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Original Article

Design, Synthesis and Biological Screening of Novel Carbazole Tethered Oxyethylamino Derivatives as Antimicrobial Agent

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ABSTRACT

Background: Carbazole is an important scaffold known to be associated with several biological activities including antimicrobial activities. Incorporation 4-oxothiazolidine moiety in carbazole moiety may lead to a new series of antimicrobials compounds. **Aim:** In this study, design and synthesis of novel carbazole tethered oxyethylamino was started with carbazole as basic pharmacophore and evaluated for antimicrobial activity. **Materials and Methods:** Molecular docking of carbazole derivatives was carried out by Schrödinger (Maestro 10.5v) active compound were Synthesized and screened for *in vitro* antimicrobial activity against *Candida albicans* and gram-positive and gram-negative bacterial strains such as *Staphylococcus aureus, Bacillus subtilis, E. coli.* MIC was calculated by standard agar tube dilution method. **Results:** All Compounds shown good antimicrobial activity at 25 (µg/ml) – 510 (µg/ml). The molecular docking studies demonstrated ligand protein interaction. **Conclusion:** carbazole represent novel set of lead for the designing of novel antimicrobial agents.

Keywords: Molecular Docking, Carbazole, Oxyethylamino, Antimicrobial activity, Antifungal activity.

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INTRODUCTION

Carbazole is tricyclic heterocyclic aromatic organic compound. It is considered as potential building block for synthesis of bioactive compounds and prominent pharmacophore which mostly found as essential in many plants' origin compound like alkaloid.[1-3] Carbazole and its derivative have attributed promising biological activities such as anti-inflammatory,[4] antitumor, anti-diabetic,[5] anti-oxidant,[6] anti-tubercular, anti-bacterial,[7] anti-fungal,[8] and anti-histaminic activity.[9] According to Drissa new carbazole alkaloids named calothrixins from cell extracts of cyanobacterial Calothrix species. They showed a unique indolo [3, 2-j] phenanthridine ring system, in antiplasmodial and anticancer assays at nanomolar concentrations it exerts *in vitro* growth inhibitory.[10] Kucukguzel reported a series of novel synthesis, characterization and screening of 1, 3-thiazolidine-4-ones derived from 1-[2-(benzoylamino)-4-(methylthio) butyryl]-4-alkyl/ arylalkyl thiosemicarbazides which is then evaluated for antimicrobial, antituberculosis, antiviral and anticancer activity.[11]

Molecular docking leads an important tool for drug design and discovery.[12] S. Vasanthkumar and coworkers in their studies have shown synthesis of 1, 4-naphthoquinone derivatives containing carbazole-6, 11-dione moiety and the molecular docking of all the synthesized compounds were carried out by using (version 8.5, Schrodinger, LLC), the aim of this study was to evaluate the *in vitro* antibacterial activity against different Gram-positive and Gram-negative bacteria.[10,13]

MATERIALS AND METHODS

All reagents are analytical reagent grade used were procured commercially from S.D. Fine chemicals, Spectrochem and Qualigens. Chemicals and solvents were purified by distillation according to conventional procedures before use. All moisture free operations were performed in oven dried glassware's. Melting points were measured using VEEGO make microprocessor apparatus and are uncorrected. NMR spectra were measured in BRUKER AVANCE II in DMSO with TMS as internal standard at 400 MHz instrument, Chemical shift values are mentioned in δ, ppm. Mass spectra were carried out on Shimadzu LC MS 2010 spectrometer. BRUKER ALPHA T FT-IR spectrophotometer were used for recording IR spectra (wave numbers in cm^{-1}) using potassium bromide discs. TLC on 2 cm X 5 cm pre-coated silica

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gel 60 F_{254} (Merck) plates of thickness of 0.25 mm were used for monitoring of reaction.

Molecular Docking Study

Molecular docking study was carried out by Schrödinger software (Maestro10.5) in order to develop selective antimicrobial agents. The molecules were docked on the DNA gyrase protein enzyme (PDB ID: 1KZN) and Lanosterol 14α-demethylase protein enzyme (PDB ID: 1EA1) retrieved from the Protein Data Bank (www.rscb.org).

Ligand Preparation

The two-dimensional structures were drawn in 2D Sketcher in MAESTRO workspace using build panel. Three-dimensional ligand preparation was done by using LigPrep panel application and optimize the structure by minimizing its energy through OPLS-3 force field.

Protein Preparation and Minimization

In Protein preparation X ray crystalline structures of DNA Gyrase and Lanosterol 14-α-Demethylase proteins were imported from Protein Data Bank with PDB ID (1KZN and1EA1) respectively. Through protein preparation Wizard protein structures were refine, minimize and optimized.

Receptor Grid Generation

Grid generation required to be performing prior to running a virtual screen with glide. The shape and properties of the receptor has represented in a grid by field that provides progressively more accurate scoring of the ligand poses.

Validation of Protein

Validation of DNA Gyrase and Lanosterol 14-α-Demethylase protein to test the reliability and reproducibility of the docking protocols for the study was shown by Ramachandran Plot.

Molecular Docking

The ligand docking was done flexibly using Standard Precision (SP) mode of GLIDE module and further refinement was done by using extra precision (XP) mode. The ligand docking process helps to predict ligand conformation and orientation within a targeted binding site and thus results in an accurate structural modeling and correct prediction of activity of ligands.

Chemical Work

Scheme

General Procedure

As mentioned in Figure 1 Intermediate 1 (a-f) were obtained by reacting chloroacetyl chloride (10 ml, 0.09 moles) with carbazole (5.00 g, 0.02 mole) in dry acetone by refluxing for 4 hr to get 1-(9H-carbazole-9-yl)-2-chloroethanone, further reacted with Hydrazine hydrate (1.73 ml, 0.05 moles) in ethanol: dioxane 18:2 v/v (9:1 v/v) to get 1-(9*H*-Carbazole-9-*yl*)-2-hydrazinylethanone, further reacted with substituted benzaldehyde. Compound 2 (a-f) were synthesized by cyclization of compound 1 with thioglycolic acid.[14]

Biological Work

The microbiological assay is based upon measurement of minimum Inhibitory Concentration (MIC) to check the lowest concentration of the compound at which visible growth of microorganism was inhibited. The assay was tested against *Staphylococcus aureus* (Gram positive), *Bacillus subtilis* (Gram positive), *E. coli* (Gram Negative) bacteria's and *C. albicans* fungi including Streptomycin and Chloramphenicol as reference standard. Procedure for all over the assay was followed as per reported procedure.[15]

RESULTS AND DISCUSSION

Synthesis and Characterization

Naturally carbazole is an alkaloid, tricyclic scaffold with large number of pharmacological profiles. The current work emphasized on synthesis of novel carbazole derivatives as antibacterial and antifungal activities with molecular docking studies. Our scheme was initiated with carbazole which was condensed with reactive chloroacetyl chloride with formation of 1-(9H-carbazol-9-yl)-2-chloroethanone, reactive towards hydrazine hydrates with formation of second intermediate (1-9H-carbazol-9-yl)-2-hydrazinyl ethanone) further second intermediate reacted with substituted benzaldehyde, in solvent ethanol with formation of compound 1 (a-f), having benzylidenehydrazineyl moiety. Aldehyde is very reactive towards hydrazine and carbazole doesn't has any substitution from starting, so the formation of compound 1 (a-f) was confirmed by TLC, and was further confirmed by spectral analysis. After having compound 1 (a-f), a series of novel carbazole derivatives (2a-2f), were synthesized and characterized. All carbazole derivatives (2a-2f) prepared by stirring compound 1(a-f) with thioglycolic acid, ethylidine cyclized to thiazolidinone scaffold in final carbazole derivatives. Completion of reaction was confirmed by TLC, crystallized with suitable solvent and column chromatography used for purification of the compounds with silica gel (60-120 mesh). Analysis of compounds were done by spectral analysis that is elemental analysis, IR, ^{1}HNMR, ^{13}C NMR, MS, was supporting successful analysis of (2a-2f).

IR spectra of compound 1 (a-f) showed absorbance at 3345 cm^{-1} for secondary amine and peaks at 3356 cm-1 (asymmetric stretching) and 3313 cm^{-1} (symmetric stretching) for primary amine were disappeared, C-N stretching observed at 1245 cm^{-1}, peak for carbonyl was observed at 1660 cm^{-1}, in 1(a-f) additional peaks observed at 810 cm^{-1} for C-Cl, 1260 cm^{-1} for methyl, 1550 cm^{-1} for NO_2, 2810 cm^{-1} for methoxy, 660 cm^{-1} for C-Br. IR

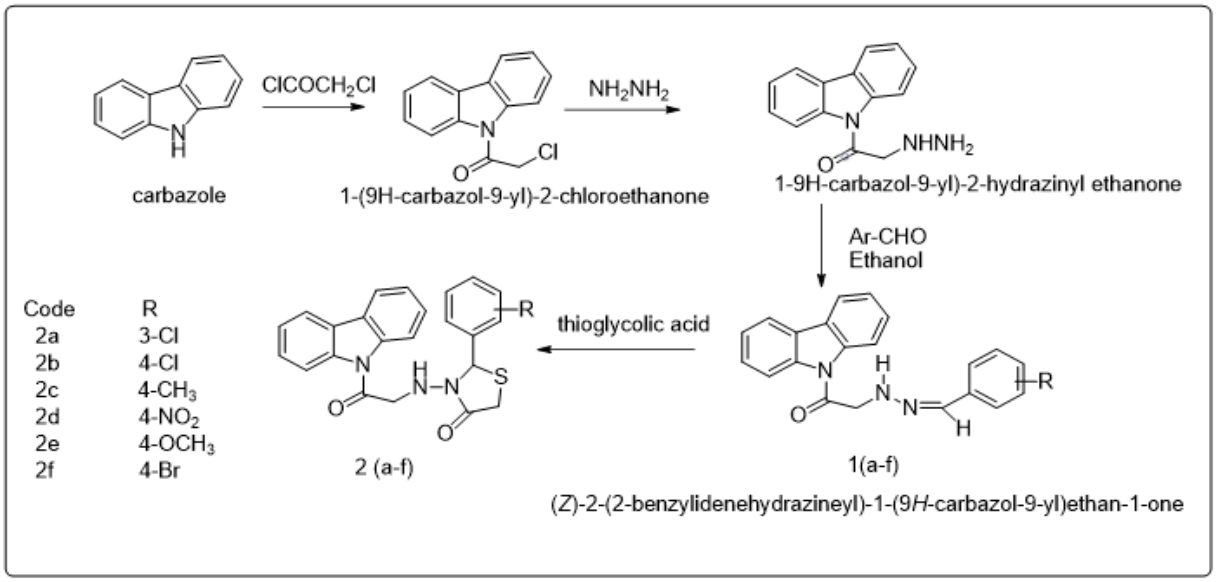

Figure 1: Scheme for the synthesis of Carbazolyl thiazolidin-2-one derivatives.

spectra of compounds 2 (a-f) showed absorbance at 3332 cm^{-1} for secondary amine, C-N stretching observed at 1240 cm^{-1}, Carbonyl peak observed at 1670 cm^{-1} in compound 2a additional peak observed at 840 cm^{-1} for C-Cl, in NMR signal shift at downfield region, H-5 and H-3 of phenyl ring appeared at same ppm at δ7.8 as three doublet due to substitution of 4-Cl. Three doublets at δ7.38 corresponds to H-2 and H-6 due to substitution of thiazolidinone moiety. In Mass spectrum base peak was appeared at 436 (MH^+). In compound 2d, absorbance at 1560 cm^{-1} observed in IR spectrum for C-NO_2, in NMR signal shifted towards downfield region, where H-5 and H-3 appeared at same ppm, at δ 7.54 as three doublets, due to the substitution of C-NO_2 at C-4 of phenyl ring, three doublets at δ 8.20 corresponds to H-2 and H-6 due to substitution of thiazolidinedione moiety. In mass spectrum base peak appeared at 447 (MH^+). In compound 2e, absorbance at 2850 cm^{-1} observed in IR spectrum for C-OCH_3, in NMR, signal shifted towards downfield region, where H-5 and H-3 appeared at same ppm, at δ 6.89 as three doublets, due to the substitution of C-OCH_3 at C-4 of phenyl ring, three doublets at δ 7.83 corresponds to H-2 and H-6 due to substitution of thiazolidinedione moiety. In mass spectrum base peak appeared at 430 (MH^+).

In compound 2f, absorbance at 680 cm^{-1} observed in IR spectrum for C-Br, in NMR, signal shifted towards downfield region, where H-5 and H-3 appeared at same ppm, at δ 7.17 as three doublets, due to the substitution of C-Br at C-4 of phenyl ring, three doublets at δ7.85 corresponds to H-2 and H-6 due to substitution of thiazolidinedione moiety. In mass spectrum base peak appeared at 481 (MH^+).

Anal. Calcd. for 3-((2-(9H-carbazol-9-yl)-2-oxoethyl)amino)-4-(4-chlorophenyl)thiazolidin-2-one ($C_{23}H_{18}ClN_3O_2S$) (2b)

C,63.37; H, 4.16; Cl, 8.13; N,9.64; O,7.34; S,7.35; IR (KBr, cm^{-1}) 3132, 1621, 1400, 820, ^{1}H NMR (DMSO) δ: 7.54 (2H, aromatic proton), 7.56 (2H, aromatic proton), 6.3 (1H, triazole proton, s), 3.85(2H, Methylene, s), 3.81(1H, triazole proton, s), 4.2 (s, NH), 7.8(2H, aromatic proton), 7.38 (2H, aromatic proton), 7.53(2H, aromatic proton), 7.98 (2H, aromatic proton), ^{13}CNMR (DMSO) δ: 115.6, 124.3, 119.8, 121.4, 125.1, 138, 125.1, 138, 121.4, 119.8, 124.3, 115.6, 168.3, 50, 164.9, 32.7, 62.0, 141.6, 127.2, 127.2, 128.6, 128.6, 132.3, MS(m/z) 436 (MH^+), m.p.: 177-180°C.

Anal. Calcd. for 3-((2-(9H-carbazol-9-yl)-2-oxoethyl)amino)-2-(4-nitrophenyl)thiazolidin-4-one, ($C_{23}H_{18}O_4N_4S$) (2d)

C, 61.87; H, 4.06; N, 12.55; O, 14.33; S, 7.18 IR (KBr, cm^{-1}) 3133, 1601, 1400, ^{1}H NMR (DMSO) δ: 4.2 (s, NH), 5.92 (s CH Thiazole proton), 3.80, 3.70 (s, CH_2, Thiazole proton), 7.54, 8.20, (4H aromatic proton), 7.97(2H, aromatic proton), 7.38(2H, aromatic proton), 7.53(2H, aromatic proton), 7.9 (2H, aromatic proton), 3.85(s, 2H, CH_2), ^{13}CNMR (DMSO) δ: 115.6, 124.3, 119.8, 121.4, 125.1, 138, 125.1, 138, 121.4, 119.8, 124.3, 115.6, 168.3, 49.3, 168.8, 35.9, 64.1, 145.3, 129.6, 123.8, 146.3, 123.8, 129.5 MS(m/z) 447 (MH^+), m.p.: 166-170°C.

Anal. Calcd. for 3-((2-(9H-carbazol-9-yl)-2-oxoethyl)amino)-2-(4-methoxyphenyl)thiazolidin-4-one ($C_{24}H_{21}N_3O_3S$) (2e)

C, 66.80; H, 4.91; N, 9.74; O, 11.12, S, 7.42, IR (KBr, cm^{-1}) 3112, 1619, 1404, 1215, ^{1}H NMR (DMSO) δ: 4.2 (s, NH), 5.92 (s CH

Thiazole proton), 3.80, 3.70 (s, CH_2, Thiazole proton), 6.89, 7.83, (4H aromatic proton), 3.81 (s, OCH_3), 7.97(2H, aromatic proton), 7.38(2H, aromatic proton), 7.53(2H, aromatic proton), 7.9 (2H, aromatic proton), 3.85(s, 2H, CH_2), ^{13}CNMR (DMSO) δ:119.8,124.3, 115.6, 138.0, 121.4, 125.1, 125.1, 121.4, 119.8, 128.6, 124.3, 126.9, 139.2, 115.6, 138.0, 61.5, 168.3, 49.3, 168.8, 42.8, 126.9, 128.6, 127.1, 55.8, 159.5, 114.8, 114.8, 131.9, 131.9, 127.1 MS(m/z) 430 (MH^+), m.p.: 160-162°C.

Anal. Calcd. for 3-((2-(9H-carbazol-9-yl)-2-oxoe thyl)amino)-2-(4-bromophenyl)thiazolidin-4-one ($C_{23}H_{18}BrN_3O_2S$) (2f)

C, 57.51; H, 3.78; Br, 16.63; N, 8.75; O, 6.66; S, 6.67, IR (KBr, cm^{-1}) 3133, 1601, 1400, 601, ^{1}H NMR (DMSO) δ: 4.2 (s, NH), 5.92 (s CH Thiazole proton), 3.80, 3.70 (s, CH_2, Thiazole proton), 7.17, 7.85, (4H aromatic proton), 7.97(2H, aromatic proton), 7.38(2H, aromatic proton), 7.53(2H, aromatic proton), 7.9 (2H, aromatic proton), 3.85(s, 2H, CH_2), ^{13}CNMR (DMSO) δ: 115.6, 124.3, 119.8, 121.4, 125.1, 138, 125.1, 138, 121.4, 119.8, 124.3, 115.6, 168.3, 49.3, 186.8, 35.9, 64.1, 138.2, 130.9, 131.5, 130.9, 131.5, 121.5 MS(m/z) 481 (MH^+), m.p.: 169-172°C.

Molecular Docking

In molecular Modelling, molecular docking is one of the tools which predict the possible orientation of one molecule to another molecule, after bound to each other to form the stable complex, where free binding energy is calculated in the form of Glide score. In this work molecular docking of total 13 compounds were done in Schrodinger software (Maestro 10.5v) against DNA Gyrase (PDB-1KZN) and Lanosterol 14-α-Demethylase proteins (PDB-1EA1) for antibacterial and antifungal activities respectively. All compounds have shown good interaction with imported proteins against standard. Compound 2e with C-OCH_3

Table 1: Result of Molecular Docking Analysis (Glide score).

Compound Code	Substitution (R)	Glide Score (1KZN)	Glide Score (1EA1)
2a	3-Cl	-4.231	-5.435
2b	4-Cl	-4.374	-4.786
2c	4-CH_3	-4.890	-5.346
2d	4-NO_2	-5.120	-7.854
2e	4-OCH_3	-6.213	-8.112
2f	4-Br	-3.325	-6.576
2g	4-OH	-4.645	-5.678
2h	4-CF_3	-3.536	-4.478
2i	3,4,5-OCH_3	-4.345	-5.768
2j	2,4-Cl	-5.108	-7.768
2k	3-NH_2	-3.167	-3.124
2l	4-NH_2	-3.107	-3.245
2m	4-F	-4.243	-5.345
Chloramphenicol	-	-5.110	-
Fluconazole	-	-	-7.789

Table 2: Results of Anti-Microbial Study.

Tested Compounds	*S. aureus*		*B. subtilis*		*E. coli*		*C. albicans*	
	MIC_{50}	MIC_{100}	MIC_{50}	MIC_{100}	MIC_{50}	MIC_{100}	MIC_{50}	MIC_{100}
2a	255	510	510	510	250	500	55	110
2b	75	150	125	250	250	500	25	50
2c	25	50	125	250	255	510	25	50
2d	255	510	510	510	25	50	25	25
2e	510	510	255	510	250	500	55	110
2f	255	255	255	510	75	150	55	55
Streptomycin	75	75	75	150	75	150	25	25
Ketoconazole	-	-	-	-	-	-	15	30

DMSO Negative control

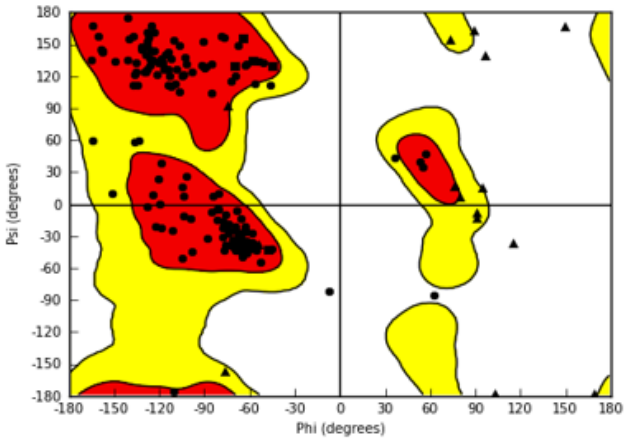

Figure 2: Ramachandran Plot for DNA Gyrase Enzyme (PDB ID- 1KZN).

substitution have shown highest G-Score (-6.213), (-8.112) on 1KZN and 1EA1 respectively, followed by compound 2d with C-NO_2 substitution as illustrated in Table 1 and Figure 2. On the basis of G-Score top ranked compounds were selected for the synthesis.

Antimicrobial study

All novel carbazole derivative were evaluated for their antibacterial and anti-fungal activity against *S. aureus, B. subtilis, E. coli* and *C. albicans* respectively. The minimum inhibitory concentration of every compound was determined by standard agar dilution method with streptomycin and Ketoconazole as reference. Compound 2c (with CH_3 substitution at C-4)

Shown excellent activity against *S. aureus*, remaining compound also shown good to moderate activity against *S. aureus*. Compound 2b (with Cl substitution at C-4) and 2c (with CH_3 substitution at C-4) were strongly active against *B. subtilis*. Compound 2d (with NO_2 substitution at C-4) was strongly active against *E. coli* and *C. albicans*, remaining compound also shown good to moderate antifungal activity as shown in Table 2.

CONCLUSION

Present work emphasized on design, synthesis and evaluation of novel carbazole derivative. The molecule with carbazole moiety already known to possess wide range of pharmacological activities. The research focused on synthesizing potential antimicrobial agents as new antimicrobial agent are urgently required and carbazole represent novel set of lead. In future structural modification of compound may allow development of pharmacologically acceptable compounds.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

ABBREVIATIONS

NMR: Nuclear magnetic resonance; **LC-MS:** Liquid chromatography-Mass spectrometry; **FT-IR:** Fourier Transform infrared spectroscopy; **MIC:** Minimum inhibitory concentration; **TMS:** Tetramethylselane; **TLC:** Thin layer chromatography.

SUMMARY

- Being a potential pharmacophore carbazole for antimicrobial activities a series was made for their possible activities in present studies.
- Molecular docking studies showed good results
- All Compounds shown good antimicrobial activity at 25 (µg/ml) – 510 (µg/ml).
- Synthesis of novel carbazole tethered oxyethylamino was started with carbazole as basic pharmacophore and evaluated for antimicrobial activity.

REFERENCES

1. Bashir M, Bano A, Ijaz AS, Chaudhary BA. Recent developments and biological activities of N-substituted carbazole derivatives: A review. Molecules. 2015;20(8):13496-517. doi: 10.3390/molecules200813496, PMID 26213906.
2. Burckhalter JH, Stephens VC, Hall LAR. Antihistaminics: The N-beta-dimethylaminoethyl derivatives of carbazole and diphenylamine. J Am Pharm Assoc Am Pharm Assoc. 1950;39(5):271-3. doi: 10.1002/jps.3030390508, PMID 15421917.
3. Ho FM, Lai CC, Huang LJ, Kuo TC, Chao CM, Lin WW. The anti-inflammatory carbazole, LCY-2-CHO, inhibits lipopolysaccharide-induced inflammatory mediator expression through inhibition of the p38 mitogen-activated protein kinase signaling pathway in macrophages. Br J Pharmacol. 2004;141(6):1037-47. doi: 10.1038/sj.bjp.0705700, PMID 14980980.
4. Jejurkar VP, Mali SN, Kshatriya R, Chaudhari HK, Saha S. Synthesis, antimicrobial screening and in silico appraisal of Iminocarbazole derivatives. ChemistrySelect. 2019;4(32):9470-5. doi: 10.1002/slct.201901890.
5. Kazmi M, Khan I, Khan A, Halim SA, Saeed A, Mehsud S, et al. Developing new hybrid scaffold for urease inhibition based on carbazole-chalcone conjugates: Synthesis, assessment of therapeutic potential and computational docking analysis. Bioorg Med Chem. 2019;27(22):115123. doi: 10.1016/j.bmc.2019.115123, PMID 31623971.
6. Meng XY, Zhang HX, Mezei M, Cui M. Molecular docking: A powerful approach for structure-based drug discovery. Curr Comput Aided Drug Des. 2011;7(2):146-57. doi: 10.2174/157340911795677602, PMID 21534921.
7. Patel AB, Chikhalia KH, Kumari P. An efficient synthesis of new thiazolidin-4-one fused s-triazines as potential antimicrobial and anticancer agents. J Saudi Chem Soc. 2014;18(5):646-56. doi: 10.1016/j.jscs.2014.02.002.
8. Prasad D, Kumar A, Shukla PK, Nath M. Design, synthesis and antimicrobial evaluation of novel 2-aryl-thiazolidin-4-one derivatives. Org Med Chem Lett. 2011;1(1):4. doi: 10.1186/2191-2858-1-4, PMID 22373323.
9. Raj K, Misra N, Pachauri G, Sharma M, Tamrakar AK, Singh AB, *et al.* Novel class of hybrid natural products as antidiabetic agents. Nat Prod Res. 2009;23(1):60-9. doi: 10.1080/14786410701824940, PMID 19140071.

10. Ravichandiran P, Premnath D, Vasanthkumar S. Synthesis, molecular docking and antibacterial evaluation of new 1,4-naphthoquinone derivatives contains carbazole-6,11-dione moiety. J Chem Biol. 2014;7(3):93-101. doi: 10.1007/s12154-014-0115-z, PMID 25077006.
11. Saini N, Sharma A, Thakur VK, Makatsoris C, Dandia A, Bhagat M, *et al*. Microwave assisted green synthesis of thiazolidin-4-one derivatives: A perspective on potent antiviral and antimicrobial activities. Curr Res Green Sustain Chem. 2020;3. doi: 10.1016/j.crgsc.2020.100021, PMID 100021.
12. Salih N, Salimon J, Yousif E. Synthesis and antimicrobial activities of 9H-carbazole derivatives. Arab J Chem. 2016;9:S781-6. doi: 10.1016/j.arabjc.2011.08.013.
13. Tatar E, Küçükgüzel İ, Clercq ED, Şahin F, Güllüce M. Synthesis, characterization and screening of antimicrobial, antituberculosis, antiviral and anticancer activity of novel 1,3-thiazolidine-4-ones derived from 1-[2-(benzoylamino)-4-(methylthio) butyryl]-4-alkyl/arylalkyl thiosemicarbazides. Arkivoc. 2008(14):191-210. doi: 10.3998/ark.5550190.0009.e19.
14. Yaqub G, Hannan A, Akbar E, Usman M, Hamid A, Sadiq Z, *et al*. Synthesis, antibacterial, and antifungal activities of novel pyridazino carbazoles. J Chem. 2013;2013:1-7. doi: 10.1155/2013/818739.
15. Zhang Y, Tangadanchu VKR, Cheng Y, Yang RG, Lin JM, Zhou CH. Potential antimicrobial isopropanol-conjugated carbazole azoles as dual targeting inhibitors of Enterococcus faecalis. ACS Med Chem Lett. 2018;9(3):244-9. doi: 10.1021/acsmedchemlett.7b00514, PMID 29541368.

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