

RESEARCH ARTICLE

Synthesis, Characterization and Molecular Docking Studies of Benzyl Scaffold Bearing 1, 3, 4-oxadiazole as Promising Antimicrobial Agents

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ABSTRACT

Background: The derivatives of heterocyclic ring 1,3,4-Oxadiazole are used as an antimicrobial agent for the treatment of microbial infections.

Objective: In this study, a new series of benzyl moiety possessing 1,3,4-oxadiazole derivatives have been synthesized by the reaction of 4-(benzylamino) benzohydrazide with substituted aromatic acids in the presence of cyclizing agent phosphorus oxychloride.

Method: The structures of synthesized compounds were analyzed by chromatographic data and characterized by spectral analysis (FT-IR, ¹H-NMR, C¹³NMR and mass spectrum). All synthetic derivatives were evaluated for their *in-vitro* antimicrobial activity against selected microbial strains; few listed in “priority pathogens” by World Health Organization (WHO). Antibacterial activity of synthetic compounds were assayed against two gram-positive strains *Bacillus subtilis*, *Escherichia coli*, and two gram-negative strains *Staphylococcus aureus*, *Pseudomonas aeruginosa*. Antifungal activity of synthetic compounds was screened against *Candida albicans* and *Aspergillus spp*. The potent derivatives were subjected to in-silico molecular docking studies with enzyme peptide deformylase.

Results and discussion: *in-vitro* antimicrobial assay indicated that compounds 1f, 1j, 1i, 1h and 1g exhibited good antimicrobial activity as compared to commercially available antibiotics Cefixime and Econazole drugs.

Conclusion: In this novel series of benzyl moiety containing 1,3,4-oxadiazole derivatives, five compounds exhibited potent antimicrobial activity against selected microbial strains.

Keywords: Benzyl, priority pathogens, *in-vitro* antimicrobial activity, in-silico molecular docking study, peptide deformylase, WHO.

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INTRODUCTION

Molecular modification^{1,2} of a previously known lead structure is the most suitable approach for the discovery of a new structure with an improved pharmacokinetic profile and therapeutic effect.³ Antimicrobial agents are widely used for the treatment of microbial infections in humans and animals.⁴ Due to excessive use of antimicrobial drugs, antimicrobial resistance is a serious problem in both human and animal medicine, adapted by various mechanism.^{5,6} Hence, considering the future aspects of antimicrobials, screening of novel structures is a substantial need for new and potent antimicrobial agents with minimum toxic effects.^{7,8} Heterocyclic derivatives have attracted attention of researchers due to their many medicinal values.⁹ Oxadiazoles are five-

membered heterocyclic compounds bearing two nitrogen and one oxygen atom.¹⁰ Among them, 1,3,4-oxadiazole have shown a broad range of pharmacological properties including antiviral¹¹, antineoplastic,¹² anti-mycobacterium,¹³ anti-inflammatory,¹⁴ and antimicrobial activities. During the last few decades, many researchers reported new antimicrobial agents having 1,3,4-oxadiazole ring.¹⁵⁻¹⁷

As per a previous literature survey gram-positive bacterial pathogens are not readily resistant to antimicrobial agents as compared to gram-negative bacterial pathogens.¹⁸ These differences in resistance mechanism may be due to their distinctive cell wall composition.¹⁹ Gram-negative bacteria have a multilayered cell wall and a specific periplasmic space in the outer cell membrane, which is not present in gram-positive

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bacterial pathogens.²⁰ Hence, the gram-negative bacterial cell wall is more lipophilic in contrast to gram-positive bacteria.²¹ WHO has published a list of antibiotic-resistant pathogens hazardous for human in 2017. In WHO list, the maximum number of priority pathogens belongs to gram negative bacteria category.²²

Computational techniques or virtual screening (VS) are important ways for drug designing and pharmacophore identification.^{23,24} In-silico molecular docking is one of the basic approaches for structural based drug design, which has been used since the 1980s.^{25,26} Computer programs based on various algorithms have been developed to perform molecular modeling as well as molecular docking studies.^{27,28} So, computational studies and other bioinformatics tools are highly effective steps in drug design and discovery.^{29,30} Molecular docking studies requires two basic components viz. ligand and active site of selected / target protein.³¹

Peptide deformylase (PDF) is an active and specific mononuclear iron-containing enzyme, belongs to the subclass of the metalloprotease category.^{32,33} This enzyme is required for protein maturation by removal of N-formyl group from N-terminal methionine polypeptide chain through iron-mediated catalysis.^{34,35} Peptide deformylase is vital and extremely conserved enzyme in various bacterial pathogens but it is not essential for protein synthesis in eukaryotic cells³⁶ and hence it is an interesting target for creating new antibacterial agents.^{37,38}

This research paper reports the synthesis of a novel series of benzyl moiety contains 2,5-disubstituted 1,3,4-oxadiazole derivatives and evaluation of their antimicrobial activity supported with molecular docking studies using peptide deformylase as target enzyme.

MATERIALS AND METHODS

Chemistry

Synthetic approach for a series of 2,5-disubstituted 1,3,4-oxadiazole analogs holding benzyl moiety is depicted in Scheme-1. The *para* aminobenzoic acid was used as a starting

material and masking the carboxylic group by esterification process (Fischer method) before benzylation.^{39,40} Benzylated product was converted into respective hydrazide by using hydrazine hydrate through simple reactions. Further, respective hydrazide was made to react with various substituted aromatic acids in the presence of cyclo-dehydrating agent POCl₃ under specified conditions and the desired products were obtained. The completion of reactions and purity of synthesized compounds were examined by thin-layer chromatography (TLC) method. The synthetic strategy for obtaining benzyl moiety bearing 2,5-disubstituted 1,3,4-oxadiazole derivatives is depicted in Scheme-1.

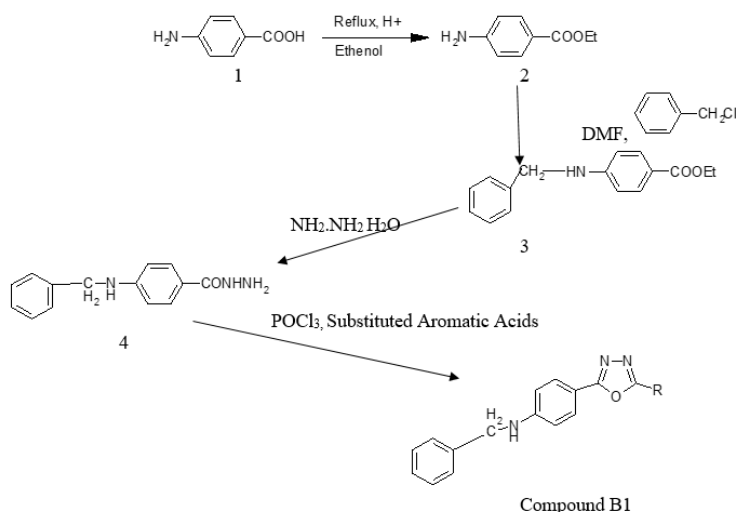
Experimental Methods

Chemical reagents and solvent were procured from local commercial suppliers. Silica gel G coated TLC plate was used for reaction monitoring and for identification of retardation factor (*R_f*) values with hexane, ethyl acetate and ethanol as a mobile phase. Spot visualization of TLC plate was done by iodine chamber. Melting points of synthesized compounds were determined by open capillary method using digital melting point apparatus and found uncorrected. The λ_{max} of synthesized compounds was obtained by using double beam UV-visible spectrophotometer (Shimadzu Pharma Spec 1700). The physical descriptions and UV data of synthesized compounds are given in Table 1. The Perkin Elmer IR spectrometer was used for obtaining IR spectra using the KBr pellet method. Mass spectra were obtained through a mass spectrometer by the ESI method. ¹H NMR and ¹³C NMR spectra were recorded by operating 400 MHz JNM-ECS spectrometer using DMSO-D₆, showing chemical shift values on δ ppm scale. Auto Dock Vina version software was applied for molecular docking studies.

General procedure for synthesis of N-benzyl-4-[5-(pyridine-4-yl)-1,3,4-oxadiazol-2-yl]aniline (B1 a-j)

• Synthesis of 4-amino benzoic Acid Ethyl Ester

To ethanolic solution of PABA (0.1mol), concentrated H₂SO₄ (1 ml) was added drop-wise. The reaction mixture was gently



Scheme 1: for synthesis of 1,3,4-oxadiazole derivatives.

Compound no.	R	Compound no.	R
B1a		B1f	
B1b		B1g	
B1c		B1h	
B1d		B1j	
B1e		B1i	

Table 1: Analytical description of synthesized 2,5 disubstituted Oxadiazole derivatives

S.No	Comp.	Molecular Formula	Solubility	R _f Value	λ _{max} (nm)
1	B1 a	C ₂₀ H ₁₆ ON ₄	DMSO,Ethanol,CHCl ₃	0.52	271
2	B1 b	C ₂₂ H ₁₇ O ₃ N ₃	DMSO,Ethanol,CHCl ₃	0.69	277
3	B1 c	C ₂₁ H ₁₇ O ₂ N ₃	DMSO,Ethanol,CHCl ₃	0.64	276
4	B1 d	C ₂₃ H ₁₉ O ₃ N ₃	DMSO,Ethanol,CHCl ₃	0.34	271
5	B1 e	C ₂₁ H ₁₇ ON ₃	DMSO,Ethanol,CHCl ₃	0.39	263
6	B1 f	C ₂₁ H ₁₅ O ₅ N ₅	DMSO,Ethanol,CHCl ₃	0.52	320
7	B1 g	C ₂₁ H ₁₆ O ₃ N ₄	DMSO,Ethanol,CHCl ₃	0.48	291
8	B1 h	C ₂₁ H ₁₈ ON ₄	DMSO,Ethanol,CHCl ₃	0.46	320
9	B1 i	C ₂₂ H ₁₉ O ₂ N ₃	DMSO,Ethanol,CHCl ₃	0.68	277
10	B1 j	C ₂₂ H ₁₉ ON ₃	DMSO,Ethanol,CHCl ₃	0.51	263

Mobile Phase for TLC: Hexane: Ethyl acetate: Ethanol (5:3:2); λ_{max} in Ethanol

refluxed for 60–75 minutes, then cooled, poured in 30 mL ice-cold water and then slowly added 10% Na₂CO₃ solution to make the mixture neutral to slightly basic (approx. pH 8). The resulting solid was filtered, dried, and recrystallized from ethanol to obtain ester compound 1 (Lit. Reported MP 90-92°C)

General Procedure for the Synthesis of 4-(benzyl amino) benzoic Acid Ethyl Ester

Taken solution of compound 1 (1g) and KOH (0.6g) in DMF (20 mL) and added benzyl chloride (1.5mL) drop-wise at low temperature. The reaction mixture was refluxed for appropriate time. The completion of reaction was checked by TLC. After the completion of the reaction, the reaction mixture was poured in to a separating funnel containing 20mL ethyl acetate. Mixture was shaken vigorously and allowed to stand for some time forming two separate layers. Upper layer was collected and neutralized by using sodium carbonate solution. Finally DMF was distilled off and desired compound 2 was obtained.⁴¹ Yield: 65%, B.P.: 148-150°C; IR (cm⁻¹): 3343.99 (NH),3000.0 (CH aromatic), 2983.3 (CH methylene), 2878.20(CH methyl), 1680.88 (C=O),1598.09 (C-O),1310.92(CN),1172.21(C-C); ¹H-NMR (CDCl₃, ppm): 7.84 (d, 2H, J=3.9),7.52(d, 2H,J=3.3),7.04 (s,3H), 6.62-6.60(d, 2H, J=3.9),4.32-4.02(m, 4H, Methylene), 1.35-1.32(t,3H, methyl); MS: [M+H]⁺326.1

General Procedure for the Synthesis of 4-(Benzyl amino) Benzoic acid hydrazide

Taken solution of Compound 2 (0.01 mol) in ethanol (20 mL), added hydrazine hydrate (0.02 mol) and refluxed the mixture for about 5 hrs on steam bath. After cooling, the resulting solid was filtered, dried and recrystallized from ethanol to obtain compound 3. Yield: 62%, M.P.: 152-154°C; IR (cm⁻¹): 3339.05(NH₂) 3005.0 (CH aromatic), 2908.3 (CH methylene), 1679.80 (C=O), 1309.92(CN), 1170.89 (C-C); MS: [M+H]⁺328.3

General Procedure for Synthesis of N-benzyl-4-[5-(pyridine-4-yl)-1,3,4-oxadiazol-2-yl]aniline (B1 a-j)

A mixture of respective aryl hydrazide (3) (0.01 mol) and nicotinic acid (0.01 mol) was dissolved in about 5ml of phosphorus oxychloride. The reaction mixture was refluxed

on a water bath for 7-8 hrs. After completion of the reaction, the mixture was cooled at room temperature. Excess of phosphorous oxychloride was distilled off, and the mixture was gradually poured into crushed ice by continuous stirring for 10 minutes and sodium bicarbonate (20%) was added for neutralization. The resulting mixture was filtered, and the residue was washed with cold water and NaHCO₃ solution. The separated yellow solid was dried and recrystallized from ethanol to obtain the final compound B1 a. A similar procedure was adopted for synthesis of compound B1b-j.⁴² The corresponding R for B1a-j is shown below.

Characterization of Synthesized Compounds B1a-j

2-(pyridine-4-yl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (a)

Yield: 70.6%, M.P: 174-178°C, light yellow solid; IR (cm⁻¹): 3416.01(NH),3093.07,3059.6(CH aromatic),2889.27(Aliphatic CH) 1676.50(CN), 1605.98,1575.15,1457.30 (C – C = C), 1346.86,1289.19(CN), 1053.16 (C-O-C), 899.73,784.24,757.61(oop bending); ¹H NMR (DMSO-D₆,400 MHz,δ ppm): 7.91 (d, 2H, pyridyl, (J = 3.9), 7.6-7.5 (t,2H, aromatic), 7.47-7.44 (m, 9H, Aromatic, (J = 3.7), 5.81(s, H, NH), 4.50 (d, 2H, methylene, (J = 1.9)); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm)164.98, 164.81, 149.77, 144.30, 133.30,131.70, 131.27, 129.72, 127.98, 123.22, 120.00, 117.37, 113.04, 44.04; MS: m/z calculated for C₂₀H₁₆N₄O [M+H]⁺329.3, found : 328.3

2-(o-carboxyphenyl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (b)

Yield: 55.8%, M.P/B.P: 192-194°C, light yellow liquid; IR (cm⁻¹): 3390.07(OH,NH),3001.09(CH aromatic),2941.99(Aliphatic CH), 1791.62 (C=O) 1602.90(CN),1534.66,1466.38 (C – C = C),1413.18 (OH), 1282.22(CN),1233.66(C-O-C), 1071.75 (C-O-C), 845.73,794.24,708.08 (oop bending); ¹H NMR (DMSO-D₆,400 MHz,δ ppm): 10.32 (s,1H, benzoic acid), 8.73 (d, 2H, carboxyphenyl, (J = 1.9), 8.23 (d,2H, aromatic, (J = 2.0), 7.57-7.47 (m, 9H, Aromatic,), 5.82(s,b, H, NH), 4.43 (d, 2H, methylene, (J = 2.2)); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm) 172.43,167.68, 161.63, 142.04, 136.18, 131.72,130.79, 129.71, 119.81, 117.60, 113.08, 42.03; MS: m/z calculated for C₂₂H₁₇N₃O₃ [M+H]⁺372.2, found : 371.12

2-(o-hydroxyphenyl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (c)

Yield: 40.2%, M.P/B.P: 180-182°C, yellowish brown solid; IR (cm⁻¹): 3359.00(OH,NH),3009.07,3059.6(CH aromatic),2954.56, 2821.24(Aliphatic CH) 1633.44(CN), 1605.54,1573.27,1540.34 (C – C =C), 1454.93 (OH), 1346.86,1292.66(CO)), 1078.59,1044.56 (C-O-C), 875.84,547.48(oop bending); ¹H NMR (DMSO-d₆,400 MHz,δ ppm): 7.76-7.73(dd, 4H, aromatic),7.57-7.44 (m,5H, aromatic), 6.91-6.86 (dd, 4H, Aromatic),6.48(s, 1H, OH) 5.68(s,b, H, NH), 4.50 (d, 2H, methylene, (J = 2.0)); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm) 172.43,166.63, 161.63, 151.36, 143.08, 136.08, 131.72,130.79, 119.61, 117.70, 113.28, 45.81.04; MS: m/z calculated for C₂₁H₁₇N₃O₂ [M+H]⁺344.13 , found : 343.13

2-{5-[4-(benzylamino) phenyl]-1,3,4-oxadiazol-2yl};phenyl acetate B 1 (d)

Yield: 69.5%, M.P/B.P: 198-200°C, light brown solid; IR (cm⁻¹): 3405.02(NH),3095.72, (CH aromatic),2873.02, 2761.42(Aliphatic CH), 1708.96(C=O), 1693.67, 1579(CN), 1602.35, 1473.46 (C – C =C), 1258.53,1220.15(CO)), 1075.16, (C-O-C), 892.71, 823.32,755.14.48(oop bending); ¹H NMR (DMSO-D₆,400 MHz,δ ppm): 7.89-7.73(m, 4H, aromatic),7.65-7.55 (m,4H, aromatic), 7.48-7.731 (m, 5H, Aromatic), 4.08(s,b, H, NH), 4.90 (d, 2H, methylene, (J = 2.5),2.1(s,3H, methyl); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm)168.02, 165.65, 144.00, 134.46,131.73, 130.06, 128.23, 124.28, 117.39, 113.06, 53.07, 29.03; MS: m/z calculated for C₂₃H₁₉N₃O₃ [M+H]⁺386.3 , found : 385.14

2-phenyl-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (e)

Yield: 71.4%, M.P/B.P: 166-168°C, Off white solid; IR (cm⁻¹): 3423.29(NH),3082.72(CH aromatic),2883.02(Aliphatic CH) 1676.50(CN), 1643.67,1579.04 (C – C =C), 1303.17(CN),1258.53(C-O str), 1075.16 (C-O-C), 892.17,823.32, 755.14(oop bending); ¹H NMR (DMSO-D₆,400 MHz,δ ppm): 7.91 (d, 2H, aromatic),7.60-7.44 (m,12H, aromatic), 5.01(s, H, NH), 4.10(d, 2H, methylene, J=2.06);¹³ C NMR (DMSO-d₆,400 MHz, δ ppm)167.98,167.81, 164.31, 154.01, 143.02, 133.30,131.70, 131.70131.27, 129.72,129.01, 128.00, 117.37, 113.04, 46.30; MS: m/z calculated for C₂₁H₁₇N₃O [M+H]⁺328.3, found : 327.13

2-(3,5-dinitrophenyl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (f)

Yield: 47.2%, M.P / B.P: 212-214°C, light yellowish brown solid; IR (cm⁻¹): 3405.29(NH),3095.02, (CH aromatic),2873.02(Aliphatic CH) 1693.67(CN), 1602.54,1540.38.15, (C – C =C),1523.45,1393.17(N-O asymm, symm), 1247.66,1200.90(C-O str), 1075.59 (C-O-C), 836.73,745.24,706.61(oop bending); ¹H NMR (DMSO-d₆,400 MHz,δ ppm): 9.02 (s, 3H, nitrophenyl), 8.23 (d,2H, aromatic, (J = 4.1)), 7.57-7.47 (m, 7H, Aromatic), 6.50 (d, 1H, NH, (J = 3.2)), 4.43(d, 2H, methylene, J=2.2); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm) 169.70,166.13,161.66, 150.69, 144.40,136.16,134.30, 131.90,131.73,130.89, 130.79, 126.58, 124.57, 124.29, 119.68, 117.60, 113.07, 46.45; MS:

m/z calculated for C₂₁H₁₅N₅O₅ [M+H]⁺418.3, found : 417.10

2-(p-nitrophenyl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (g)

Yield: 58.9%, M.P / B.P: 202-204°C, light yellow solid; IR (cm⁻¹): 3323.29(NH), 3007.94(CH aromatic),2855.05(Aliphatic CH) 1650.48(CN), 1453.64 (C – C =C), 1377.59 (N-O asymm.),1241.21(CO), 1097.57 (C-O-C), 858.49,724.49,757.61(oop bending); ¹H NMR(DMSO-d₆,400 MHz,δ ppm): 8.50 (d, 2H, nitrophenyl, J=4.6), 7.91 (d,2H, nitrophenyl, (J=3.9), 7.40-7.24 (m, 9H, Aromatic), 6.50 (d, 1H, NH, (J = 3.0)), 4.41(s, 2H, methylene, J=2.2)); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm)166.10, 164.66, 154.09,150.69, 144.36, 131.90, 131.73,130.89,130.79, 126.58, 124.57, 124.29, 119.68, 117.60, 113.07, 43.64; MS: m/z calculated for C₂₁H₁₈N₄O₃ [M+H]⁺373.4 , found : 372.12

2-(p-aminophenyl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (h)

Yield: 66.3%, M.P/B.P: 170-172°C, yellowish brown solid; IR (cm⁻¹): 3430.68(NH),3064.96 (CH aromatic),2930.89(Aliphatic CH), 1696.47, 1595.66(CN),1635.46 (NH bending, m) 1602.98, (C – C =C), 1282.32, 1233.42 (CO), 1070.97 (C-O-C), 878.76,707.53,706.61(oop bending); ¹H NMR (DMSO-d₆,400 MHz,δ ppm): 7.86 (d,4H, aromatic, (J = 3.9)), 7.56 (4, 2H, Aromatic J=3.78), 7.33 (d, 5H, Aromatic, (J = 3.6)),6.50(d, 2H, NH, J=3.3), 6.2(s, 2H, NH₂) 4.18(d, 2H, methylene, J=2.0) ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm)168.0, 164.72, 148.86, 143.84, 133.11,131.72, 129.44, 128.72,127.94, 113.11, 44.43; MS: m/z calculated for C₂₁H₁₈N₄O [M+H]⁺343.1 , found : 342.14

2-(p-methoxyphenyl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (i)

Yield: 45.1%, M.P /B.P: 196-198°C, dark brown solid; IR (cm⁻¹): 3359.00(NH),3009.93(CH aromatic),2821.24(Aliphatic CH), 1633.44(CN), 1605.95,1535.00,1498.38 (C – C =C), 1281.97,1233.25(CO), 1011.24 (C-O-C), 876.23,764.06,708.18(oop bending); ¹H NMR(DMSO-d₆,400 MHz,δ ppm): 7.89-7.13 (m, 13H, Aromatic), 6.30 (d, 1H, NH, (J = 3.2)), 4.33(d, 2H, methylene, J=2.1),3.82 (s, 3H, Methoxy); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm)166.81, 159.97,153.62, 143.72, 133.30,131.70, 131.27, 129.72,129.00 128.90,117.37, 113.04, 54.62, 45.25; MS: m/z calculated for C₂₂H₁₆N₃O₂ [M+H]⁺358.2 , found : 357.14

2-(benzyl)-5-[4-(benzylamino)-phenyl]-1,3,4-oxadiazole B 1 (j)

Yield: 71.9%, M.P / B.P: 158-160°C, light yellow liquid; IR (cm⁻¹): 3323.29(NH), 3055.24(CH aromatic),2954.74,2870.26(Aliphatic CH), 1644.31, 1543.84(CN),1543.84,1455.24 (C – C =C), 1310.66,1282.08(CO), 1078.45 (C-O-C), 875.66,845.07 (oop bending); ¹H NMR (DMSO-d₆,400 MHz,δ ppm): 7.76-7.73 (q, 4H, Aromatic), 7.5-7.4(m, 10H, Aromatic), 6.50 (d, 1H, NH, (J = 3.2)), 4.18(d, 4H, methylene, J=4.3); ¹³ C NMR (DMSO-d₆,400 MHz, δ ppm)166.0, 148.86, 143.04, 133.39,131.70, 131.72, 129.72, 127.44, 128.81,113.11, 44.23; MS: m/z calculated for C₂₂H₁₉N₃O [M+H]⁺342.1 , found : 341.15

In-vitro Antimicrobial Evaluations*Antibacterial Studies*

The novel synthesized compounds were evaluated for their antibacterial activity against *Bacillus subtilis*, *Staphylococcus aureus*, *Escherichia coli*, and *Pseudomonas aeruginosa*. The antibacterial evaluation was evaluated by disc diffusion method.^{43,44} Sterilized nutrient agar media (20 mL) was poured into each labeled petri dish and solidified. Freshly prepared bacterial inoculum was spread on the surface of agar media for the growth of the bacterial lawn. Then discs were immersed in different concentrations of test compounds and were placed on top of agar surface. Cefixime was taken as a positive control, and DMSO was used as blank. All Petri dishes were incubated at 37°C for 24–48 hrs. The results were recorded by measuring diameter of zone of inhibition produced by various concentrations of the test compounds. The bacterial zone of inhibition data for test compounds are presented in Table 2

MIC Determination

Minimum Inhibitory Concentration of synthesized compounds was determined by using broth dilution method.^{45,46} Aqueous

solution of Mueller Hinton broth was prepared, sterilized and poured into labeled tubes. The tubes were inoculated by fresh bacterial log culture, containing 5×10^5 CFU/mL concentration. DMSO was used as a solvent for preparation of stock solution of test compounds and reference drug. The reference drug and test compound solutions were added in to inoculated tubes and incubated at $35 \pm 2^\circ\text{C}$ for 20-24 hrs. One set was prepared for each test compound against test organism with 6.5, 12.5, 25, 50, 100, 200 and 400 mg/L concentration. MIC values of synthesized compounds were noted at the end of incubation time by observing the lowest concentration of tubes with visible growth. The MIC data of synthesized compounds are shown in Table 4.

Antifungal Activity

Newly synthesized compounds were also analyzed for their antifungal activity through disc diffusion method.^{47,48} Two fungal strains *Aspergillus flavus* and *Candida albicans* were taken in DMSO for this experiment. Sterile sabourands agar media was poured into pre-sterilized Petri plates and allowed for solidification. PDA plates were inoculated with 100 μL of fresh fungal strain of log culture for lawning. Further paper

Table 2: Antibacterial activity of the synthesized 2,5-disubstituted 1,3,4-oxadiazole derivatives

Compound	Concentration ($\mu\text{g/ml}$)	Zone of inhibition in mm			
		<i>S. aureus</i>	<i>B. subtilis</i>	<i>E. coli</i>	<i>P. aeruginosa</i>
B1 (a)	100	-	-	10.0 ± 0.3	-
	200	-	-	11.0 ± 0.2	-
	400	-	9.0 ± 0.4	12.0 ± 0.2	-
B1 (b)	100	-	-	-	-
	200	-	-	-	-
	400	-	-	-	-
B1 (c)	100	07.2 ± 0.2	-	10.1 ± 0.4	-
	200	10.0 ± 0.4	-	10.0 ± 0.9	05.0 ± 0.2
	400	12.4 ± 0.1	-	12.2 ± 0.3	09.7 ± 0.1
B1 (d)	100	-	-	-	-
	200	-	-	-	1.0 ± 0.4
	400	-	5.0 ± 0.3	-	1.2 ± 0.3
B1 (e)	100	-	-	09.0 ± 0.3	-
	200	-	10.0 ± 0.6	15.2 ± 0.6	-
	400	-	12.3 ± 0.4	16.4 ± 0.2	-
B1 (f)	100	10.4 ± 0.3	07.2 ± 0.4	11.2 ± 0.5	8.1 ± 0.6
	200	15.0 ± 0.2	10.8 ± 0.1	15.7 ± 0.2	10.8 ± 0.4
	400	20.1 ± 0.4	18.1 ± 0.2	20.8 ± 0.3	11.1 ± 0.2
B1 (g)	100	06.1 ± 0.4	04.0 ± 0.4	10.4 ± 0.3	-
	200	12.5 ± 0.2	06.1 ± 0.4	13.3 ± 0.3	08.0 ± 0.2
	400	16.3 ± 0.4	13.6 ± 0.5	17.8 ± 0.1	12.2 ± 0.4
B1 (h)	100	08.2 ± 0.4	05.0 ± 0.3	10.2 ± 0.1	-
	200	11.0 ± 0.2	10.2 ± 0.2	14.6 ± 0.6	-
	400	17.2 ± 0.5	14.1 ± 0.7	18.1 ± 0.3	11.2 ± 0.4
B1 (i)	100	05.2 ± 0.5	09.0 ± 0.4	10.0 ± 0.2	09.0 ± 0.4
	200	11.0 ± 0.2	12.2 ± 0.1	16.0 ± 0.6	12.2 ± 0.2
	400	16.4 ± 0.1	18.8 ± 0.6	18.2 ± 0.3	12.5 ± 0.3
B1 (j)	100	09.2 ± 0.2	10.0 ± 0.2	10.0 ± 0.6	-
	200	10.0 ± 0.1	12.0 ± 0.6	16.6 ± 0.2	-
	400	16.3 ± 0.4	19.0 ± 0.4	20.4 ± 0.2	9.2 ± 0.7
Cefixime	100	08.6 ± 0.3	07.2 ± 0.2	10.1 ± 0.3	-
	200	11.7 ± 0.2	12.7 ± 0.4	15.4 ± 0.1	-
	400	17.2 ± 0.4	18.9 ± 0.1	20.8 ± 0.3	10.8 ± 0.1

discs immersed in different dilutions of test compounds were placed on its surface. These plates were incubated at 37°C for 24-48 hours. The fungal activity of synthesized compounds was compared with econazole as the standard drug and DMSO as blank. A fungal inhibition halo zone was created around the tested compounds. The diameter of inhibition zone of all the synthetic compounds was measured in millimeters and data are given in Table 3.

In-silico Molecular Docking Studies

Molecular Docking studies were performed for synthesized 2, 5-disubstituted 1, 3, and 4-oxadiazole derivatives by using Auto Dock/Vina software.^{49,50} In correlation to *in-vitro* antimicrobial activity, it was worthwhile to carry out *in-silico* studies to predict the binding affinity and orientation at the active site of the protein.^{51,52} The structure of synthesized compounds was drawn in Chem Sketch Draw tool (Chem-Sketch freeware) allocated with proper 2-D orientation, and also checked for structural drawing error. A 2-D structure was converted into 3D representation with minimum energy by using ChemBio3D. The energy minimized ligand molecules

were used as input for Auto Dock Vina suitable for molecular docking simulation.⁵³ The protein Peptide deformylase (PDF) was selected as target macromolecule.^{54,55,56} The PDB coordinate file named 'PDF- 1G2A.pdb' was used as a receptor molecule. Water molecules and other interfered groups were removed from receptor molecule and rebuild the missing side chain in receptors automatically.

The interesting region of macromolecule was covered by grid box in *x*, *y* and *z* direction. The graphic user interface program "MGL Tools" was utilized for a grid box set to carry out the docking simulation. The grid box volume was set to 60, 60, and 60 Å for *x*, *y*, and *z* dimensions which included all the interesting amino acids residues in the considered active pocket of selected protein/macromolecule. Auto Grid 4.0 program was utilized for obtaining grid maps, supported with Auto Dock 4.0.⁵⁷ The docking algorithm software provided with Auto Dock Vina was applied for identification of best-docked conformation between the ligand and protein. About ten conformers were considered for each ligand molecule during the docking process. PyMol was used to conclude docking

Table 3: Antifungal activity of synthesized 2,5-disubstituted 1,3,4-oxadiazole derivatives in diameter of inhibition zone (mm)

Comp. code	<i>Candida albicans</i>					<i>Aspergillus flavus</i>				
	50	100	250	500	1000	50	100	250	500	1000
4a	3.2 ± 0.1	3.9 ± 0.2	8.8 ± 0.2	10.0 ± 0.4	14.2 ± 0.1	0.0 ± 0	10.6 ± 0.2	14.5 ± 0.8	15.4 ± 0.3	18.8 ± 0.7
4b	00 ± 0.0	00 ± 0.0	00 ± 0.0	00 ± 0.0	00 ± 0.0	00	00	00	00	00
4c	00 ± 0.0	00 ± 0.0	00 ± 0.0	00 ± 0.0	00 ± 0.0	00	00	00	00	00
4d	00 ± 0.0	2.4 ± 0.6	2.0 ± 0.03	6.9 ± 0.7	10.3 ± 0.4	00 ± 0	00 ± 0	4.0 ± 0.8	7.2 ± 0.2	12.6 ± 0.3
4e	00 ± 0.0	00 ± 0.0	00 ± 0.0	00 ± 0.0	00 ± 0.0	00	00	00	00	00
4f	10.6 ± 0.7	15.8 ± 0.3	17.6 ± 0.1	19.7 ± 0.2	25.9 ± 0.1	11.0 ± 0.0	14.4 ± 0.6	20.2 ± 0.3	23.0 ± 0.6	26.8 ± 0.2
4g	3.0 ± 0.07	4.2 ± 0.05	5.0 ± 0.03	08.0 ± 0.2	12.5 ± 0.02	2.3 ± 0.05	10.4 ± 0.3	14.2 ± 0.6	15.4 ± 0.7	17.0 ± 0.2
4h	4.0 ± 0.2	9.0 ± 0.0	13.0 ± 0.3	15.2 ± 0.8	19.8 ± 0.5	8.3 ± 0.02	14.1 ± 0.2	18.4 ± 0.5	20.9 ± 0.4	22.6 ± 0.2
4i	5.3 ± 0.0	6.9 ± 0.0	10.1 ± 0.0	12.4 ± 0.07	16.1 ± 0.03	6.3 ± 0.05	12.0 ± 0.03	16.0 ± 0.02	16.0 ± 0.02	20.4 ± 0.03
4j	07.2 ± 0.4	13.6 ± 0.06	16.2 ± 0.08	19.2 ± 0.02	24.9 ± 0.02	09.2 ± 0.04	15.6 ± 0.06	21.0 ± 0.02	22.8 ± 0.06	26.2 ± 0.02
standard	15.0 ± 0.2	17.9 ± 0.7	19.0 ± 0.4	21.4 ± 0.3	26.4 ± 0.3	14.0 ± 0.6	17.4 ± 0.4	20.5 ± 0.1	26.4 ± 0.6	27.8 ± 0.4
DMSO	-	-	-	-	-	-	-	-	-	-

Table 4: Minimum Inhibitory concentration data of synthesized compounds B1a-B1j

Compound code	Gram-positive bacteria		Gram-negative bacteria	
	<i>S.aureus</i>	<i>Bacillus subtilis</i>	<i>E.coli</i>	<i>P.aureginosa</i>
B1a	NT	NT	NT	NT
B1b	NT.	NT	NT	NT
B1c	100	100	50	400
B1d	NT	NT	NT	NT
B1e	NT	NT	NT	NT
B1f	25	50	25	200
B1g	50	100	25	200
B1h	50	100	12.5	100
B1i	100	200	50	400
B1j	50	100	25	200
Standard Cefixime	25	50	12.5	100

MIC (µg/mL) value means lowest concentration of the compound to inhibit the visible growth of bacteria.

NT: not tested

simulation's final pictorial presentation between ligand and target macromolecule/ protein.⁵⁸

RESULT AND DISCUSSION

Chemistry

Benzyl moiety has good antimicrobial properties and also enhances the lipophilicity of compound.^{59,60} Therefore, benzyl ring containing 2,5-disubstituted 1,3,4-oxadiazole were synthesized as per scheme-1. The structural confirmation of newly synthesized compounds B 1 (a-j) was studied by IR, ¹H NMR, ¹³C NMR and mass spectral analysis. IR spectrum of compound (a) shows absorption band at 3416.01 cm⁻¹ due to NH group and aromaticity of compound was confirmed by absorption band aroused at 3093.07 and 3059.6 cm⁻¹. Absorption bands at 1578.50 cm⁻¹ and 1053.16 cm⁻¹ are assigned for CN and C-O-C ring stretching of Oxadiazole respectively. Medium absorption band at 3000-2800 cm⁻¹ range are shown due to aliphatic CH stretching in each IR spectrum. In ¹H NMR spectra, all proton signals appeared at an appropriate region with the expected chemical shift and integral values. Diagnostic peaks at δ 7.91 (d, 2-H), 7.6- 7.4 (m, 10-H) were observed in aromatic region for compound B1(a). A broad peak at δ 5.8 (s, 2-H) was observed due to amine (NH) protons. The signal of methylene protons was seen at δ 4.5 (d, 2-H). Fundamental peaks at δ 165.1, 164.3, 149.7, 144.3, 133-120, 44.0 were seen in ¹³C NMR spectrum which completely correlates with the proposed structure of compound B1(a). The structures of remaining derivative compounds were also characterized in a similar way. The delta (δ) values of aromatic and aliphatic protons were changed due to substitution by electron-donating groups or electron withdrawing groups at the different positions of phenyl ring. The mass spectrum of synthesized compounds was also expected as per the proposed molecular formula and molecular ion peak was coherent with calculated molecular weight. Analytical and spectral data of synthesized compounds were completely supportive with their proposed structures and detail spectral values are given in the experimental section.

Antimicrobial Studies

Antibacterial Activity

All the synthesized compounds were studied for their antibacterial activity against selected strains *Staphylococcus*

aureus, *Bacillus subtilis*, *E.coli* and *P. aeruginosa* by using disc diffusion method. Cefixime was taken as positive control and DMSO used as negative control. The antibacterial activity of test compounds was assayed on the basis of radius of inhibition zones. The average diameter of zones of inhibition (mm) were recorded and compared with standard drug Cefixime. Most of the compounds exhibited mild to moderate antibacterial activity against selected strains as per screening results (table-2). Promising inhibitory results of Compound B1f, B1j, B1h, B1i B1g, and B1c were obtained against selected bacterial strains. The compounds B1f, B1j and B1h exhibited activity nearly similar to that of cefixime ranging from 11.1 ± 0.2 to 20.1 ± 0.8 for B1f, 9.2 ± 0.7 to 20.4 ± 0.2 for B1j, 11.2 ± 0.8 to 18.1 ± 0.3 for B1h at the concentration 400 µg/ml. The potent derivatives revealed that structural variations of compounds impacts biological activity. Compounds B1f, B1g, B1h, B1j having nitro, benzyl, methoxy and amino group showed good antibacterial activity against all strains except *P. aeruginosa*. Remaining compounds did not showed remarkable antibacterial activity. MIC values of synthesized compounds also indicated good antibacterial activity given in Table 4.

Antifungal activity

Antifungal activity of synthesized compounds was performed by disc diffusion method. Two fungal strains *Aspergillus flavus* and *Candida albicans* were taken for assessing antifungal activity. Antifungal screening results revealed that four compounds B1f, B1j, B1h, and B1i showed antifungal activity (table-3). Among these compounds, B1f and B1j exhibited promising results comparable with standard drug Econazole. The descending order of antifungal activity of synthesized compounds were B1f > B1j > B1h > B1i > B1a > B1g against selected fungal strains.

Molecular Docking Studies

In silico analysis of potentially active newly synthesized 1,3,4-oxadiazole derivatives were carried out against peptide deformylase protein and the docking results were also synchronized with *in-vitro* antimicrobial screening results. The docking analysis of tested compounds was performed through auto dock process to predict the binding affinity of ligand and best orientation conformation of each ligand. The binding affinities of docked ligand were assessed as binding energy or docking scores. The hydrophobic and hydrogen bond interactions between protein and each ligand molecule

Table 5: *In silico* molecular docking results of selected 2,5-disubstituted 1,3,4-oxadiazole compounds

S.No.	Ligand	Affinity (binding energy) in cal/mol	H-bonds	Hydrophobic interactions amino acids
1.	B1 (f)	12.52	6	GLU42, GLU41, ARG97, LEU91, CYS90, GLN50, HIS136, GLU133, HIS132, GLN131, ARG97, GLY124
2.	B1 (h)	8.33	2	ARG97, GLU88, CYS90, ILE128, HIS132, CYS129, GLU133, GLY45, GLY43, LEU91, SER92
3.	B1 (i)	8.13	3	ILE128, HIS132, CYS129, GLU133, ILE44, GLY43, GLU41, LEU91, CYS90, GLU88, ARG97
4.	B1 (j)	9.19	2	GLU95, PRO94, ARG97, GLY89, CYS90, LEU91, ILE44, GLU133, CYS129, HIS132, ILE128, HIS132, ALA127
Standard	Cefixime	7.3	6	ILE44, GLU41, GLU42, GLY89, GLU95, ILE128, ILE86, HIS132, GLU133, GLU88

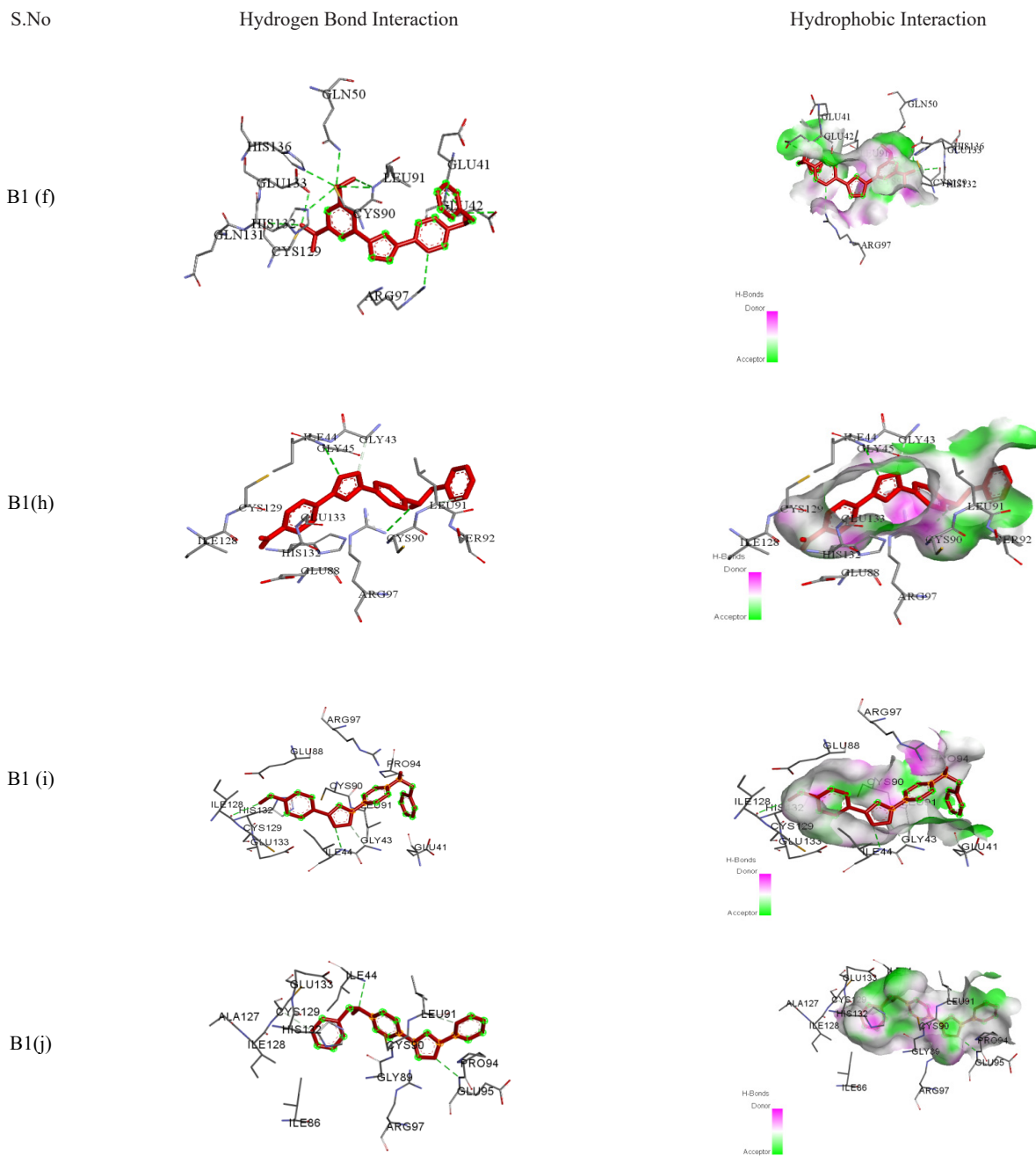


Figure 1: 3D pictorial representation of selected ligand molecule with peptide deformylase

B1f, B1h, B1i and B1j were assessed within the binding pocket of protein-peptide deformylase 1G2A. All docked molecules exhibited excellent binding posed with amino acids of active pocket of selected protein as shown in Figure 1. The docked ligand molecules B1f, B1h, B1i and B1j were found with excellent docking confirmation with minimal binding affinity (-12.52 , -8.33 , -8.13 and -9.19 kJ mol^{-1}) than standard drug Cefixime (-7.3) and Econazole (-6.9). Molecular docking scores of compound B1f, B1h, B1i, and B1j are shown in Table 5.

CONCLUSION

A series of novel 2,5-disubstituted Oxadiazole derivatives fused with benzyl ring were synthesized and evaluated for

their antimicrobial activity against microorganisms as per priority pathogens declared by WHO. Among synthesized compounds, B1f and B1j showed remarkable antimicrobial potential against tested microorganisms. *In-vitro* antimicrobial activity of tested compounds was also correlated with *in silico* molecular docking studies. Molecular docking results also conclude that the phenyl ring substituted with electron-withdrawing groups and benzyl ring attached to Oxadiazole enhanced the biological activity due to alteration in lipophilicity. Hence, based on the above results it can be concluded that the current study of Oxadiazole is suitable for further investigation in the field of antimicrobial drug designing.

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Supportive/supplementary materials:

Supplementary data will be provided on demand.

REFERENCES

- Tishler M. Molecular Modification in Modern drug Research. Advance in chemistry, American chemical society, Washington,DC,1964, 228
- Gajewski JH. Molecular Modification in Drug Design: Advance in Chemistry series 45. ROBERT F. GOULD, Ed., American Chemical Society, Washington, DC, 1964,22pp. Clinical Chemistry. 1965 May. 11(5): 612
- Deb PK, Al-Attraqchi O, Jabber, AY; Amarji, B.; Tekade, R.K.: Physicochemical Aspects to Be Considered in Pharmaceutical Product Development, Academic Press: 2018; Vol. 1, 57-83.
- Marshall BM, Levy SB. Food Animals and Antimicrobials: Impacts on Human Health. Clinical Microbiology Reviews. 2011Oct, 24(4): 718-733.
- Schwarz S, Loeffler A, Kadlec K. Bacterial resistance to antimicrobial agents and its impact on veterinary and human medicine. 2017, 28(1), 82-e19, DOI: 10.1111/vde.12362.
- Schwarz S, Cloeckeaert A, Roberts MC. In: Mechanisms and spread of bacterial resistance to antimicrobial agents:Aarestrup, F.M, Ed. Antimicrobial Resistance in Bacteria of Animal Origin; DC: ASM Press: Washington, 2006; 73–98.
- Jackson N, Czaplowski L, Piddock J.V.L. Discovery and development of new antibacterial drugs: learning from experience. Journal of Antimicrobial Chemotherapy 2018; 73(6): 1452-1459.
- Cheesman MJ, Ilanko A, Blonk B, E.Cock I. Developing new Antimicrobial therapies: Are Synergistic Combination of Plant Extract/Compounds with Conventional Antibiotics the Solution?. Pharmacognosy Review 2017; 11(22): 57-72.
- Sabir S, Alhazza MI, Ibrahim AA. A review on heterocyclic moieties and their application. Catalysis for Sustainable Energy 2015; 2: 99-115.
- Bostrom J, Hogner A, Llinas A, Wellner E, Plowright AT. Oxadiazoles in Medicinal Chemistry. Journal of Medicinal Chemistry. 2012; 55(5): 1817-1830.
- Selvakumar B, Vaidyanathan PS, Madhuri S, Elango PK. Synthesis and Antiviral Activity of Sulfonylhydrazide and 1,3,4-oxadiazole Derivatives of 6,6-Dimethyl-9-Oxo-4,5,6,7,8,9-Hexahydropyrazolo[5,1-b] Quinazoline. Journal of Chemical Research. 2017; 41(4): 221-224.
- Glomb T, Szymankiewicz K, Swiatek P. Anti-cancer Activity of derivatives of 1,3,4-Oxadiazole. Molecules. 2018; 23(12): 3361, doi: 10.3390/molecules23123361
- Karabnovich G, Zemanova J, Smunty T, Centarova I, Vocat, A. Development of 3,5-dinitrobenzylsulfanyl-1,3,4-oxadiazoles and Thiadiazoles as Selective Antitubercular Agents Active Against Replicating and nonreplicating *Mycobacterium tuberculosis*. Journal of Medicinal Chemistry. 2016; 59(6): 2362-2380.
- Singh KA, Lohani M, Parthasarthy R. Synthesis, Characterization and Anti-Inflammatory Activity of some 1,3,4- Oxadiazole Derivatives, Iranian journal of pharmaceutical research. 2013; 12(2): 319-323.
- Grewal AS, Redhu S. Synthesis, Antibacterial and Antifungal Activity of 2,5-disubstituted-1,3,4-oxadiazole Derivatives. International Journal of Pharm Tech Research .2014; 6(7): 2015-2021.
- Habibullah K, Khan S, Md.Nomani S, Ahmed B. Synthesis, characterization and antimicrobial activity of benzodioxane ring containing 1,3,4-oxadiazole derivatives. Arabian Journal of Chemistry. 2016; 9(2): S1029-S1035.
- Yurttas L, Bulbul EF, Tikinkoca S, Demirayak S. Antimicrobial activity evaluation of new 1,3,4-oxadiazole derivatives. Acta Pharmaceutica Scienica. 2017; 55(2), DOI: 10.23893/1307-2080. APS.05511.
- Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, Pulcini C, Kahlmeter G, Kluytmans J, Carmeli Y. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis, Lancet Infect Disease. 2018; 18(3):318-327.
- Reygaert WC. An overview of the antimicrobial resistance mechanisms of bacteria. AIMS Microbiology 2018; 4(3): 482-501.
- Beveridge TJ. Structures of Gram-Negative Cell walls and Their Derived Membrane Vesicles. Journal of Bacteriology 1999 Aug; 181(16): 4725-4733.
- Bala S, Kamboj S, Kajal A, Saini V, Prasad DN. 1,3,4-Oxadiazole Derivatives: Synthesis, Characterization, Antimicrobial Potential, and Computational Studies. BioMed Research International 2014, Article ID 172791, <http://dx.doi.org/10.1155/2014/172791>.
- Brejijeh Z, Jubeh B, Karaman R. Resistance of Gram-Negative bacteria to Current Antibacterial Agents and Approaches to Resolve It. Molecules 2020; 25(6): 1340, doi: 10.3390/molecules25061340.
- Lin X, Li X, Lin X. A Review on Applications of Computational Methods in Drug Screening and Design. Molecules 2020; 25: 1375 doi: 10.3390/molecules25061375.
- Yu W, Mackerell AD. Computer-Aided Drug Design Methods. Methods of Molecular Biology 2017;1520:85-106, doi: 10.1007/978-1-4939-6634-9_5.
- Meng Y, Zhang H X, Mezei M, Cui M. Molecular Docking: A powerful approach for structure-based drug discovery. Current Computer- Aided Drug design 2011;7(2):146-157.
- Ferreira LG, Dos Santos RN, Oliva G, Andricopulo AD. Molecular docking and structure-based Drug Design Strategies. Molecules 2015 Jul; 20(7): 13384-13421.
- Pagadala NS, Syed K, Tuszynski J. Software for molecular docking: a review. Biophysical Reviews 2017 Apr; 9(2): 91-102.
- Jamkhande PG, Ghante MH, Ajgunde BR. Software based approaches for drug designing and development: A systematic review on commonly used software and its applications. Bulletin of faculty of Pharmacy, Cairo University 2017 Dec; 55(2): 203-210.
- Xia X. Bioinformatics and Drug Discovery. Current Topics in medicinal Chemistry 2017 Jun; 17(15): 1709-1726.
- Slioski G, Kothiwale SK, Meiler J, Lowe EW. Computational Methods in Drug Discovery. Pharmacological Reviews 2014 Jan; 66(1): 334-395.

31. Hernandez-Santoyo A, Tenorio-Barajas AY, Altuzar V, Vivanco-Cid H. Protein-Protein and Protein-ligand Docking. Protein Engineering- Technology and Application 2013, doi: 10.5772/56376.
32. Kalembe D, Kunicka A. Antibacterial and antifungal properties of essential oils Current Medicinal Chemistry 2003; 10(10): 813–829,
33. Giglione C, Pierre M, Meinnel T. Peptide deformylase as a target for new generation, broad spectrum antimicrobial agents. Molecular Microbiology 2002; 36(6): 1197-1205.
34. Kumar S, Kanudia P, Karthikeyan S, Chakraborti PK. Identification of Crucial Amino Acids of bacterial Peptide Deformylases Affecting Enzymatic Activity in Response to Oxidative stress. Journal of Bacteriology 2014 Jan; 196(1): 90-99.
35. Becker A, Schlichting I, Kabsch W, Groche D, Schiltaz S, Volkar wagner, A F. Iron center, substrate recognition and mechanism of peptide deformylase. Nature Structural biology 1998; 5: 1053- 1058.
36. Hernick M, Fierke C. Enzymes and Enzymes Mechanisms. Comprehensive natural products II 2010; 8: 547-581.
37. Muraleedharan KM, Avery MA. Therapeutic Areas II: Cancer, Infectious Disease, Inflammation & Immunology and Dermatology. Comprehensive Medicinal Chemistry II 2007; 7: 765-814.
38. Apfel C M, Locher H, Evers S, Takacs B, Hubschwerlen C, Pirson W, Page M.G.P., Keck W. Peptide Deformylase as an Antibacterial Drug Target: Target, validation and Resistance Development. American Society for Microbiology 2001; 1058-1064.
39. Alhassan G, Merza J, Ghenim R. Fischer Esterification of glycerol by Phenylacetic acids, Phenylacetic Anhydrides and some of their Aromatic Derivatives. Journal of chemical and Pharmaceutical research 2018; 10(10): 71-79.
40. Matsumoto K, Yanagi R, Oe Y. Recent Advances in the Synthesis of Carboxylic Acids Esters. Carboxylic Acid- Key role in Life Sciences 2018, doi: 10.5772/interchopen.74543.
41. <https://erowid.org> "synthesis of benzylamine and derivatives".
42. Selvaraj K, Kulanthai K, Sadhasivam G. Synthesis, characterization and biological evaluation of novel 2,5 substituted-1,3,4-oxadiazole derivatives, Saudi Pharmaceutical Journal 2017; 25: 337-345.
43. Zeleke D, Eswaramoorthy R, Belay Z, Melaku Y. Synthesis and antibacterial, Antioxidant, and molecular docking analysis of Some Novel Quinoline Derivatives, Journal of Chemistry 2020, doi.org/10.1155/2020/1324096.
44. EI Malah T, Nour HF, Satti A.A.E., Hemdan BA, EI-Sayed WA. Design, Synthesis, and Antimicrobial Activities of 1,2,3-Triazole Glycoside Clickamers .Molecules 2020; doi: 10.3390/molecules25040790.
45. Zheng Z, Liu Q, Kim W, Tharmalingam N, Fuchs BB, Mylonakis E. Antimicrobial activity of 1,3,4-oxadiazole derivatives against planktonic cells and biofilm of *Staphylococcus aureus*. Future Medicinal Chemistry 2018; 10(3): 283-296.
46. Andrews JM. Determination of minimum inhibitory concentrations. Journal of Antimicrobial Chemotherapy 2001; 48(S1): 5-16.
47. Sengupta P, Mal M, Mandal S, Singh J, Maity TK. Evaluation of Antibacterial and Antifungal Activity of some 1,3,4 Oxadiazole. Iranian Journal Pharmacology & Therapeutics 2008;72: 165-167.
48. Moger M, Satam V, Govindaraju D.R.C., Paniraj AS, Gopinath VS, Hindupur RM, Patil HN. Synthesis and antimicrobial properties of 1,3,4-oxadiazole analogs containing dibenzosuberane moiety Journal of the Brazilian Chemical Society. 2014; 25(1): doi: 10.5935/0103-5053.20130275.
49. Azam SS, Abbasi AW. Molecular docking studies for the identification of novel melatonergic inhibitors for acetylserotonin-O-methyltransferase using different docking routines. Theoretical Biology and Medical Modelling 2013 Oct; 10(63).
50. Trott O, Olson AJ. AutoDock/Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization and multi threading. Journal of Computational Chemistry 2010; 31: 455-461.
51. Dahan A, Markovic M, Keinan S, Kurnikov I, Aponick A, Zimmermann EM, Ben-Shabat S. Computational modeling and in- vitro/in-silico correlational of phospholipid-based prodrug for targeted drug delivery in inflammatory bowel disease. Journal of computer- aided molecular design 2017; 31(11): 1021-1028.
52. Castro RI, Valenzuela-Riffo F, Morales-Quintana L. In Silico and In Vitro Analysis of the 4,4',4''-(1,3,5-Triazine-2,4,6-triyl) tris(azanediy)triphenol, an Antioxidant Agent with a possible Anti-Inflammatory Function. BioMed Research International 2019; Article ID 9165648, doi: 10.1155/2019/9165648.
53. Moris GM, GoodSell DS, Halliday RS. Automated docking using a Lamarckian genetics algorithm and an empirical binding free energy function. Journal of computational chemistry 1998; 19: 1639-1662.
54. Cali J, Han C, Hu T, Zhang J, Wu D, Wang F, Liu Y, Ding J, Chen K, Yue J, Shen X, Jiang H. Peptide deformylase is a potent target for anti- *Helicobacter pylori* drugs: Reverse docking, enzymatic assay, and X-ray crystallography validation. Protein Science 2006; 15(9): 2071-2081
55. Fieulaine S, Alves de Sousa R, Maigra L, Hamiche K, Alimi M, Bolla JM, Taleb A, Denis A, Pages JM, Artaud I, Meinnel T, Giglione C. A unique peptide deformylase platform to rationally design and challenge novel active compounds. Science report 2016; 6: 35429.
56. Gao J, Liang L, Zhu Y, Shengzhi Q, Wang T, Zhang L. Ligand and Structure-based Approaches for the identification of Peptide Deformylase Inhibitors as Antibacterial Drugs. International Journal of Molecular Sciences 2016; 17(7): 1141.
57. Sindhe MA, Bodke DY, Kenchappa R, Telkar S, Chandrashekar A. Synthesis of a series of novel 2,5-disubstituted-1,3,4-oxadiazole derivatives as potent antioxidant and anti bacterial agents. Journal of Biological Chemistry 2016; 9: 79-90.
58. Laskowski RA, Swindells MB. LigPlot+: multiple ligand-protein interaction diagrams for drug discovery. Journal of Chemical Information and Modeling. 2011; 51: 2778-2786.
59. Wang S, Jia XD, Li ML, Lu Y, Guo HY. Synthesis, antimycobacterial and antibacterial activity of ciprofloxacin derivatives containing a N- substituted benzyl moiety, Bioorganic & Medicinal Chemistry Letters. 2012; 22(18): 5971-5.
60. Aziz-ur-Rehman, Siddiqui SZ, Abbasi MA, Abbas N, Khan KM, Shahid M, Mahmood Y, Akhtar MN, Lajis NH. Synthesis, Antibacterial screening and hemolytic activity of S-substituted derivatives of 5-Benzyl-1,3,4-oxadiazole-2-thiol. International Journal of Pharmacy and Pharmaceutical Sciences. 2012; 4(2): 676-680.