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2-Acetyl quinoline analogues: Synthesis, ADME analysis and molecular docking studies

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An efficient avenue has been developed towards the synthesis of 2-acetylquinolines from 2-aminoaryl ketones and butan-1,2-dione using $Cu(OTf)_2$ as a mild catalyst through Friedländer synthesis the excellent yields. The synthesized 2-acetyl-4-phenylquinoline analogues have been optimized using at B3LYP/6-31G(d) level of theory in water to calculate the contour plot of frontier molecular orbital (FMO) and molecular electrostatic potential (MEP) map. Subsequently, the biological activity of 2-acetylquinolines has been analyzed using molecular docking and ADME properties. Finally, it has been found that **3g** and **3f** are the best candidates for this inhibiting of EGFR.

Keywords: 2-Acetyl quinolines, Friedländer synthesis, Molecular docking studies, ADME studies

Quinoline derivatives have emerged in recent years as favoured scaffolds that are present in both natural drugs like alkaloids and synthetic medicines with significant and varied pharmacological effects[1-7]. There are a number of established techniques for making quinoline core, including the Skraup[8], Doebner von Miller[9], Pfitzinger[10], Conrad-Limpach[11], Combes syntheses[12] and Povarov reaction[13]. Among them, the Friedland synthesis, which dates back to 1882, is still used by scientists as a recognised method for the synthesis of quinoline analogues in heterocyclic chemistry[14,15], by condensing readily available 2-aminoarylketones with carbonyl chemicals to achieve a reactive methylene group, researchers created the Friedlander synthesis to create quinoline derivatives. Cyclodehydration[16-18]. Recently, this method has been focused on producing a large amount of output using a variety of catalysts and methodologies, including ionic liquids, Lewis acids, Brϕnsted acids, greener processes, nano catalysts, and a variety of solvents[19-48]. In recent years, a number of heterogeneous catalysts, including metal-organic framework (MOF) materials, reusable eco-friendly polymeric catalysts, and metal catalysts, have been created for Friedland synthesis[49-53]. A Friedland synthesis has been developed. A notable method for creating ester-substituted quinoline cores was the cyclization of 2-aminoaryl ketones and alkynoates, which was frequently employed to find bioactive and medicinal compounds[54].

The outlook of approachable safe chemical procedures or techniques is the significant synthetic strategy from the solvent free organic reaction. Heterogeneous catalysts including sulfonic acid have emerged as user-friendly catalysts with advantages over homogeneous catalytic systems in the modern era[55-58]. The described synthetic processes for quinolines and their derivatives, even if accessed the method used to synthesize this class of chemicals most frequently.[7] The creation of a straightforward, environmentally friendly, low-cost technique is desirable because existing methods have poor yields, protracted reaction times, and a reliance on hazardous and frequently expensive catalyst systems.

The 3-acetylquinoline scaffolds are the most considerable biological analogues[59]. Based on the

Designed and synthesized compounds are optimized at B3LYP/6-31G(d) level in water. Then, the biological activity of these compounds is analyzed using molecular docking. In molecular docking calculations, the OPLS4 method is used. Furthermore, ADME properties of these compounds are investigated. Finally, it is found that **3g** and **3f** are found as the best candidate for the inhibiting of EGFR.

Results and Discussion

Chemistry

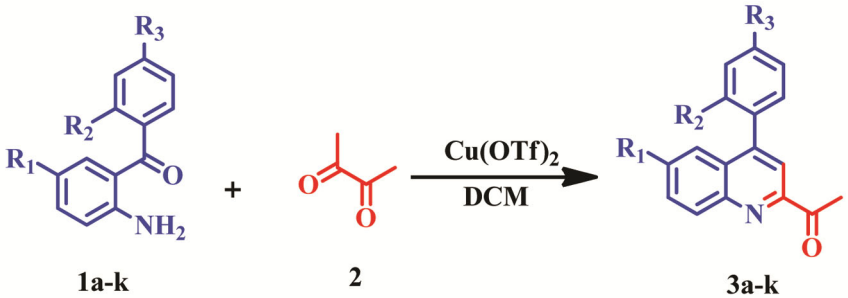
The synthesis of 2-acetyl-4-phenylquinolines derivatives under the solvent system with Copper (II) triflate catalyst ($Cu(OTf)_2$) by using in the reactions (Scheme 1, **3a-k**). The precursor 2-aminoarylketone (**1a-k**) and pentan-2,3-dione (**2**) was refluxed with new catalyst under the DCM solvent system (Table 1). The final products were confirmed FT-IR, ^{1}H NMR, m-m.p., co-TLC, and elemental analysis. Table 2 displays the suitable for 2-acetyl-4-phenylquinolines derivatives in yield of product.

In the beginning, **3a** and pentan-2,3-dione (**2**) were used to create product **3a** (Scheme 1) in the presence of ($Cu(OTf)_2$). To test the effectiveness of the catalyst at various reaction periods and temperatures, we studied the reaction in methanol, ethanol, DMF, acetonitrile, DMSO, water, toluidine, and DCM (Table 1). We discovered that the reaction in DCM produced product **3a** with an excellent yield (98%). We also noticed that the yield of product **3a** decreased as reaction time in the methanolic environment increased. The yield of product **3a** was lower in all these solvent reaction systems than it was in the ($Cu(OTf)_2$) reaction system using reflux with DCM as the solvent. Therefore, we utilized ($Cu(OTf)_2$) with DCM at reflux for 1 hour to synthesize **3a-k**. The percentage yield of **3a-k** is provided in Table 2.

For entries 2, 3, 4, 8, 10, and 11 (Table 2), respectively, the presence of electron-withdrawing groups of Cl-H, Cl-Cl, Cl-F, Br-F, H-Br, and Cl-Cl 2-aminoarylketone derivatives yielded good yields of the product as 98%, 96%, 93%, 91%, 96%, and 98%. As electron-donating groups, the aromatic NO_2-H, NO_2-Cl, NO_2-F, and 2-aminoarylketone produced yields of 90%, 89%, and 88% at entries of 5, 6, and 7, respectively (Table 2). These findings imply that electronic influences may have an impact on the product's amount.

Computational Analyses

The synthesized quinoline analogues were optimized at B3LYP/6-31G(d) level in water using Gaussian software[60,61]. IEF-PCM method was taken into consideration to consider the solute-solvent interactions. No imaginary frequency was observed in the result of IR calculations. Contour plot of frontier



Scheme 1 — Synthesis of 2-acetyl-4-phenylquinolines **3a-k**

Table 1 — Optimization of the reaction conditions with different solvents and reaction completion times

Entry	Catalyst	Solvent	Temp (°C)	Time (h)	Yield (%)
1	$Cu(OTf)_2$	MeOH	Reflux	6	80
2	$Cu(OTf)_2$	EtOH	Reflux	6	70
3	$Cu(OTf)_2$	DMF	Reflux	6	50
4	$Cu(OTf)_2$	CH_3CN	Reflux	6	75
5	$Cu(OTf)_2$	DMSO	Reflux	6	50
6	$Cu(OTf)_2$	H_2O	Reflux	6	50
7	$Cu(OTf)_2$	Toluidine	Reflux	4	75
8	$Cu(OTf)_2$	DCM	Reflux	1	98

molecular orbital and molecular electrostatic potential (MEP) map were calculated to predict electronic properties at same level of theory using Gaussian software.

Molecular docking and ADME analyses were performed using Maestro 12.8 software[62,63]. The studied compounds were re-minimized using LigPrep module. Epidermal Growth Factor Receptor was selected as target and the protein structure was downloaded from protein data bank as **1M17**. The x-y-x coordinate of receptor binding domain (RBD) was defined as 22.01-0.25-52.79, respectively. This protein was minimized using Protein Preparation module. The interaction between studied compounds and target protein was scanned using LigDocking module. Finally, the ADME properties of the mentioned compounds were studied at the same software.

Simulated Structures and Electronic Properties

The 2-acetyl-4-phenylquinolines derivatives are fully optimized at B3LYP/6-31G(d) level in water. The optimized structures of **3a** and **3b** at ground state are represented in Fig. 1. The optimized structures for the others are given in Supplemental Material.

According to optimized structures, the planar structure is more dominant on the 2-(prop-1-en-2-yl)quinolone. However, the benzene ring below stands as intersects the main structure at 90 degrees. This situation is the same for each structure. The given structures are at ground state level and no imaginary frequency is observed as the result of calculations. Electronic properties of chemicals may be vital in the determination of bioactivity of molecules and these properties can be determined using contour plot of HOMO, contour plot of LUMO and molecular electrostatic potential (MEP) map. These diagrams are calculated and are given in Fig. 2 for only compound **3a**. HOMO plot, LUMO plot and MEP maps for other compounds are given in Supplemental Material.

According to contour plot of HOMO and LUMO, electrons are delocalized on mainly benzene rings on the structure. Especially, π electrons seem so active. Therefore, this molecule can be interacted using these π electrons. As for the MEP map, there are many colors on the structure. Especially, environments of oxygen and nitrogen atoms seem as red due to the more electron density. Over the benzene ring, the color is green due to the pi electrons. As a result, these molecules can be interacted by using π electrons and heteroatoms such as nitrogen and oxygen.

Table 2 — Synthesis of 2-acetyl-4-phenylquinolines **3a-k**

Entry	R_1	R_2	R_3	Product	Yield (%) [a]
1.	H	H	H	**3a**	98
2.	Cl	H	H	**3b**	98
3.	Cl	Cl	H	**3c**	96
4.	Cl	F	H	**3d**	93
5.	NO_2	H	H	**3e**	90
6.	NO_2	Cl	H	**3f**	89
7.	NO_2	F	H	**3g**	88
8.	Br	F	H	**3h**	91
9.	H	H	F	**3i**	95
10.	H	H	Br	**3j**	96
11.	H	H	Cl	**3k**	98

[a] Isolated pure products

Molecular docking studies

Molecular docking is the significant step for the prediction of biological activity of compound using

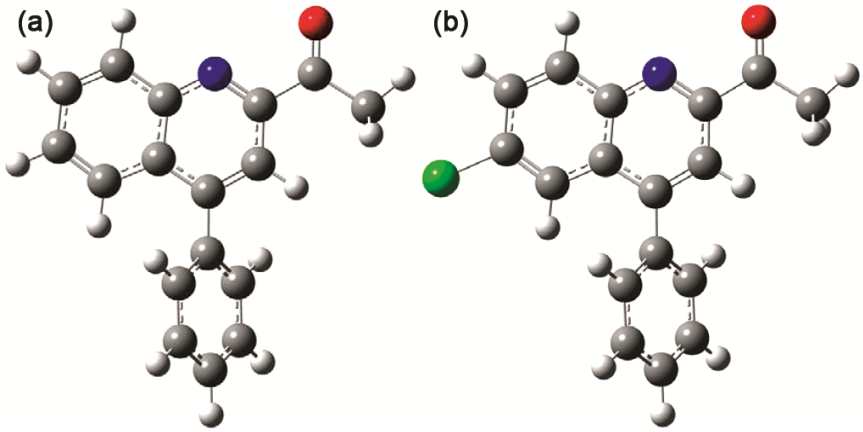


Fig. 1 — The optimized structure of 2-acetyl-4-phenylquinolines derivatives **3a** and **3b**

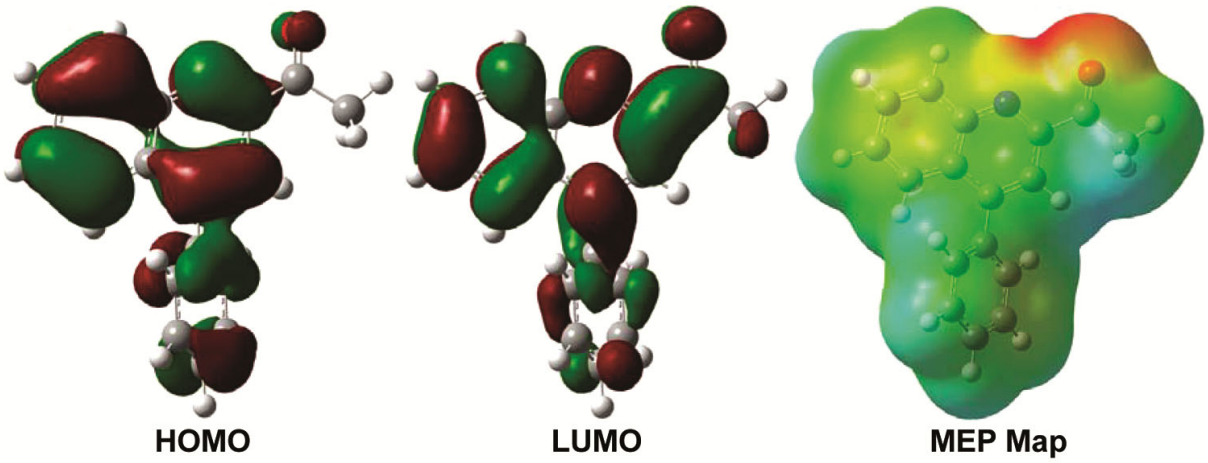


Fig. 2 — Contour plot of HOMO, LUMO and MEP map of compound **3a**

in silico techniques. In this study, epidermal growth factor receptor (EGFR) is selected as target since this receptor plays an important role in prognosis of cancer. Over-expression of EGFR is associated with the development of a wide variety of tumors. Interruption of EGFR signaling can prevent the growth of cancer that expresses the EGFR and improve the patient's condition. At this point, the target protein which PDB code is 1M17 is downloaded from protein data bank. Firstly, the studied eleven compounds are minimized at OPLS4 method using LigPrep module. Then, selected protein is minimized at same method using Protein Preparation module. Then x-y-z coordinate of receptor binding domain of this protein is defined as 22.01-0.25-52.79, respectively. Molecular docking calculations are performed using Ligand Docking module. The results which are docking score (DS), van der Walls energy (E_{vdW}), Coulomb energy (E_{Coul}), and interaction energy (E_{Int}) are given in Table 3.

Table 3 — The molecular docking results

Compd	DS	E_{vdW}	E_{Coul}	E_{Int}
3a	–7.001	–35.739	–2.547	–38.286
3b	–7.062	–36.961	–2.363	–39.324
3c	–7.131	–38.609	–2.345	–40.954
3d	–7.120	–37.146	–2.014	–39.161
3e	–7.123	–38.700	–2.623	–41.324
3f	–7.259	–41.371	–2.577	–43.948
3g	–7.332	–39.925	–2.459	–42.384
3h	–7.065	–37.719	–2.029	–39.748
3i	–6.748	–32.964	–3.615	–36.579
3j	–5.369	–33.027	–2.537	–35.565
3k	–6.024	–33.077	–2.428	–35.505

According to Table 3, docking scores for all studied compounds are more than -7.0 kcal/mol. The best docking score is obtained for compound **3g**. However, compound **3f** result is like compound **3g**, there is only a small difference. Considering the total interaction energies obtained, it is seen that the energies obtained for compounds **3f** and **3g** are better than other compounds. So, it can be said that compound **3f** and **3g** could be good inhibitors for the EGFR.

ADME studies

ADME is an abbreviation for "absorption, distribution, metabolism and excretion" in pharmacokinetics and pharmacology and describes the localization of a pharmaceutical compound within an organism. The whole criteria affect drug levels and drug exposure kinetics to tissues and so affect the performance and pharmacological activity of the drug candidates. QikProp descriptors of studied boron containing compounds are calculated using Maestro 12.8 software to determine the ADME properties. QikProp parameters for compound 1-7 are given in Table 4. QikProp parameters for other compounds are given in supplemental material.

According to Table 4, calculated parameters are in good agreement with the recommended value for each parameter. These parameters reveal the drug likeness properties of the investigated compounds. Additionally, some compounds can be taken part in metabolic reactions which is undesirable. In such cases, the dose of the drugs taken into the body should be adjusted.

Table 4 — Calculated QikProp parameters of studied compounds for ADME analyses

Parameters[a]	**3a**	**3b**	**3c**	**3d**	**3e**	**3f**	**3g**	RV[b]
Stars	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0-5
Amine	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0-1
rtvFG	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0-2
SASA	513.3	537.2	551.6	544.3	553.8	565.4	558.8	300.0-1000.0
FOSA	84.0	84.0	84.9	84.0	84.0	84.9	84.0	0.0-750.0
FISA	59.1	59.1	57.3	59.1	156.7	152.8	156.4	7.0-330.0
PISA	370.2	322.7	286.2	294.3	313.2	276.5	283.0	0.0-450.0
WPSA	0.0	71.4	123.2	106.9	0.0	51.2	35.5	0.0-175.0
donorHB	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0-6.0
AccptHB	3.0	3.0	3.0	3.0	4.0	4.0	4.0	2.0-20.0
QPpolrz	30.7	32.0	33.0	32.3	32.5	33.4	32.7	13.0-70.0
QPPCaco	2724.9	2724.6	2836.2	2725.0	323.5	352.7	325.8	<25 poor >500 great
QPlogBB	–0.1	0.1	0.2	0.1	–1.1	–0.9	–1.0	-3.0- 1.2
QPPMDCK	1461.9	3598.8	7220.1	5632.0	146.1	305.9	230.3	<25 poor >500 great
QPlogKp	–1.1	–1.3	–1.4	–1.4	–3.0	–3.1	–3.1	–8.0 –1.0
metab	0.0	0.0	0.0	0.0	1.0	1.0	1.0	1-8
QPlogKhsa	0.2	0.4	0.5	0.4	0.1	0.2	0.2	–1.5- 1.5
Percent Human-Oral Absorption	100.0	100.0	100.0	100.0	88.0	90.9	89.1	>80% is high <25% is poor
PSA	38.6	38.6	39.1	38.6	83.6	84.0	83.6	7.0- 200.0
RuleOfFive	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Max is 4
RuleOfThree	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Max is 3

[a] **Stars**: Number of property or descriptor values that fall outside the 95% range of similar values for known drugs; **Amine**: Number of non-conjugated amine groups; **rtvFG**: Number of reactive functional groups; **SASA**: Total solvent accessible surface area; FOSA: Hydrophobic component of the SASA; **FISA**: Hydrophilic component of the SASA; **PISA**: π (carbon and attached hydrogen) component of the SASA; **WPSA**: Weakly polar component of the SASA; **donorHB**: Estimated number of hydrogen bonds that would be donated; **AccptHB**: Estimated number of hydrogen bonds that would be accepted; **QPpolrz**: Predicted polarizability in cubic angstroms; **QPPCaco**: Predicted apparent Caco-2 cell permeability in nm/sec; **QPlogBB**: Predicted brain/blood partition coefficient; **QPPMDCK**: Predicted apparent MDCK cell permeability in nm/sec; **QPlogKp**: Predicted skin permeability; **metab**: Number of likely metabolic reactions; **QPlogKhsa**: Prediction of binding to human serum albumin; **Percent Human-Oral Absorption**: Predicted human oral absorption on 0 to 100% scale; **PSA**: Van der Waals surface area of polar nitrogen and oxygen atoms; **RuleOfFive**: Number of violations of Lipinski's rule of five; **RuleOfThree**: Number of violations of Jorgensen's rule of three.

[b] RV: Recommended Value

Conclusion

An efficient $Cu(OTf)_2$ acts as a moderate catalyst in the Friedlander synthesis of 2-acetylquinolines from 2-aminoaryl ketones and butan-1,2-dione to produce the compounds in high yields. The optimized 2-acetyl-4-phenylquinoline analogues were calculated using the frontier molecular orbital (FMO) and molecular electrostatic potential (MEP) map contour plot at the B3LYP/6-31G(d) level of theory in water. Utilizing molecular docking and ADME characteristics, the biological activity of 2-acetylquinolines is then examined. In the end, it is discovered that **3g** and **3f** are the best candidates for suppressing EGFR.

Supplementary Information

The data that supports the findings of this study are available from the supplementary information of this article. Supplementary information is available in the website http://nopr.niscpr.res.in/handle/123456789/58776.

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Conflict of Interest

The authors declare no conflict of interest.

References

1 Morimoto Y, Matsuda F & Shirahama H, *Synlett*, 3 (1991) 202.
2 Micheal JP, *Nat Pro Rep*, 14 (1997) 605.
3 Micheal JP, *Nat Pro Rep*, 19 (2002) 742.
4 Markees DG, Dewey VC & Kidder GW, *J Med Chem*, 13 (1970) 324.
5 Campbell SF, Hardstone JD & Palmer MJ, *J Med Chem*, 31 (1988) 1031.
6 Yadav P & Shah K, *Bioorg Chem*, 109 (2021) 104639.
7 Nainwal LM, Tasneem S, Akhtar W, Verma G, Khan M F, Parvez S, Shaquiquzzaman M, Akhter M & Alam M M, *Eur J Med Chem*, 164 (2019) 121.
8 Li J J, in *Named React* (Springer, Berlin, Heidelberg), (2003), pp.378–379.
9 Doebner O & Miller WV, *Berichte Der Dtsch Chem Gesellschaft*, 14 (1881) 2812.
10 Pfitzinger W, *J für Prakt Chemie*, 33 (1886) 100.
11 Conrad M & Limpach L, *Berichte der Dtsch Chem Gesellschaft*, 20 (1887) 944.
12 Surrey AR, *Combes Quinoline Synthesis*, (Academic Press Inc.), 1961.
13 Povarov LS, *Russ Chem Rev*, 34 (1965) 639.
14 Friedlaender P, *Berichte der Dtsch Chem Gesellschaft*, 15 (1882) 2572.
15 Ghobadi N, Nazari N & Gholamzadeh P, *Adv Heterocycl Chem*, 132 (2020) 85.
16 Satheeshkumar R, Shankar R, Kaminsky W, Kalaiselvi S, Padma V V & Rajendra Prasad KJ, *J Mol Struct*, 1109 (2016) 247.
17 Satheeshkumar R, Sayin K, Kaminsky W & Rajendra Prasad K J, *J Mol Struct*, 1128 (2017) 279.
18 Satheeshkumar R, Shanmugaraj K, Delgado T, Bertrand J, Brito I & Salas CO, *Org Prep Proced Int*, 53 (2021) 138.
19 Cheng C C & Yan S J, *Org React*, 28 (1982) 37.
20 Strekowski L, Czarny A & Lee H, *J Fluor Chem*, 104 (2000) 281.
21 Yadav JS, Reddy BVS & Premalatha K, *Synlett*, 2004 (2004) 963.
22 Yadav JS, Reddy BVS, Sreedhar P, Rao RS & Nagaiah K, *Synthesis (Stuttg)*, 2004 (2004) 2381.
23 Bose DS & Kumar RK, *Tetra Lett*, 47 (2006) 813.
24 Mogilaiah K & Reddy CS, *Syn Comm*, 33 (2003) 3131.
25 De SK & Gibbs RA, *Tetra Lett*, 46 (2005) 1647.
26 Arumugam P, Karthikeyan G, Atchudan R, Muralidharan D & Perumal P T, *Chem Lett*, 34 (2005) 314.
27 Wu J, Zhang L & Diao T N, *Synlett*, 17 (2005) 2653.
28 Varala R, Enugala R & Adapa S R, *Synthesis (Stuttg)*, 22 (2006) 3825.
29 Ryabukhin S V, Volochnyuk D M, Plaskon A S, Naumchik V S & Tolmachev A A, *Synthesis (Stuttg)*, 8 (2007) 1214.
30 Palimkar SS, Siddiqui SA, Daniel T, Lahoti RJ & Srinivasan K V, *J Org Chem*, 68 (2003) 9371.
31 Hu Y Z, Zhang G & Thummel R P, *Org Lett*, 5 (2003) 2251.
32 Karthikeyan G & Perumal P T, *J Heterocycl Chem*, 41 (2004) 1039.
33 Song S J, Cho S J, Park D K, Kwon T W & Jenekhe S A, *Tetra Lett*, 44 (2003) 255.
34 Muscia G C, Bollini M, Carnevale J P, Bruno A M & Asís S E, *Tetra Lett*, 47 (2006) 8811.
35 Satheeshkumar R, Sayin K, Kaminsky W & Rajendra P K J, *Syn Comm*, 47 (2017) 1940.
36 Xie R, Lu G P, Jiang H F & Zhang M, *J Cat*, 383 (2020) 239.
37 Satheeshkumar R, Shankar R, Kaminsky W & Rajendra Prasad K J, *Chem Sel*, 1 (2016) 6823.
38 Satheeshkumar R, Edatt L, Muthusankar A, Sameer Kumar V B & Rajendra Prasad K J, *Polycycl Aromat Comp*, 41 (2021) 1631.
39 Satheeshkumar R, Rajamanikandan R, Ilanchelian M, Sayin K & Prasad K J R, *Spectrochim Acta - Part A Mol Biomol Spect*, 221 (2019) 117196.
40 Satheeshkumar R, Kaminsky W, Sparkes H A & Rajendra Prasad K J, *Synth Comm*, 45 (2015) 2203.
41 Satheesh K R, Kaminsky W & Rajendra Prasad K J, *Synth Comm*, 47 (2017) 245.
42 Yadav J S, Rao P P, Sreenu D, Srinivasa R R, Kumar V N, Nagaiah K & Prasad A R, *Tetra Lett*, 46 (2005) 7249.
43 Wang G W, Jia C S & Dong Y W, *Tetra Lett*, 47 (2006) 1059.
44 Desai U V, Mitragotri S D, Thopate T S, Pore D M & Wadgaonkar P P, *Arkivoc*, 2006 (2007) 198.
45 Narasimhulu M, Reddy T S, Mahesh K C, Prabhakar P, Rao C B & Venkateswarlu Y, *J Mol Catal A Chem*, 266 (2007) 114.
46 Fehnel E A, *J Hetero Chem*, 4 (1967) 565.
47 Arcadi A, Chiarini M, Di G S & Marinelli F, *Synlett*, 2 (2003) 203.
48 McNaughton B R & Miller B L, *Org Lett*, 5 (2003) 4257.
49 Das B, Damodar K, Chowdhury N & Kumar RA, *J Mol Catal A Chem*, 274 (2007) 148.
50 Lotfi S, Nikseresht A & Rahimi N, *Polyhedron*, 173 (2019) 114148.
51 Hasaninejad A, Zare A, Shekouhy M & Ameri-Rad J, *Green Chem*, 13 (2011) 958.
52 Dhakshinamoorthy A & Garcia H, *Chem Soc Rev*, 43 (2014) 5750.
53 Pérez-Mayoral E & Čejka J, *Chem Cat Chem*, 3 (2011) 157.
54 Lenoci A, Tomassi S, Conte M, Benedetti R, Rodriguez V, Carradori S, Secci D, Castellano S, Sbardella G, Filetici P, Novellino E, Altucci L, Rotili D & Mai A, *Chem Med Chem*, 9 (2014) 542.
55 Hara M, Yoshida T, Takagaki A, Takata T, Kondo J N, Hayashi S & Domen K, *Angew Chemie Int Ed*, 43 (2004) 2955.
56 Toda M, Takagaki A, Okamura M, Kondo JN, Hayashi S, Domen K & Hara M, *Nature*, 438 (2005) 178.
57 Reddy B V S, Venkateswarlu A, Reddy G N & Reddy Y V R, *Tetra Lett*, 54 (2013) 5767.
58 Fareghi-Alamdari R, Golestanzadeh M & Zekri N, *New J Chem*, 40 (2016) 3400.
59 Satheeshkumar R, Kalaiselvi S, Rajendra Prasad K J, Wang W L & Salas C O, *Chem Biol Drug Des*, 100(6) (2022) 1042.
60 Frisch M J, Trucks G W, Schlegel H B, Scuseria G E, Robb M A, Cheeseman J R, Scalmani G, Barone V, Petersson G A, Nakatsuji H, Li X, Caricato M, Marenich A V, Bloino J, Janesko B G, Gomperts R, Mennucci B, Hratchian H P, Ortiz J V, Izmaylov A F, Sonnenberg J L, Williams-Young D, Ding F, Lipparini F, Egidi F, Goings J, Peng B, Petrone A, Henderson T, Ranasinghe D, Zakrzewski V G, Gao J, Rega N, Zheng G, Liang W, Hada M, Ehara M, Toyota K, Fukuda R, Hasegawa J, Ishida M, Nakajima T, Honda Y, Kitao O, Nakai H, Vreven T, Throssell K, Montgomery J A J, Peralta J E, Ogliaro F, Bearpark M J, Heyd J J, Brothers E N, Kudin K

N, Staroverov V N, Keith T A, Kobayashi R, Normand J, Raghavachari K, Rendell A P, Burant J C, Iyengar S S, Tomasi J, Cossi M, Millam J M, Klene M, Adamo C, Cammi R, Ochterski J W, Martin R L, Morokuma K, Farkas O, Foresman J B & Fox D J, *Gaussian 16 Revision C01*, 2016

61 Frisch M J, Trucks G W, Schlegel H B, Scuseria G E, Robb M A, Cheeseman J R, Scalmani G, Barone V, Petersson G A, Nakatsuji H, Li X, Caricato M, Marenich A V, Bloino J, Janesko B G, Gomperts R, Mennucci B, Hratchian H P, Ortiz J V, Izmaylov A F, Sonnenberg J L, Williams-Young D, Ding F, Lipparini F, Egidi F, Goings J, Peng B, Petrone A, Henderson T, Ranasinghe D, Zakrzewski V G, Gao J, Rega N, Zheng G, Liang W, Hada M, Ehara M, Toyota K, Fukuda R, Hasegawa J, Ishida M, Nakajima T, Honda Y, Kitao O, Nakai H, Vreven T, Throssell K, Montgomery J A J, Peralta J E, Ogliaro F, Bearpark M J, Heyd J J, Brothers E N, Kudin K N, Staroverov V N, Keith T A, Kobayashi R, Normand J, Raghavachari K, Rendell A P, Burant J C, Iyengar S S, Tomasi J, Cossi M, Millam J M, Klene M, Adamo C, Cammi R, Ochterski J W, Martin R L, Morokuma K, Farkas O, Foresman J B, Fox D J, *Gaussian 09 Revision A02*, 2009

62 Gedikli MA, Tuzun B, Aktas A, Sayin K & Ataseven H, *Bratislava Med J*, 122 (2021) 101.

63 Satheeshkumar R, Prabha K, Vennila K N, Sayin K, Güney E, Kaminsky W & Acevedo R, *J Mol Struc*, 1267 (2022) 133552.