds 4E and 4D are potential inhibitors of enoyl reductase and specifically bind to the enzyme.

About Authors

Judy Jays is an Assistant Professor in the Department of Pharmaceutical Chemistry, Faculty of Pharmacy, MS Ramaiah University of Applied Sciences, Bangalore, Karnataka. She has about 21 years of teaching experience. Her area of research is drug discovery using CADD tools, synthesis of novel heterocyclic compounds and their evaluation as antimicrobials. She has published several papers in national and international journals.

Dr. S Mohan is the Director of PES College of Pharmacy, Bangalore, Karnataka. He has 36 years of teaching experience. His research interest is the synthesis of some novel heterocycles of biological importance. He has numerous publications in national and international journals and guided several MPharm and Ph.D students.

Dr. J Saravanan is the principal of PES College of Pharmacy, Bangalore, Karnataka. He has 26 years of teaching experience. His research interest is the synthesis and characterization of some NCEs. He has guided several MPharm and Ph.D students and have a number of publications in national and international journals to his credit.

Cite this article: Jays J, Mohan S, Saravanan J. Molecular Docking Studies of Novel Furan-azetidinone Hybrids as Potential Inhibitors of *Escherichia coli.* Indian J of Pharmaceutical Education and Research. 2019;53(3 Suppl 2):s325-s331.