RSC Advances

PAPER

View Article Online
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Cite this: *RSC Adv.*, 2023, **13**, 14631

Novel quinoline/thiazinan-4-one hybrids; design, synthesis, and molecular docking studies as potential anti-bacterial candidates against MRSA†

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In an attempt to develop effective and safe antibacterial agents, we synthesized novel thiazinanones by combining the quinolone scaffold and the 1,3-thiazinan-4-one group by reaction between ((4-hydroxy-2-oxo-1,2-dihydroquinolin-3-yl)methylene)hydrazinecarbothioamides and 2,3-diphenylcycloprop-2-enone in refluxing ethanol in the presence of triethyl amine as a catalyst. The structure of the synthesized compounds was characterized by spectral data and elemental analysis, IR, MS, ^{1}H and ^{13}C NMR spectroscopy which showed two doublet signals for CH-5 and CH-6 and four sharp singlets for the protons of thiazinane NH, CH=N, quinolone NH and OH, respectively. Also, the ^{13}C NMR spectrum clearly showed the presence of two quaternary carbon atoms which were assigned to thiazinanone-C-5 and C-6. All the 1,3-thiazinan-4-one/quinolone hybrids were screened for antibacterial activity. Compounds **7a**, **7e** and **7g** showed broad spectrum antibacterial activity against most of the tested strains either G +ve or G −ve. Compound **7e** is the most potent antibacterial agent against MRSA with the minimum inhibitory concentration against MRSA found to be 48 μg mL^{-1} compared to the drug ciprofloxacin (96 μg mL^{-1}). Additionally, a molecular docking study was performed to understand the molecular interaction and binding mode of the compounds on the active site of *S. aureus Murb* protein. *In silico* docking assisted data strongly correlated with the experimental approach of antibacterial activity against MRSA.

Received 16th March 2023
Accepted 28th April 2023

DOI: 10.1039/d3ra01721d

rsc.li/rsc-advances

1. Introduction

Thiazinanones, despite their an appropriate term, are very interesting because of their significant role in pharmaceutical chemistry.[1–3] Substituted thiazinanones displayed antitumor,[4] antifungal[5] and antimalarial activity which was assessed by Kumawat *et al.*,[6] as well as anti-oxidant activity.[7] Thiazinanone derivatives were obtained through a multicomponent condensation or a two-step process involving an amine, mercapto acid, and carbonyl compounds.[5] 3-Alkyl-2-aryl-1,3-thiazinan-4-ones with methylsulfonyl pharmacophore exhibited inhibition activity against cyclooxygenase-2-[COX-2].[8] As well, 3-pyridin-2-ylmethyl-1,3-thiazinan-4-ones displayed anti-oxidant activities.[7] 3-(3-(6-Chloro-2-methoxyacridin-9-ylamino)propyl)-2-(thiophen-2-yl)-1,3-thiazinan-4-one (**I**) showed activity against various cancer cell types, such as prostate cancer, two lung cancer cell lines, and eight breast cancer cell lines with varying genetic background (Fig. 1).[9]

Quinolones are a fascinating class of heterocycles having a nitrogen atom. They are also essential moieties in medicinal chemistry. Scientists around the world have been interested in quinolones' biological applications.[10,11] Quinolone derivatives have revealed anti-cancer,[12] anti-malarial,[13] anti-inflammatory,[14] anti-viral,[15] anti-bacterial and anti-fungal activities.[16] 3-((7-Chloroquinolin-4-ylamino)methyl)-2-phenyl-1,3-thiazinan-4-one derivatives **II** (Fig. 1) were screened for their *in vitro* anti-bacterial activity against a panel of pathogenic bacterial strains,

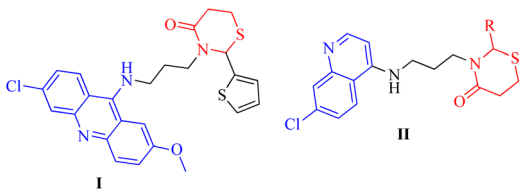

Fig. 1 Anticancer and antibacterial thiazinanones I and II.

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† Electronic supplementary information (ESI) available. See DOI: https://doi.org/10.1039/d3ra01721d

antitubercular activity against *Mycobacterium tuberculosis* H37Rv and also for their *in vitro* antimalarial activity against *Plasmodium falciparum*. Several of the synthesized compounds exhibited excellent antibacterial activity against *C. tetani*. Some of them showed excellent antitubercular and antimalarial activity.[17]

Many chemists have been interested in the chemistry of cyclopropenones throughout the last three decades,[18,19] with a special emphasis on diphenylcyclopropenone's behavior.[20] The formation of aza-cyclopentanones (pyrrolidinones) has been reported, *via* the reaction of 2,3-diphenylcyclopropenone with compounds containing C=N moieties.[21–24] Triphenylpyrimidinones were obtained through the reaction of amidrazones with 2,3-diphenylcyclopropenone in EtOH/Et_3N accompanied by elimination of ammonia.[25] The reaction of alkenylidenehydrazine-carbothioamides with cyclopropenone, as well as the presence of nucleophilic sites like azomethine carbon and sulfur atoms, resulted in 3,5-disubstituted 1,3,4-thiadiazolyl-2,3-diphenylpropenones.[26] The reaction of cyclopropenone with various aldehyde 4-phenyl thiosemicarbazones in acetic acid afforded pyrrolo[2,1-*b*]oxadiazoles through [2 + 3] cycloaddition; H_2S was eliminated.[27] Moreover, 2,4-disubstituted thiosemicarbazides reacted with cyclopropenone to afford the corresponding pyridazines.[28] 2,3-Diphenylcyclopropenone reacted with *N*-imidoyl-thiourease accompanied by elimination of phenylisothiocyanate; 3-substituted 2,5,6-triphenylpyrimidin-4-ones were obtained.[29] The reaction of pyrazolylthiourea with cyclopropenone, followed by oxidation with DDQ, yielded 5,6-diphenyl-1,3-thiazinones *via* the formation of pyrazolylimino-3,5,6-triphenyl-1,3-thiazinan-4-ones.[30] Racemic 2-((2,4-dinitrophenyl)-hydrazono)-5,6-diphenyl-1,3-thiazinan-4-ones and (*Z*)-*N*′-(2,4-dinitrophenyl)-2,3-diphenylacrylo-hydrazides were obtained *via* the diastereoselective reaction between 2,3-diphenylcyclopropenone and 4-substituted 1-(2,4-dinitrophenyl) thiosemicarbazides.[31]

The serious medical problem of Multi Drug Resistance (MDR) of bacteria leads to increasing levels of resistance to classical antibiotics among Gram-positive organisms such as *pneumococci*, *enterococci*, and *staphylococci*.[32] In communities worldwide, MRSA (methicillin-resistant *Staphylococcus aureus*) is a severe health hazard. The World Health Organization (WHO) has identified MRSA as one of the top threats to people causing developed resistance to almost all classes of antimicrobial agents.[33] Treatments for MRSA infections are limited and thus it has become a leading cause of morbidity and mortality across the globe after cancer.[34] In spite of enormous amounts of research works, these MDR pathogens remain a challenge in developing new drug candidates.

Large amounts of effort towards further research of quinolones are performed to develop new more effective antibacterial agents with broader antimicrobial spectrum and better therapeutic index. The azolylthioether quinolones **III** (Fig. 2) exhibited good antimicrobial activities that displayed remarkable anti-MRSA and anti-*P. aeruginosa* efficacies with low MIC values of 0.25 μg mL^{-1}, even superior to reference drugs. They induced bacterial resistance more slowly than clinical drugs.[35] Also, compound **IV** (Fig. 2), 3-aminothiazolquinolones, 3-(2-aminothiazol-4-yl)-7-chloro-6-(pyrrolidin-1-yl)quinolone exhibited potent antibacterial activity, low cytotoxicity to hepatocyte cells, strong inhibitory potency to DNA gyrase and a broad antimicrobial spectrum including against multidrug-resistant strains. This active molecule **IV** also induced bacterial resistance more slowly than norfloxacin.[36] Moreover, thiazinane was taken into consideration in MDR challenge whereas the monoiodinated thiazine derivative **V** (Fig. 2) showed good antibacterial activity against methicillin-sensitive *Staphylococcus aureus* (*S. aureus*, MSSA) ATCC 29213 and methicillin-resistant *Staphylococcus aureus* (MRSA) ATCC 43300. Among strategies by which resistance can be achieved, overexpression of efflux pumps such as NorA of *Staphylococcus aureus* leads to a sub-lethal concentration of 3-phenyl-1,4-benzothiazine **VI** (Fig. 2), at the active site that in turn may predispose the organism to the development of high-level target-based resistance. With an aim to improve both the chemical stability and potency of our previously reported 3-phenyl-1,4-benzothiazine.[37]

In response to the previously mentioned findings, we here designed novel compounds based on the concept of merging more than one scaffold in one compact structure. Hybrids **7a–h** gather two types of anti-MRSA scaffolds; 2-quinolones and 1,3-thiazines in one novel hybrid aims to develop simpler and more efficient antibacterial compounds with synergistic effect and less bacterial resistance. Testing against G +ve and G −ve bacteria align with examining against methicillin-resistant *S. aureus* (MRSA) to investigate the anti-MDR activity as well as anti-bacterial spectrum. This is illustrated in a summarized schematic diagram (Fig. 2).

2. Results and discussion

2.1. Chemistry

The target ((*E*)-((4-hydroxy-2-oxo-1,2-dihydroquinolin-3-yl) methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one derivatives **7a–h** were obtained through the route outlined in Scheme 1. The strategy starts by preparing compounds **2a–h**, **3a–h** and **5a–h** according to reported methods. Treating aniline derivatives **1a–h** with polyphosphoric acid (PPA), and diethyl malonate (DEM) at 220 °C afforded 2-quinolones **2a–h**.[38] Gentle heating of **2a–h** with $CHCl_3$ and 15% NaOH gave the corresponding 4-hydroxy-2-oxo-1,2-dihydroquinoline-3-carbaldehydes **3a–h**. Reaction of **3a–h** with thiosemicarbazide (**4**) gave the corresponding thiosemicarbazones **5a–h** (Scheme 1), and their structures were confirmed by comparing their spectral data to those previously published. Accordingly, thiosemicarbazones **5a–h** were treated with 2,3-diphenylcyclopropenone (**6**) in dry EtOH using a few drops of Et_3N under reflux for 4–6 h to give 1,3-thiazinan-4-ones **7a–h** as the only products in excellent yields.

Diastereomeric mixtures **7a–h** were formed as a result of the development of two new stereo centers at C-5 and C-6 positions. As a result, most signals in the ^1H and ^{13}C NMR spectra were duplicated. The expected diastereomeric forms were not separable by column chromatography. In the ^1H NMR spectra, the signals of the respective protons of the synthesized compounds were confirmed based on their chemical shifts and multiplicities. The compounds reported in this study have been

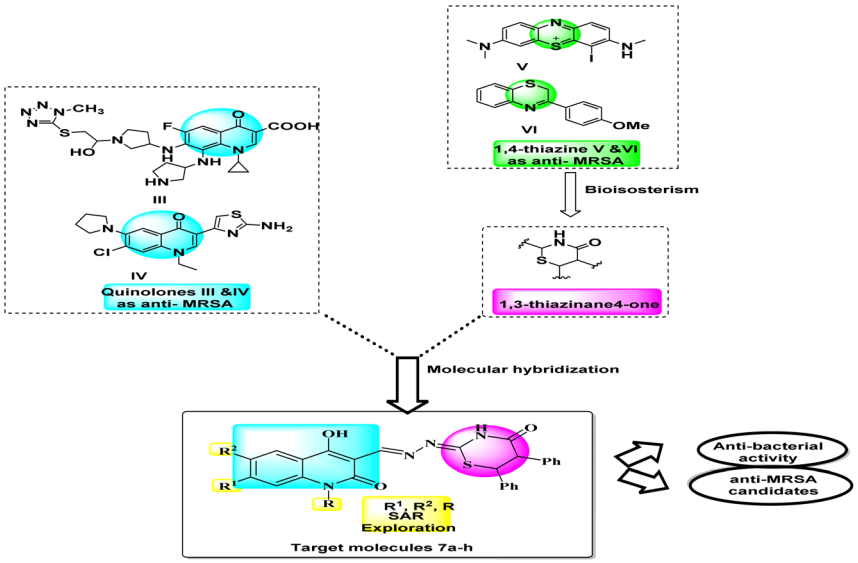
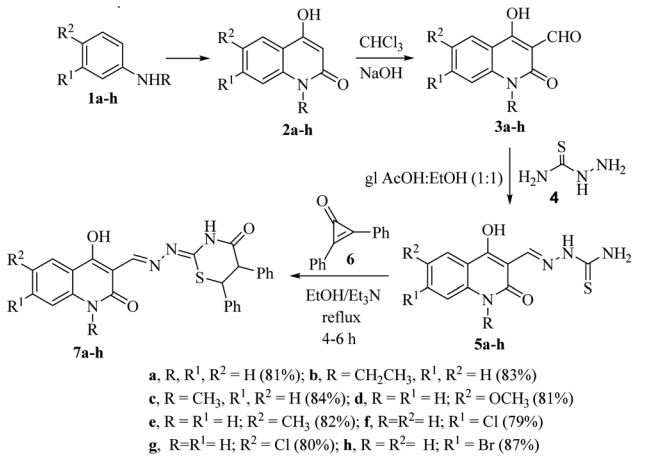


Fig. 2 Design of target compounds **7a–h**.



Scheme 1 Synthesis of hydrazono-5,6-diphenyl-1,3-thiazinan-4-ones **7a–h**.

thoroughly characterized by elemental analysis and mass spectral data. The ^{1}H NMR spectrum of **7a** showed, in addition to the aromatic protons, two doublet signals for CH-6 and CH-5 at δ_H = 4.50 ppm and 5.44 ppm with coupling constant J = 4.0 Hz and four sharp singlets at δ_H = 8.15, 8.55, 11.60 and 12.03 ppm related to the protons of thiazinane NH, CH=N, quinolone NH and OH, respectively. As the saturated thiazinanes belong to the cyclohexane confirmation structure, the coupling constant values of CH-5 and CH-6 = 4 Hz. Moreover, the ^{13}C NMR spectrum clearly showed the presence of two quaternary carbon atom which resonated at δ_C = 43.36 and 56.06 ppm which were assigned to thiazinanone-CH-6,5. Furthermore, the ^{13}C NMR spectrum revealed the presence of carbonyl-thiazinanone and carbonyl-quinolone, quinolone C-4, CH=N and C=N at δ_C = 168.17, 165.88, 163.30, 161.45 and 158.07 ppm, respectively (see the Experimental section). According to elemental analysis and mass spectrometry, compound **7a** has a molecular formula of $C_{26}H_{20}N_4O_3S$, resulting from the addition of one molecule of hydrazinecarbothioamide **5a** with one molecule of **6** without any elimination.

In case of **7b**, its ^{1}H NMR spectrum showed triplet and quartet signals for CH_3 and CH_2 groups appeared at δ_H = 1.23 and δ_H = 4.28 ppm. Whereas the OH, CH=N and thiazinanone-NH protons resonated as three singlets at δ_H = 12.03, 8.83 and 8.03 ppm, respectively. Also, doublet signals for CH-5 and CH-6 at δ_H = 4.50 ppm and δ_H = 5.44 ppm (J = 4.0 Hz). The ^{13}C NMR spectrum revealed CH_3, CH_2, C-6, C-5, C=N, CH=N, C–OH, carbonyl-quinolone and carbonyl-thiazinanone at δ_C = 15.09, 38.11, 44.19, 56.98, 157.16, 161.34, 164.28, 165.28 and 168.81, respectively (Fig. 3).

The plausible mechanism for the formation of 1,3-thiazinan-4-ones **7a–h** was based upon the conjugate double bond of **6** was attacked by the thione lone pair forming zwitterion salts **8a–h**. Subsequently, a proton was transferred in **8a–h** to give the intermediates **9a–h**, which on rearrangement and ring opening of cyclopropenone would give the intermediate **10a–h**. The carbonyl carbon was then attacked by the lone-pair of nitrogen to form intermediates **11a–h**, which rearranged to give the final products **7a–h** (Scheme 2).

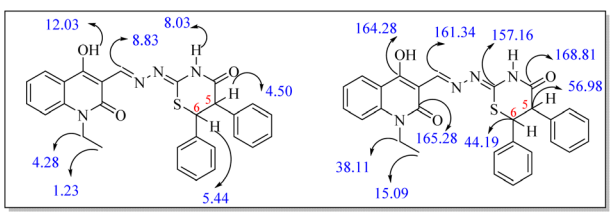


Fig. 3 δ values of some distinctive carbons and protons of compound **7b**.

Using compound **7a** as an example, we carried out the reaction in various settings after optimizing the reaction conditions. When the reaction was refluxed in DMF/Et_3N and dioxane/Et_3N, it was found that the yield of **7a** was reduced to 60% and 64%, respectively. In addition, side products were obtained from the reaction. As a result, utilizing ethanol in the presence of Et_3N as a catalyst is the best way to get high yields.

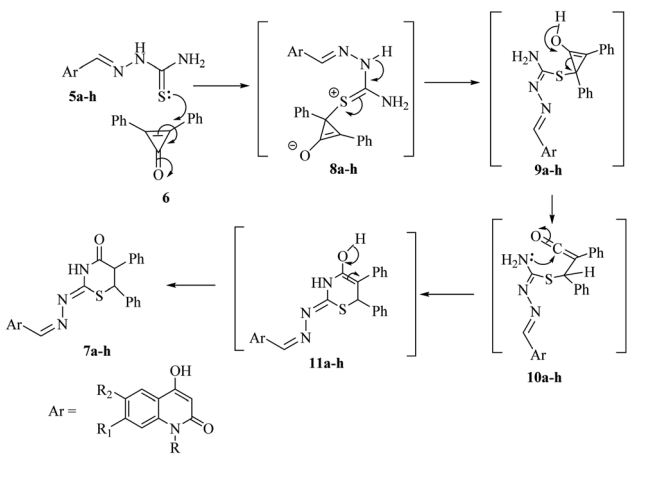
2.2. Screening of antibacterial activity

The antibacterial and antifungal activities of compounds **7a–h** were evaluated *in vitro* against three-Gram positive (G +ve) strains; non-resistant *S. aureus* (ATCC 6538), methicillin resistant *Staphylococcus aureus* (MRSA) and *Escherichia coli* (ATCC 25922) and two-Gram negative (G −ve) strains; *Pseudomonas aeruginosa* (ATCC 10145) and *Salmonella*. The tested compounds were assayed against ciprofloxacin as an antibacterial reference using standard agar cup diffusion method. Results of the antibacterial screening are listed in Table 1.

According to the MICs recorded in Table 1, it can be deduced that most of the tested compounds showed a higher antibacterial activity than the reference ciprofloxacin against G +ve bacteria. It was found that compound **7a**, **7e** and **7h** displayed potent activity against non-resistant *S. aureus* compared with the reference with MICs of 12, 48, and 48 μM, respectively. Meanwhile, compounds **7e** displayed significant antibacterial activity against MRSA better than the reference with MICs 48 and 96 μM, respectively, however **7a** showed remarkable activity of MIC 96 μM.

Moreover, compounds **7g** exhibited the good activity against *E. coli* with MICs of 24 μM when compared to the reference, however, both **7a** and **7d** showed moderate activity against *E. coli*.

Concerning activity against G −ve strains; compounds **7e** and **7g** revealed a high potency against *P. aeruginosa* with MICs of 12 and 12 μM. On contrast, other compounds displayed moderate to weak activity (Fig. 4). Furthermore, the derivatives **7d–f** showed moderate activity against *Salmonella* with MICs of 96 μg mL^{-1}, respectively (Table 1 and Fig. 4).



Scheme 2 The rationale for the formation of 1,3-thiazinan-4-ones 7a–h.

2.2.1. Structure–activity relationship.

Based on the aforementioned results, it is obvious that compounds **7a**, **7e** and **7g** showed broad spectrum antibacterial activity against all the tested strains either G +ve or G −ve. In general, the quinolone-based thiazine derivatives **7c** and **7f** exhibited weak activity almost against most of the tested strains. From the above results, it can be concluded that, there is no specific substituent on the *quinolone nucleus* of tested compounds to enhance the antibacterial activity in a broad-spectrum manner. So, the enhanced activity of some of the tested derivatives may be due to improvement of the physicochemical properties and consequently enhancing permeability to microbial cells.

In summary, compound **7e** presented a significant broad spectrum anti-bacterial activity that was probably attributed to when (R^1 = CH_3), it would enhance the physicochemical parameters and hence increase cell permeability against either nonresistant or resistant strains.

2.3. Molecular modeling studies

Docking studies have been carried out to elucidate the binding mode of the quinolone/thiazine hybrids **7a–h** with the protein active site of *S. aureus Murb* (PDB ID: IHSK). Prior to the molecular docking studies, the receptor protein was prepared for docking by omitting additional water and co-factors, followed by the addition of polar hydrogens and computing charges fixation. Also, the docking scores of the tested compounds are depicted in Table 2 that used to calculate the inhibition constant (K_i value) according to the reported equation[7] (see ESI†). Typically, a high potency is implied by a low K_i value and it has to be in the micromolar range for a molecule to be qualified as a lead compound or hit. Compounds **7b**, **7c**, **7e** and **7h** have the least K_i value of 0.62×10^{-6}, 0.83×10^{-6}, 0.78×10^{-6} and 0.76×10^{-6} μM, respectively to qualify as a drug and hence, the most potent among the other tested compounds.

Docking results of the known antibacterial reference; ciprofloxacin into active site of *S. aureus Murb* protein (Fig. 5 and Table 2) revealed that ciprofloxacin showed CDOCKER energy of −6.53 kcal mol^{-1} and engaged in two hydrogen bonds with amino acid residues SER82 and GLY79.

Most of the tested compounds have high binding affinity to protein of *S. aureus Murb* as the binding free energy (ΔG) values of them range from 0.0 to −2.6 kcal mol^{-1}. The docking study results of target **7b**, **7c** and **7f** showed interactions typically as the reference with amino acid residues SER82 and GLY79.

Although, all the tested compounds **7a–h** showed interaction with amino acid residues SER82 and TYR149, hybrids **7a**, **7e** and **7h** lack interaction with the last residue.

Moreover, compounds **7e** and **7h** exhibited potential interactions with both amino acid residues ASN80 and ARG255, while the hybrid **7d** interacted with the first residue and the second residue engaged with the **7a**.

Interestingly, compound **7f** showed additional two hydrophobic interactions with ILE140 amino acid residue which is not observed with the others.

Collectively, the docking results were in agreement with the biological study, and we could conclude that hybrid **7e** entitled

Table 1 The MICs of antibacterial activity of the tested compounds, ciprofloxacin (μg mL^{-1})

	MIC[a] (μM)				
	Gram +ve			Gram −ve	
Compound	Non-resistant *S. aureus*	MRSA	*E. coli*	*P. aeruginosa*	*Salmonella*
7a	48	96	48	48	768
7b	768	>2000	768	96	>2000
7c	>2000	>2000	768	768	>2000
7d	48	334	48	24	96
7e	12	48	96	12	96
7f	142	>2000	768	320	96
7g	96	768	24	12	>2000
7h	48	384	768	96	320
Ciprofloxacin	12	96	24	12	24

[a] MIC = lowest conc. inhibit the growth + highest conc. allow the growth/2.

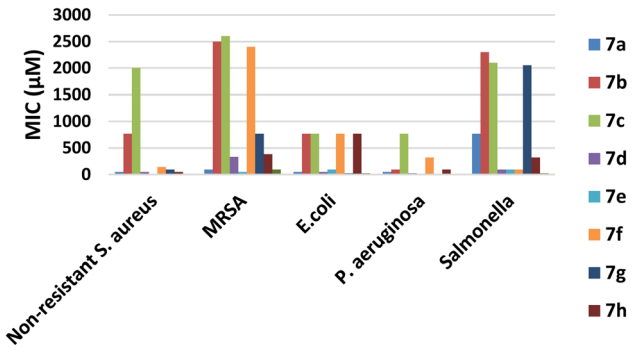


Fig. 4 MICs of the tested compounds **7a–h**.

to be promising as attractive future lead candidate for the development of broad-spectrum antibacterial activity.

3. Experimental

3.1. Chemistry

A list of chemicals and instrumentation is provided in the ESI.†

3.1.1. Starting materials. Carbaldehydes **3a–c**,[39–41] **3e–h**[42] and thiosemicarbazones **5a–c**[43,44] and **5e–h**[45] were prepared according to literature methods.

3.1.2. General procedure. Equimolar amounts of 2,3-diphenylcycloprop-2-enone **6** and the appropriate hydrazinecarbothioamides **5a–e** were mixed in absolute EtOH and a few drops of Et_3N was added as a catalyst and refluxed for about 4–6 h, furnished yellow precipitates (*i.e.* the reaction was followed up by TLC analysis). The precipitate was filtered, washed with ethanol, dried and recrystallized from the stated solvents to give the final products **7a–h**.

(Z)-2-((E)-((4-Hydroxy-2-oxo-1,2-dihydroquinolin-3-yl) methylene)-hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one ***(7a).*** Yellow crystals (DMF/EtOH), yield: 0.379 g (81%); mp 300–302 °C; R_f = 0.22 (toluene–ethyl acetate, 1 : 1); IR (KBr): ν = 3392 (OH), 3230, 3215 (NH), 3066 (Ar-CH), 2934 (aliph-CH), 1662 and 1649 (CO), 1628 cm^{-1} (C=N); ^{1}H NMR (400 MHz, DMSO-d_6): δ_H = 4.50 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.44 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 6.84 (dd, 2H, J = 8.0 Hz, Ar-H), 6.96 (dd, 2H, J = 8.0 Hz, Ar-H), 7.18–7.30 (m, 5H, Ar-H), 7.58–7.60 (m, 5H, Ar-H), 8.15 (brs, 1H, thiazinanone-NH), 8.55 (s, 1H, CH=N), 11.60 (s, 1H, quinolone-NH), 12.03 (s, 1H, quinolone-OH); ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 43.36 (thiazinanone-CH-6), 56.06 (thiazinanone-CH-5), 109.90 (quinolone-C3), 114.87, 116.49, 117.75, 118.41, 120.03, 122.02, 122.68, 123.27, 125.56, 126.59, 127.55, 128.30, 129.83, 132.05 (Ar-CH), 134.99, 136.98, 139.57, 143.77 (Ar-C), 158.07 (C=N), 161.45 (CH=N), 163.30 (C-OH), 165.88 (quinolone-C=O), 168.17 (thiazinanone-C=O). MS (Fab, 70 eV, %): m/z = 468 (M^+, 70), 391 (25), 307 (100), 289 (15), 273 (5). Anal. calcd for $C_{26}H_{20}N_4O_3S$ (468.53): C, 66.65; H, 4.30; N, 11.96; S, 6.84. Found: C, 66.80; H, 4.34; N, 12.10; S, 6.98.

(Z)-2-((E)-((1-Ethyl-4-hydroxy-2-oxo-1,2-dihydroquinolin-3-yl)-methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one ***(7b).*** Yellow crystals (DMF/EtOH), yield: 0.412 g (83%); mp 281–283 °C; R_f = 0.30 (toluene–ethyl acetate, 10 : 8); IR (KBr) ν = 3390 (OH), 3230 (NH), 3070 (Ar-CH), 2970 (aliph-CH), 1672 and 1668 (CO), 1611 cm^{-1} (C=N); ^{1}H NMR (400 MHz, DMSO-d_6): δ_H = 1.23 (t, 3H, J = 8.0 Hz, CH_3), 4.28 (q, 2H, J = 8.0 Hz, CH_2), 4.50 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.44 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 6.84 (dd, 2H, Ar-H), 6.97 (dd, 2H, Ar-H), 7.28–7.31 (m, 10H, Ar-H), 8.03 (brs, 1H, thiazinanone-NH), 8.83 (s, 1H, CH=N), 12.03 (s, 1H, quinolone-OH); ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 15.09 (CH_3), 38.11 (CH_2), 44.19 (thiazinanone-CH-6), 56.98 (thiazinanone-CH-5), 109.89 (quinolone-C3), 115.30, 123.90, 123.99, 127.94, 128.02, 128.59 (Ar-CH), 128.79, 128.90, 129.24, 129.39 (Ar-2CH), 133.50, 133.63, 134.62, 139.80 (Ar-C), 157.16 (C=N), 161.34 (CH=N), 164.28 (C-OH), 165.28 (quinolone-C=O), 168.81 (thiazinanone-C=O); MS (Fab, 70 eV, %): m/z = 496 (M^+, 100), 468 (70), 307 (50), 316 (88), 288 (45), 280 (20), 216 (15), 189 (30). Anal. calcd for $C_{28}H_{24}N_4O_3S$ (496.58): C, 67.72; H, 4.87; N, 11.28; S, 6.46. Found: C, 67.81; H, 4.92; N, 11.15; S, 6.33.

(Z)-2-((E)-((1-Methyl-4-hydroxy-2-oxo-1,2-dihydroquinolin-3-yl)-methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one ***(7c).*** Yellow crystals (DMF/H_2O), yield: 0.405 g (84%); mp 280–282 °C; R_f = 0.22 (toluene–ethyl acetate, 10 : 8); IR (KBr) ν = 3308 (OH), 3276 (NH), 3109 (Ar-CH), 2965 (aliph-CH), 1639 and 1615 (CO),

Table 2 Energy scores for the complexes formed by the optimized structures of tested **7a–h** in the active site of the *S. aureus Murb* (PDB ID: IHSK)

Compound	*S* score	C-Docker energy (kcal mol^{-1})	Inhibition constant, K_i (μM)	Ligand–receptor interaction		
				Residue	Type	Length (Å)
7a	−7.43	−0.7	3.64×10^{-6}	SER82	H-donor	3.68
		−0.8		ARG225	Pi-cation	4.32
7b	−8.48	−2.3	0.62×10^{-6}	SER82	H-donor	2.86
		−2.2		GLY79	H-acceptor	3.00
		−1.4		GLY81	H-acceptor	3.24
		−0.0		TYR149	Pi–Pi	3.94
7c	−8.27	−2.1	0.83×10^{-6}	SER82	H-donor	2.94
		−2.2		GLY79	H-acceptor	3.00
		−1.2		GLY81	H-acceptor	3.26
		−0.0		TYR149	Pi–Pi	3.94
7d	−8.00	−2.1	1.39×10^{-6}	GLY146	H-donor	3.19
		−2.2		SER82	H-acceptor	3.12
		−1.6		SER82	H-acceptor	2.60
		−0.7		TYR149	H–Pi	4.10
		−2.6		ASN83	Pi–H	4.15
7e	−8.34	−1.7	0.78×10^{-6}	AS80	H-acceptor	3.30
		−1.9		SER143	H-acceptor	3.28
		−0.7		SER82	Pi–H	4.55
		−0.9		ARG225	Pi-cation	4.36
7f	−7.95	−2.0	1.51×10^{-6}	SER82	H-donor	2.99
		−2.1		GLY79	H-acceptor	2.99
		−0.9		GLY81	H-acceptor	3.32
		−0.6		ILE140	Pi–H	4.51
		−0.6		ILE140	Pi–H	4.10
		−0.0		TRY149	Pi–Pi	3.93
7g	−7.69	−0.9	2.34×10^{-6}	SER82	H-acceptor	3.99
		−1.5		SER82	H-acceptor	2.86
		−0.7		TRY149	Pi–H	4.08
7h	−8.36	−2.4	0.76×10^{-6}	ASN80	H-acceptor	3.14
		−1.0		SER143	H-acceptor	3.49
		−0.7		SER80	Pi–H	4.52
		−0.9		ARG225	Pi-cation	4.36
Ciprofloxacin	−6.53	−1.5	14.49×10^{-6}	SER82	H-acceptor	3.19
		−2.7		GLY79	H-acceptor	2.74

1584 cm^{-1} (C=N); ^{1}H NMR (400 MHz, DMSO-d_6): δ_H = 3.61 (s, 3H, CH_3), 4.51 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.45 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 6.84–6.86 (m, 2H, Ar-H), 6.97 (dd, 2H, Ar-H), 7.23–7.30 (m, 10H, Ar-H), 7.97 (brs, 1H, thiazinanone-NH), 8.83 (s, 1H, CH=N), 12.03 (s, 1H, quinolone-OH); ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 34.48 (CH_3), 44.19 (thiazinanone-CH-6), 55.76 (thiazinanone-CH-5), 108.56 (quinolone-C3), 114.11, 122.27, 122.75, 126.61, 126.93, 128.07 (Ar-CH), 128.40, 128.52, 129.47, 129.73 (Ar-2CH), 133.74, 133.77, 134.81, 141.52 (Ar-C), 157.97 (C=N), 161.29 (CH=N), 164.65 (C-OH), 165.69 (quinolone-C=O), 168.38 (thiazinanone-C=O); MS (Fab, 70 eV, %): m/z = 482 (M^+, 70), 468 (50), 316 (80), 307 (100), 286 (45), 280 (90), 202 (10), 175 (30), 161 (50). Anal. calcd for $C_{27}H_{22}N_4O_3S$ (482.55): C, 67.20; H, 4.60; N, 11.61; S, 6.64. Found: C, 67.31; H, 4.64; N, 11.55; S, 6.58.

*(Z)-2-((E)-((4-Hydroxy-6-methoxy-2-oxo-1,2-dihydroquinolin-3-yl)methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one (**7d**).* Yellow crystals (DMF/H_2O), yield: 0.403 g (81%); mp 295–297 °C; R_f = 0.18 (toluene–ethyl acetate, 1 : 1); IR (KBr): ν = 3334 (OH), 3276, 3190 (NH), 3110 (Ar-CH), 2865 (aliph-CH), 1661 and 1625 (CO), 1593 cm^{-1} (C=N); ^{1}H NMR (400 MHz, DMSO-d_6): δ_H = 3.77 (s, 3H, OCH_3), 4.48 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.45 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 6.85–6.86 (m, 2H, Ar-H), 6.95–6.97 (m, 1H, Ar-H), 7.23–7.31 (m, 10H, Ar-H), 7.98 (brs, 1H, thiazinanone-NH), 8.76 (s, 1H, CH=N), 11.48 (s, 1H, quinolone-NH), 12.03 (s, 1H, quinolone-OH); ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 44.20 (thiazinanone-CH-6), 55.36 (OCH_3), 56.30 (thiazinanone-CH-5), 109.31 (quinolone-C3), 116.61 (Ar-2CH), 125.26, 126.92, 127.15, 127.24 (Ar-CH), 128.06, 128.31 (Ar-2CH), 128.47 (Ar-CH), 130.09 (Ar-2CH), 132.54, 133.10, 136.90, 138.83, 143.80 (Ar-C), 153.64 (C=N), 156.61 (CH=N), 162.78 (C-OH), 164.81 (quinolone-C=O), 167.09 (thiazinanone-C=O); MS (Fab, 70 eV, %): m/z = 498 (M^+, 30), 468 (60), 307 (100), 280 (85), 218 (14), 191 (20). Anal. calcd for $C_{27}H_{22}N_4O_4S$ (498.55): C, 65.05; H, 4.45; N, 11.24; S, 6.43. Found: C, 65.17; H, 4.48; N, 11.17; S, 6.53.

*(Z)-2-((E)-((4-Hydroxy-6-methyl-2-oxo-1,2-dihydroquinolin-3-yl)-methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one (**7e**).* Yellow crystals (DMF/MeOH), yield: 0.314 g (82%); mp = 304–306 °C; R_f = 0.20 (toluene–ethyl acetate, 10 : 8); IR (KBr): ν =

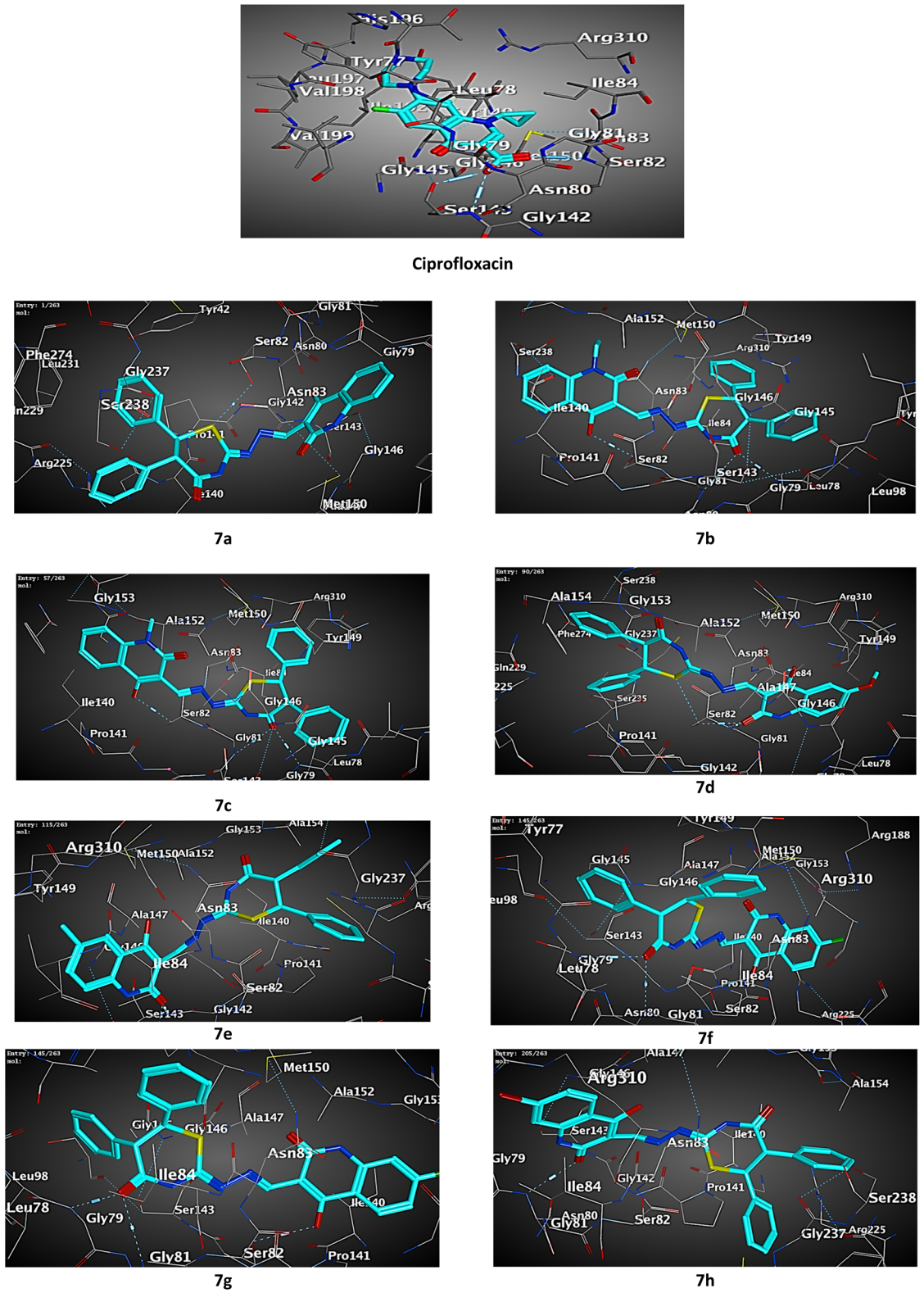


Fig. 5 3D diagram illustrating the binding modes of the optimized structures of tested **7a–h** in the active site of the *S. aureus Murb* (PDB ID: IHSK).

3410 (OH), 3215, 3211 (NH), 3062 (Ar-CH), 2925 (aliph-CH), 1668 and 1648 (CO), 1620 cm^{-1} (C═N); ^1H NMR (400 MHz, DMSO-d_6): δ_H = 2.78 (s, 3H, CH_3), 4.55 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.53 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 7.01 (dd, 2H, J = 8.0 Hz, Ar-H), 7.25–7.54 (m, 10H, Ar-H), 7.89 (s, 1H, Ar-H), 8.10 (brs, 1H, thiazinanone-NH), 8.56 (s, 1H, CH═

N), 11.55 (s, 1H, quinolone-NH), 12.56 (s, 1H, quinolone-OH); ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 20.02 (CH_3), 51.26 (thiazinanone-CH-6), 54.88 (thiazinanone-CH-5), 109.27, (quinolone-C3), 110.26, 110.35, 114.08, 114.17, 114.94, 115.05, 116.35, 117.17, 118.22, 123.91, 124.93, 125.54, 129.71, (Ar-CH), 131.14, 137.80 (Ar-C), 139.29 (Ar-2C), 140.12 (Ar-C), 160.72 (C=N), 161.45 (CH=N), 164.99 (C-OH), 165.10 (quinolone-C=O), 166.16 (thiazinanone-C=O). MS (Fab, 70 eV, %): m/z = 482 (M^+, 58), 391 (26), 316 (78), 309 (100), 286 (45), 282 (35), 202 (10), 175 (28), 161 (36). Anal. calcd for $C_{27}H_{22}N_4O_3S$ (482.55): C, 67.20; H, 4.60; N, 11.61; S, 6.64. Found: C, 67.36; H, 4.64; N, 11.75; S, 6.73.

(Z)-2-((E)-((7-Chloro-4-hydroxy-2-oxo-1,2-dihydroquinolin-3-yl) methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one ***(7f).*** Yellow crystals (DMF), yield: 0.295 g (79%); mp = 310–312 °C; R_f = 0.15 (toluene–ethyl acetate, 1 : 1); IR (KBr): ν = 3402 (OH), 3221, 3216 (NH), 3042 (Ar-CH), 2920 (Ali-CH), 1670, 1640 (CO), 1588 cm^{-1} (C=N). ^{1}H NMR (400 MHz, DMSO-d_6): δ_H = 4.54 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.49 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 6.81 (dd, 2H, J = 8.0 Hz, Ar-H), 7.19–7.58 (m, 10H, Ar-H), 7.90 (s, 1H, Ar-H), 8.12 (brs, 1H, thiazinanone-NH), 8.76 (s, 1H, CH=N), 12.62 (s, 1H, quinolone-NH), 13.21 (s, 1H, quinolone-OH); ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 45.05 (thiazinanone-CH-6), 56.14 (thiazinanone-CH-5), 100.10 (quinolone-C3), 113.65, 114.91, 115.12, 115.85, 116.20, 122.02, 123.01, 123.27, 125.50 (Ar-CH), 126.05 (Ar-2CH), 128.41, 129.98 (Ar-CH), 131.89, 135.02, 136.98, 138.86, 142.78 (Ar-C), 156.12 (C=N), 161.46 (CH=N), 163.45 (C-OH), 165.35 (quinolone-C=O), 166.24 (thiazinanone-C=O); MS (Fab, 70 eV, %): m/z = 504 (M + 2, 40), 503 (M + 1, 15), 502 (M^+, 7), 391 (10), 309 (5), 308 (12), 307 (40), 289 (17), 260 (5), 154 (100). Anal. calcd for $C_{26}H_{19}ClN_4O_3S$ (502.97): C, 62.09; H, 3.81; N, 11.14; S, 6.38. Found: C, 62.24; H, 3.85; N, 11.28; S, 6.48.

(Z)-2-((E)-((6-Chloro-4-hydroxy-2-oxo-1,2-dihydroquinolin-3-yl) methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one ***(7g).*** Yellow crystals (DMF/EtOH), yield: 0.402 g (80%); mp 270–272 °C; R_f = 0.18 (toluene–ethyl acetate, 1 : 1); IR (KBr): ν = 3330 (OH), 3282, 3178 (NH), 3089 (Ar-CH), 2860 (aliph-CH), 1670 and 1652 (CO), 1627 cm^{-1} (C=N); ^{1}H NMR (400 MHz, DMSO-d_6): δ_H = 4.50 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.44 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 6.85–6.86 (m, 2H, Ar-H), 6.95–6.97 (m, 1H, Ar-H), 7.23–7.30 (m, 10H, Ar-H), 8.03 (brs, 1H, thiazinanone-NH), 8.63 (s, 1H, CH=N), 11.62 (s, 1H, quinolone-NH), 12.03 (s, 1H, quinolone-OH); ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 44.19 (thiazinanone-CH-6), 56.89 (thiazinanone-CH-5), 109.86 (quinolone-C3), 115.32, 122.10, 123.90, 127.92, 128.01, 128.53, 128.95, 129.24, 129.39 (Ar-CH), 133.54, 134.80 (Ar-2CH), 132.40, 133.30, 133.60, 136.32, 143.76 (Ar-C), 157.26 (C=N), 161.32 (CH=N), 162.57 (C-OH), 164.89 (quinolone-C=O), 168.71 (thiazinanone-C=O); MS (Fab, 70 eV, %): m/z = 503 (M + 1, 30), 502 (M^+, 55), 468 (40), 307 (20), 280 (16), 223/222 (7/50), 196/195 (100/64). Anal. calcd for $C_{26}H_{19}ClN_4O_3S$ (502.97): C, 62.09; H, 3.81; N, 11.14; S, 6.38. Found: C, 62.16; H, 3.86; N, 11.26; S, 6.48.

(Z)-2-((E)-((7-Bromo-4-hydroxy-2-oxo-1,2-dihydroquinolin-3-yl)-methylene)hydrazono)-5,6-diphenyl-1,3-thiazinan-4-one ***(7h).*** Yellow crystals (DMF/EtOH), yield: 0.325 g (87%); mp = 338–340 °C; R_f = 0.20 (toluene–ethyl acetate, 1 : 1); IR (KBr): ν = 3390 (OH), 3219, 3215 (NH), 3072 (Ar-CH), 2914 (aliph-CH), 1661 and 1650 (CO), 1600 cm^{-1} (C=N). ^{1}H NMR (400 MHz, DMSO-d_6): δ_H = 4.54 (d, 1H, J = 4.0 Hz, thiazinanone-H6), 5.55 (d, 1H, J = 4.0 Hz, thiazinanone-H5), 6.99 (dd, 2H, J = 8.0 Hz, Ar-H), 7.13–7.33 (m, 10H, Ar-H), 7.90 (m, 1H, Ar-H), 8.12 (brs, 1H, thiazinanone-NH), 8.55 (s, 1H, CH=N), 12.20 (s, 1H, quinolone-NH), 12.91 (s, 1H, quinolone-OH). ^{13}C NMR (100 MHz, DMSO-d_6): δ_C = 46.14 (thiazinanone-CH-6), 55.34 (thiazinanone-CH-5), 109.33 (quinolone-C3), 110.50, 112.35, 114.15, 114.98, 115.22, 116.32, 117.22, 119.54, 122.65, 123.34, 125.30 (Ar-CH), 129.80 (Ar-2CH), 131.14 (Ar-2C), 136.89, 138.40, 141.09 (Ar-C), 160.80 (C=N), 161.14 (CH=N), 164.98 (C-OH), 165.24 (quinolone-C=O), 167.23 (thiazinanone-C=O). MS (70 eV, %): m/z 549 (M + 2, 25), 547 (M^+, 25), 530 (17), 529 (14), 476 (15), 460 (100), 443 (25), 391 (30), 375 (22), 330 (38), 305 (40), 154 (100). Anal. calcd for $C_{26}H_{19}BrN_4O_3S$ (547.42): C, 57.05; H, 3.50; N, 10.23; S, 5.86. Found: C, 57.23; H, 3.55; N, 10.38; S, 5.96.

3.2. Biology

3.2.1. Screening of antibacterial activity. The antibacterial activity was screened according to serial dilution method. Minimal inhibition concentration (MIC) is the lowest concentration of an antimicrobial agent that can inhibit the visible growth of a microorganism after overnight incubation (see ESI†).

3.2.2. Molecular docking study. The docking simulation study was carried out using Molecular Operating Environment (MOE®) version 2014.09 (Chemical Computing Group Inc., Montreal, QC, Canada). The computational software operated under "Windows XP" installed on an Intel Pentium IV PC with a 1.6 GHz processor and 512 MB memory. The target compounds were constructed into a 3D model using the builder interface of the MOE program and docked into the active site of caspase-3 (PDB: 3GJQ). Checking their structures and the formal charges on atoms by 2D depiction was carried out and the energy, was minimized until an RMSD (root mean square deviations) gradient of 0.01 kcal mol^{-1} and RMS (Root Mean Square) distance of 0.1 A with MMFF94X (Merck molecular force field 94X) force-field and the partial charges were automatically calculated (see ESI†).

4. Conclusions

In short, a series of 1,3-thiazinanone derivatives have been synthesized in excellent yields *via* nucleophilic attack of thiosemicarbazones on 2,3-diphenylcyclopropenone. The target compounds were identified and characterized using ^{1}H NMR, ^{13}C NMR, MS and elemental analysis. The suggested mechanism for the formation of the final products was remembered. The biological results revealed that some target compounds exhibited good antibacterial activity against most of the tested G +ve and G −ve strains, especially compound **7e** against MRSA even superior to reference drug. They induced bacterial resistance more slowly than clinical drugs. Molecular docking study indicated strong binding interaction of the tested compounds.

In conclusion, compound **7e** revealed potential broad spectrum anti-bacterial activity that should be taken into consideration as good candidates for further study.

Author contributions

A. H. M. (writing, editing, and revision); S. M. M. (revision), A. A. A. (concept, writing, edit, revision, and submitting), A. A. H. (editing), E. M. O. (experimental), A. B. B. (editing and revision), E.-S. M. N. A. (biology, writing, and editing). All authors have read and agreed to the published version of the manuscript.

Conflicts of interest

The authors declare no conflict of interest. The authors declare that they have no known competing interests.

Acknowledgements

The authors thank DFG for providing Ashraf A. Aly with a one-month fellowship, enabling him to conduct the compound analysis at the Karlsruhe Institute of Technology, Karlsruhe, Germany, in July and August 2019.

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