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Synthesis and antibacterial evaluation of novel Schiff's base derivatives of nitroimidazole nuclei as potent *E. coli* FabH inhibitors[†]

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Series of novel Schiff's base derivatives have been synthesized by combining 2-(2-methyl-5-nitro-1*H*imidazol-1-yl)ethyl 4-formylbenzoate **5**, **6** with aromatic/heterocyclic amine **7a**–**r**, **8**, **9a**–**r** in ethanol. All compounds were evaluated for antibacterial assay and inhibition against *E. coli* FabH. Among the compounds studied, most of the compounds showed effective antibacterial and potential inhibitory activity against *E. coli* FabH. Compound **10q** showed most potent inhibitory activity ($IC_{50} = 2.6883 \mu M$) by binding tightly to the active site of the *E. coli* FabH receptor with minimum binding energy ($\Delta G_b =$ -55.3117 kcal mol⁻¹), in which molecular docking study indicated the binding mode was stabilized by one hydrogen bond and five π – π interactions.

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1 Introduction

An alarming increment in pathogenic resistance to existing first-line standard drugs is a serious problem in antimicrobial cure.¹ Moreover, the progression of drug-resistant strains has contributed to the inefficiency of the straight antimicrobial therapy. This sets up an enormous interest in antibacterial research and we strongly believe that there is an urgent call for the development of novel antibacterial drugs with divergent and unique structures. Consequently, this area of research is accorded an enormous significance and continues to attract considerable attention from an increasing number of medicinal chemists. In order to prevent the serious medical problems caused by microorganisms, the discovery of new types of antibacterial agents is a crucial task at present. Fortunately, considerable research effort is made for the design of new antibacterial agents with high efficiency.²

In the last 10 years, the research has been focused toward new antibacterial agents, which may act through different kinds of targets in key areas of the bacterial cell cycle, to surpass the problem of acquired resistance. The fatty acid synthesis (FAS) pathway in bacteria is a promising target in the recent research and fatty acid biosynthesis (FAB) is a fundamental metabolic process for microorganisms and essential for cell viability and growth.^{3,4}

β-Ketoacyl-acyl carrier protein synthase III (FabH) is the key enzyme responsible for the first reaction in the pathway and plays an important regulatory role.5 FabH has also been demonstrated to be essential for initiating the fatty acid elongation cycles and is involved in the feedback regulation of the biosynthetic pathway via product inhibition.6,7 Some novel compounds had been demonstrated to inhibit FabH found in Gram-positive and Gram-negative bacteria, including multi-drug resistant strains. FabH proteins from Gram-positive and Gram-negative bacteria are highly conserved at the sequence and structural level whereas there are no significantly homologous proteins in humans. Importantly, the residues that comprise the active site are essentially invariant in various bacterial FabH molecules.8,9 FabH has been proved to be a promising target for the design of novel antimicrobial drugs because it adjusts and controls the fatty acid biosynthesis rate in an initiation pathway, and its substrate specificity is a key factor in membrane fatty acid composition.¹⁰⁻¹² These facts indicate that small molecule inhibitors of FabH enzymatic activity could be potential candidates for selective, nontoxic, and broad spectrum antibacterials.

Because of varied biological activities, nitroimidazole derivatives have gained constant interests in drug research for antimicrobial chemotherapeutics and antiangiogenic hypoxic cell radiosensitizers. The metabolism and toxicology of nitroimidazole derivatives, particularly for secnidazole, have been characterized in recent reports.^{13,14} Secnidazole (α ,2-dimethyl-5nitro-1*H*-imidazole-1-ethanol) is extraordinarily effective in the treatment of giardiasis, amebiasis and bacterial vaginosis. By oral administration, secnidazole can be rapidly and completely absorbed, and has a longer terminal elimination half-life

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(17–29 h) than popular medication.¹⁵ Also, the treatment achieved with secnidazole is more effective and displays fewer side effects.¹⁶

Moreover, Schiff bases are compounds with the structure of AC = NB, which are usually synthesized from the condensation of active carbonyl groups and primary amines. Schiff's bases constitute an important class of biologically active drug molecules, which have attracted attention of medicinal chemists due to their wide range of pharmacological properties. These compounds are being synthesized as drugs by many researchers in order to combat diseases with minimal toxicity and maximal effects. These predictions have provided therapeutic pathways to develop new effective biologically active Schiff's base derivatives. Many researchers have studied the synthesis, characterization and structure-activity relationship (SAR) of Schiff bases and some Schiff bases were reported to have antibacterial activities.17 Moreover, Kim and co-workers reported the YKAs3003, a Schiff base condensed by 4-hydroxy salicylaldehyde and cyclohexanamine, as a potent inhibitor of Escherichia coli (E. coli) FabH with antimicrobial activity.18

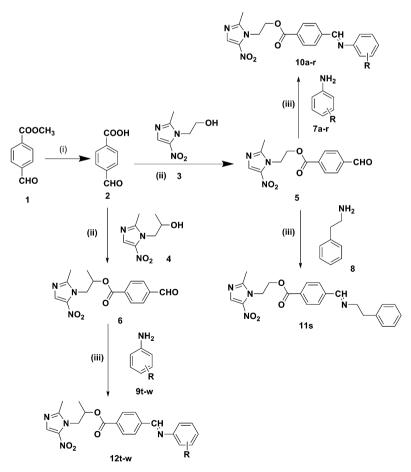
Along the studies on FabH of our group based on nitroimidazole¹⁹ and Schiff's base,²⁰ we report here the synthesis and structure-activity relationship of a new series of Schiff base derivatives of nitroimidazole nuclei in a single scaffold and their antibacterial activities against *Escherichia coli*, *Pseudomonas aeruginosa* (*P. aeruginosa*), *Bacillus subtilis* (*B. subtilis*) and *Staphylococcus aureus* (*S. aureus*) and also *E. coli* FabH inhibitory activities.

2 Results and discussion

2.1 Chemistry

Schiff's base derivatives **10a-r** have been synthesized by reaction between the intermediate **5** (Intermediate **5** can be obtained by the simple two steps using compound **1** and metronidazole **3**) and various substituted aniline **7a-r** in ethanol and when refluxed overnight provides good yield (45–87%) (Scheme 1). Moreover, the addition of 2-phenyl-ethanamine **8** into the intermediate **5** could produce target compound **11s** in ethanol, when refluxed overnight. Other compounds **12t-w** were derived from the reaction between compound **2** and secnidazole **4**, subsequently interacting with four substituted aniline **9t-w** in ethanol, refluxed overnight.

The structures of all the new synthesized compounds were established by ¹H NMR, elemental analysis, and molecular



(i)CH₃OH/H₂O=1:1, 2M NaOH, rt,4h (i

(ii) EDC.HCl, DMAP, CH₂Cl₂, refulx, overnight (iii) CH₃CH₂OH, reflux, overnight

Scheme 1 Synthesis of the titled compounds.

weight of compounds confirmed by mass spectrometry. Mass spectroscopy of compounds showed molecular ion peak (M^+) corresponding to the exact mass.

2.2 Biological activity

2.2.1 In vitro antibacterial and *E. coli* FabH inhibitory activity. All the synthesized compounds were screened for their antibacterial activities against two Gram-negative bacterial strains, *i.e.*, *E. coli* ATCC 35218 and *Pseudomonas aeruginosa* ATCC 13525 (*P. aeruginosa*), and two Gram-positive bacterial strains, *i.e.*, *Bacillus subtilis* ATCC 6633 (*B. subtilis*) and *Staphylococcus aureus* ATCC 6538 (*S. aureus*) by serial dilution method. The MICs (minimum inhibitory concentrations) of the compounds against these bacteria were presented in Table 1. Kanamycin B and penicillin G were taken as reference compounds under identical conditions for comparison.

Upon investigation of antibacterial activity (Table 1), it has been observed that a majority of the compounds have shown effective activity against the strains used. Against Gram-negative bacteria *E. coli*, compound **10q** (MIC = 1.56 µg mL⁻¹) showed more effective activity compared to penicillin G (MIC = 3.13 µg mL⁻¹) and comparable activity to kanamycin B (MIC = 1.56 µg mL⁻¹), whereas compounds **10f**, **10l**, **10o**, **10r**, **12v** and **12w** (MIC = 3.13 µg mL⁻¹) showed comparable activity to penicillin G (MIC = 3.13 µg mL⁻¹). Against *P. aeruginosa*, compound **10q** $(MIC = 3.13 \ \mu g \ mL^{-1})$ showed comparable activity to kanamycin B (MIC = 3.13 $\mu g \text{ mL}^{-1}$). Against Gram-positive bacteria S. aureus, compound 10q (MIC = 3.13 $\mu g m L^{-1}$) showed the most effective activity. As well compounds 10b, 10f, 10k, 10o and **10p** (MIC = 6.25 μ g mL⁻¹) showed comparable activity as compared to penicillin G (MIC = 6.25 $\mu g m L^{-1}$) but less compared to kanamycin B (MIC = $1.56 \ \mu g \ mL^{-1}$). Compound **10q** (MIC = 1.56 μ g mL⁻¹) showed comparable activity and compounds 10b, 10f, 10g, 10k, 10p, 10t and 12v (MIC = 3.13 µg mL^{-1}) showed less activity as compared to penicillin G (MIC = 1.56 μ g mL⁻¹) against *B. subtilis*. Of the compounds studied for *E. coli* FabH inhibitory activity (Table 2), compounds 10q (IC₅₀ = 2.6883 μ M), **12v** (IC₅₀ = 4.928 μ M) and **10r** (IC₅₀ = 5.5923 μ M) showed more potent activity as compared to secnidazole ($IC_{50} =$ 28.5 μ M) and metronidazole (IC₅₀ = 17.6 μ M) as well as other compounds of the series.

Structure activity relationship (SAR) was carried out from *E. coli* FabH inhibitory and antibacterial activities. According to the activity data, it has been observed that the change in R substitution may lead to change in the activity against employed strains as well as *E. coli* FabH. Compounds **100**, **10p**, **10q**, **10r**, **12v** and **12w** having sulfonamide linkage (-SO₂NH) showed potent activity compared to other compounds. Electron releasing group R = 3-OCH₃ in compound **10f** gave better activity than **10e** (R = 3-CH₃), while

Table 1 The MICs (minimum inhibitory concentrations) of the compounds against these bacteria

Compound	Minimum inhibitory concentrations ($\mu g m L^{-1}$) of 10a-r , 11s , 12t-w				
	Gram-negative		Gram-positive		
	<i>E. coli</i> ATCC 35218	P. aeruginosa ATCC 13525	B. subtilis ATCC 6633	S. aureus ATCC 6538	
10a	25	100	25	50	
10b	6.25	12.5	3.13	6.25	
10c	25	100	25	50	
10d	12.5	100	25	25	
10e	50	100	25	100	
10f	3.13	12.5	3.13	6.25	
10g	6.25	25	3.13	12.5	
10h	6.25	100	12.5	12.5	
10i	25	100	25	50	
10j	12.5	100	12.5	25	
10k	6.25	12.5	3.13	6.25	
10l	3.13	25	12.5	25	
10m	12.5	50	6.25	25	
10n	12.5	50	12.5	25	
100	3.13	12.5	6.25	6.25	
10p	6.25	25	3.13	6.25	
10q	1.56	3.13	1.56	3.13	
10r	3.13	12.5	6.25	12.5	
11s	6.25	25	6.25	12.5	
12t	12.5	25	3.13	12.5	
12u	12.5	100	12.5	25	
12v	3.13	25	3.13	12.5	
12w	3.13	12.5	6.25	12.5	
Penicillin G	3.13	6.25	1.56	6.25	
Kanamycin B	1.56	3.13	0.78	1.56	

Table 2E. coliFabH inhibitory activities of compounds10a-r,11s,12t-w

Compounds	IC_{50} (μM)	Hemolysis LC_{30} (mg ml ⁻¹
10a	31.4738	>10
10b	9.9087	>10
10c	39.0767	>10
10d	30.8408	>10
10e	31.0767	>10
10f	6.4994	>10
10g	12.2729	>10
10h	17.3407	>10
10i	43.4738	>10
10j	30.7389	>10
10k	11.1688	>10
10l	11.9535	>10
10m	14.8985	>10
10n	28.0284	>10
100	6.1688	>10
10p	6.9193	>10
10q	2.6883	>10
10r	5.5923	>10
11s	10.0336	>10
12t	10.0857	>10
12u	28.4504	>10
12v	4.928	>10
12w	6.8125	>10
DCCP	3.1542	>10

there is no activity difference observed in 2-, 3- and 4-position of $-CH_3$ group. Secnidazole derivatives **12t-w** gave better activity than derivatives. Introduction of alkyl chain in compound **11s** gave better activity than simple amine moiety in compound **10n**; moreover, different halogen groups at 2-, 3and 4-position gave different activity. The decreasing order of activity in halogen compounds is (4-Br > 4-F > 2-Cl > 2-Br > 4-Cl > 2, 4-Cl > 2-F). Moreover, reviewing and comparing the activity data, it is worthy to mention that the antibacterial activity against *E. coli* FabH of the target compounds depends not only on the heteroaromatic pharmacophore, but also on the nature of the substituents.

In addition, an acute oral toxicity test was conducted with mice to determine the toxicity from a single dose *via* the oral route. Based on the results (not listed), the single dose acute oral LD_{50} (half maximal concentration of lethal dose) values of the compounds (**10b**, **10f**, **10q**, **10r**, **12v**) are all greater than 5000 mg kg⁻¹ of bodyweight.

2.2.2 Molecular docking. Molecular docking of all compounds and *E. coli* FabH was performed on the binding model based on the *E. coli* FabH–CoA complex structure (1HNJ.pdb).²¹ All docking runs were applied using Ligand Fit Dock protocol of Discovery Studio 3.5. The binding energy calculation of the synthesized compounds is listed in Table 3. Among them, compound **10q** showed the lowest interaction energy ($\Delta G_{\rm b} = -55.3117$ kcal mol⁻¹). The binding model of compound **10q** and *E. coli* FabH is depicted in Fig. 1 and 2. In the binding model, compound **10q** was nicely bound to the FabH kinase with one hydrogen bond and five π - π

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	R	CDOCKER interaction 1^{-1}
Compounds	(substitution)	energy – $\Delta G_{\rm b}$ (kcal mol ⁻¹)
10a	4-CH ₃	38.5262
10b	4-OCH ₃	45.0913
10c	2-CH ₃	37.9892
10d	2-OCH ₃	39.1592
10e	3-CH ₃	38.9233
10f	3-OCH ₃	48.5006
10g	2-Cl	41.7271
10h	2-Br	40.6593
10i	2 F	36.9981
10j	4-Cl	39.2611
10k	4-Br	44.8312
10l	4 F	42.0465
10m	2,4-Cl	41.1015
10n	H	39.9716
100	$\overset{O}{\overset{H}{\overset{H}}}_{\overset{H}{\overset{H}}} \overset{N}{\overset{H}{\overset{H}}} \overset{N}{\overset{H}} \overset{N}{\overset{N}} \overset{N}{\overset{N}} \overset{N}{\overset{N}} \overset{N}{\overset{N}} \overset{N}{\overset{N} \overset{N}{\overset{N}} \overset{N} N$	48.8312
10p	$\begin{array}{c} 0 \\ H \\ 4 - S - N \\ 0 \\ N \end{array}$	48.0807
10q	$\begin{array}{c} O \\ H \\ 4 - S - N \\ O \\ N \end{array} $	55.3117
10r	$\begin{array}{c} O \\ H \\ 4-S-N \\ 0 \\ NH_2 \end{array}$	49.4077
11s	Н	44.9664
12t	4-OCH ₃	44.9143
12u	$4-CH_3$	39.5496
12v	$\begin{array}{c} 0 \\ H \\ 4 - S - N \\ 0 \\ N \end{array}$	51.0720
12w	$\begin{array}{c} O \\ H \\ 4-S \\ 0 \\ NH_2 \end{array} \xrightarrow{\text{NH}} $	48.1875

interactions. Among hydrogen bonds formed between Oatom of C=O (carbonyl group) and ARG151 with distance: 1.948 Å; DHA angle: 133.0° and HAY angle: 149.3°, one π - π interaction formed between imidazole ring and ARG151 with distance 3.61222 Å, two π - π interactions formed between imidazolering and TRP32 with distance 4.53889 Å and 5.83906 Å and two π - π interactions formed between -NO₂ group of imidazole ring and TRP32 with distance 3.57476 Å and 4.05855 Å. Moreover, the binding model of compound **10f** and *E. coli* FabH is depicted in Fig. 3 and 4. In the binding model, compound **10f** was nicely bound to the FabH kinase

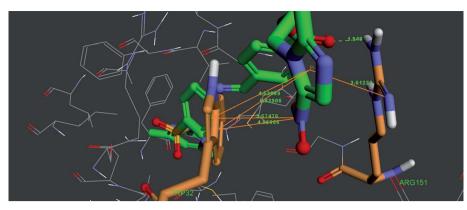


Fig. 1 3D binding model of compound 10q into the active site of FabH.

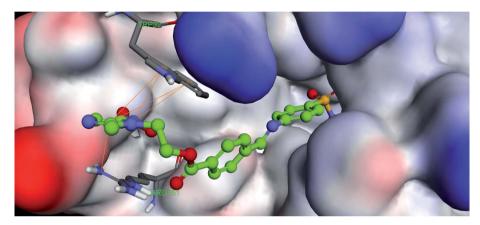


Fig. 2 Surface model of compound 10q into the active site of FabH (3D-model).

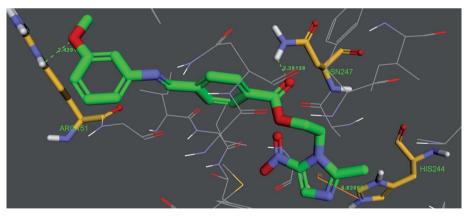


Fig. 3 3D binding model of compound 10f into the active site of FabH.

with two hydrogen bonds and one π - π interaction. A hydrogen bond formed between O-atom of -OCH₃ and ARG151 with distance: 2.4297 Å; DHA angle: 107.1° and HAY angle: 100.2°, while another one formed between O-atom of C=O (carbonyl group) and ASN247 with distance: 2.3913 Å; DHA angle: 125.3° and HAY angle: 117.0°. One

 π - π interaction formed between imidazole ring and HIS244 with distance 6.62666 Å. This molecular docking result, along with the biological assay data, suggests that compounds **10q** and **10f** prove to be potential inhibitors of *E. coli* FabH.

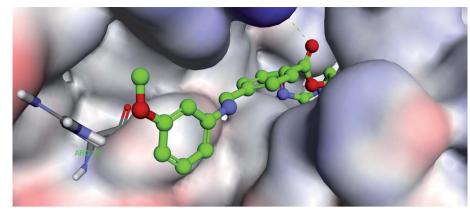


Fig. 4 Surface model of compound 10f into the active site of FabH (3D-model)

3 Conclusions

New Schiff's base derivatives **10a–r**, **11s** and **12t–w** have been synthesized by reaction between 2-(2-methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-formylbenzoate **5**, **6** and aromatic/heterocyclic amine in ethanol. This synthetic strategy allows the assimilation of two promising bioactive nuclei in a single scaffold through an easy method. Reviewing the biological activity data, it has been concluded that a majority of the compounds have been found most effective against applied bacterial strains. Compound **10q** showed most effective inhibition by binding into the active site of *E. coli* FabH receptor with a minimum binding energy. According to this, it is worthy to mention that the Schiff's base derivatives having nitroimidazole nuclei have become a vital spot of antibacterial and *E. coli* FabH inhibition medicine research.

4 Experiments

4.1 Materials and measurements

All chemicals and reagents used in the current work were of analytical grade. Melting points were determined using an XT4 MP apparatus (Taike Corp., Beijing, China). All the ¹H NMR and ¹³C NMR spectra were recorded using a Bruker DPX300 model spectrometer in DMSO-d6 and chemical shifts were reported in ppm (d). ESI-MS spectra were recorded using a Mariner System 5304 mass spectrometer. Elemental analyses were performed using a CHN–O-Rapid instrument. TLC was performed using glass backed silica gel sheets (Silica Gel 60 GF254) and visualized in UV light (254 nm).

4.2 General method for synthesis of Schiff's base derivatives

2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-formylbenzoate 5, 6 (1 mol) and aromatic/heterocyclic amine **7a–r**, **8**, **9t–w** (1.1 mol) were mixed together in ethanol as a solvent. The reaction mixture was stirred and refluxed overnight. After the completion of reaction (checked by TLC), the separated solid was filtered, washed well with ethanol (10 mL) and water (10 mL), and finally dried and recrystallized from ethanol to get the pure solid samples **10a–r**, **11s**, **12t–w**. Physical, analytical, and

spectroscopic characterization data of the compounds are presented hereafter.

4.2.1 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-((*p*-tolylimino)methyl)benzoate (10a). White powder, yield: 83%. Mp 191–193 °C; ¹H NMR (DMSO-d6) δ ppm: 2.33, 2.48 (s, 6H, 2 × CH₃), 4.66–4.77 (t, 4H, 2 × CH₂), 7.24–8.06 (m, 9H, ArHs), 8.73 (s, 1H, CH=N); anal. calcd for C₂₁H₂₀N₄O₄ (392.15 g mol⁻¹): C, 64.28; H, 5.14; N, 14.28 (%); found: C, 64.49; H, 5.22; N, 14.33 (%); MS (*m*/*z*): 392.1 (M⁺).

4.2.2 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4-methoxyphenyl)imino)methyl) benzoate (10b). White powder, yield: 87%. Mp 197–199 °C; ¹H NMR (DMSO-d6) δ ppm: 2.48 (s, 3H, CH₃), 3.79 (s, 3H, OCH₃), 4.65–4.77 (t, 4H, 2 × CH₂), 6.99–8.05 (m, 9H, ArHs), 8.74 (s, 1H, CH=N); anal. calcd for C₂₁H₂₀N₄O₅ (408.41 g mol⁻¹): C, 61.76; H, 4.94; N, 13.72 (%); found: C, 61.80; H, 5.12; N, 13.82 (%); MS (*m*/*z*): 408.1 (M⁺).

4.2.3 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-((*o*-tolylimino)methyl)benzoate (10c). White powder, yield: 75%. Mp 187–188 °C; ¹H NMR (DMSO-d6) δ ppm: 2.35, 2.48 (s, 6H, 2 × CH₃), 4.68–4.76 (t, 4H, 2 × CH₂), 7.09–8.07 (m, 9H, ArHs), 8.70 (s, 1H, CH=N); anal. calcd for C₂₁H₂₀N₄O₄ (392.15 g mol⁻¹): C, 64.28; H, 5.14; N, 14.28 (%); found: C, 64.49; H, 5.22; N, 14.33 (%); MS (*m*/*z*): 392.1 (M⁺).

4.2.4 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((2-methoxyphenyl)imino)methyl)benzoate (10d). White powder, yield: 80%. Mp 196–197 °C; ¹H NMR (DMSO-d6) δ ppm: 2.48 (s, 3H, CH₃), 3.80 (s, 3H, OCH₃), 4.68–4.76 (t, 4H, 2 × CH₂), 6.95–8.05 (m, 9H, ArHs), 8.63 (s, 1H, CH=N); anal. calcd for C₂₁H₂₀N₄O₅ (408.41 g mol⁻¹): C, 61.76; H, 4.94; N, 13.72 (%); found: C, 61.80; H, 5.12; N, 13.82 (%); MS (*m*/*z*): 408.1 (M⁺).

4.2.5 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-((*m*-tolylimino)methyl)benzoate (10e). White powder, yield: 75%. Mp 185–187 °C; ¹H NMR (DMSO-d6) δ ppm: 2.35, 2.48 (s, 6H, 2 × CH₃), 4.68–4.76 (t, 4H, 2 × CH₂), 7.09–8.07 (m, 9H, ArHs), 8.70 (s, 1H, CH=N); anal. calcd for C₂₁H₂₀N₄O₄ (392.15 g mol⁻¹): C, 64.28; H, 5.14; N, 14.28 (%); found: C, 64.49; H, 5.22; N, 14.33 (%); MS (*m*/*z*): 392.1 (M⁺).

4.2.6 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((3-methoxyphenyl)imino)methyl)benzoate (10f). White powder, yield: 77%. Mp 195–197 °C; ¹H NMR (DMSO-d6) δ ppm: 2.49 (s, 3H, CH₃), 3.81 (s, 3H, OCH₃), 4.68–4.78 (t, 4H, 2 × CH₂),

6.86–8.08 (m, 9H, ArHs), 8.74 (s, 1H, CH=N); anal. calcd for $C_{21}H_{20}N_4O_5$ (408.41 g mol⁻¹): C, 61.76; H, 4.94; N, 13.72 (%); found: C, 61.80; H, 5.12; N, 13.82 (%); MS (*m*/*z*): 408.1 (M⁺).

4.2.7 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((2chlorophenyl)imino)methyl)benzoate (10g). White powder, yield: 76%. Mp 199–200 °C; ¹H NMR (DMSO-d6) δ ppm: 2.45 (s, 3H, CH₃), 4.64–4.75 (s, 4H, 2 × CH₂), 7.21–8.02 (m, 9H, ArHs), 8.75 (t, 1H, CH=N); anal. calcd for C₂₀H₁₇ClN₄O₄ (412.83 g mol⁻¹): C, 58.19; H, 4.15; N, 13.57 (%); found: C, 58.25; H, 4.31; N, 13.62 (%); MS (*m*/*z*): 412.1 (M⁺).

4.2.8 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((2-bromophenyl)imino)methyl)benzoate (10h). White powder, yield: 78%. Mp 202–203 °C; ¹H NMR (DMSO-d6) δ ppm: 2.45 (s, 3H, CH₃), 4.64–4.75 (s, 4H, 2 × CH₂), 7.21–8.02 (m, 9H, ArHs), 8.76 (t, 1H, CH=N); anal. calcd for C₂₀H₁₇BrN₄O₄ (457.28 g mol⁻¹): C, 52.53; H, 3.75; N, 12.25 (%); found: C, 52.65; H, 3.81; N, 12.42 (%); MS (*m*/*z*): 456.1 (M⁺).

4.2.9 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((2-florophenyl)imino)methyl)benzoate (10i). White powder, yield: 75%. Mp 198–199 °C; ¹H NMR (DMSO-d6) δ ppm: 2.45 (s, 3H, CH₃), 4.64–4.75 (s, 4H, 2 × CH₂), 7.21–8.02 (m, 9H, ArHs), 8.74 (t, 1H, CH=N); anal. calcd for C₂₀H₁₇FN₄O₄ (396.37 g mol⁻¹): C, 60.60; H, 4.32; N, 14.13 (%); found: C, 60.65; H, 4.40; N, 14.20 (%); MS (*m*/*z*): 396.4 (M⁺).

4.2.10 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4chlorophenyl)imino)methyl)benzoate (10j). White powder, yield: 86%. Mp 201–202 °C; ¹H NMR (DMSO-d6) δ ppm: 2.49 (s, 3H, CH₃), 4.68–4.78 (s, 4H, 2 × CH₂), 7.35–8.08 (m, 9H, ArHs), 8.74 (t, 1H, CH=N); anal. calcd for C₂₀H₁₇ClN₄O₄ (412.83 g mol⁻¹): C, 58.19; H, 4.15; N, 13.57 (%); found: C, 58.25; H, 4.31; N, 13.62 (%); MS (*m*/*z*): 412.1 (M⁺).

4.2.11 (*E*)-2-(2-methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4-bromophenyl)imino)methyl)benzoate (10k). White powder, yield: 87%. Mp 203–204 °C; ¹H NMR (DMSO-d6) δ ppm: 2.49 (s, 3H, CH₃), 4.68–4.78 (s, 4H, 2 × CH₂), 7.35–8.08 (m, 9H, ArHs), 8.74 (t, 1H, CH=N); anal. calcd for C₂₀H₁₇BrN₄O₄ (457.28 g mol⁻¹): C, 52.53; H, 3.75; N, 12.25 (%); found: C, 52.65; H, 3.81; N, 12.42 (%); MS (*m*/*z*): 456.1 (M⁺).

4.2.12 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4-florophenyl)imino)methyl)benzoate (10l). White powder, yield: 85%. Mp 199–200 °C; ¹H NMR (DMSO-d6) δ ppm: 2.49 (s, 3H, CH₃), 4.68–4.78 (s, 4H, 2 × CH₂), 7.35–8.08 (m, 9H, ArHs), 8.74 (t, 1H, CH=N); anal. calcd for C₂₀H₁₇FN₄O₄ (396.37 g mol⁻¹): C, 60.60; H, 4.32; N, 14.13 (%); found: C, 60.65; H, 4.40; N, 14.20 (%); MS (*m*/*z*): 396.4 (M⁺).

4.2.13 *(E)*-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((2,5-dichlorophenyl)imino)methyl)benzoate (10m). White powder, yield: 65%. Mp 205–206 °C; ¹H NMR (DMSO-d6) δ ppm: 2.45 (s, 3H, CH₃), 4.64–4.75 (t, 4H, 2 × CH₂), 7.31–8.07 (m, 8H, ArHs), 8.66 (s, 1H, CH=N); anal. calcd For C₂₀H₁₆C₁₂N₄O₄ (447.27 g mol⁻¹): C, 53.71; H, 3.61; N, 12.53 (%); found: C, 53.82; H, 3.49; N, 12.43 (%); MS (*m/z*): 446.1 (M⁺).

4.2.14 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-((phenylimino)methyl)benzoate (10n). White powder, yield: 67%. Mp 189–190 °C; ¹H NMR (DMSO-d6) δ ppm: 2.49 (s, 3H, CH₃), 4.68–4.78 (t, 4H, 2 × CH₂), 7.28–8.09 (m, 10H, ArHs), 8.73 (s, 1H, CH=N); anal. calcd for C₂₀H₁₈N₄O₄ (378.38 g mol⁻¹): C, 63.48; H,

4.79; N, 14.81 (%); found: C, 63.64; H, 4.63; N, 14.91 (%); MS (m/z): 378.1 (M^+).

4.2.15 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4-(*N*-(**pyridin-2-yl)sulfamoyl)phenyl)imino)methyl)benzoate** (**100**). White powder, yield: 45%. Mp 234–235 °C; ¹H NMR (DMSO-d6) δ ppm: 2.48 (s, 3H, CH₃), 4.69–4.76 (t, 4H, 2 × CH₂), 6.87–8.08 (m, 13H, ArHs), 8.72 (s, 1H, CH=N), 11.70 (s, 1H, SO₂NH); anal. calcd for C₂₅H₂₂N₆O₆S (534.54 g mol⁻¹): C, 56.17; H, 4.15; N, 15.72 (%); found: C, 56.24; H, 3.93; N, 15.85 (%); MS (*m*/*z*): 534.1 (M⁺).

4.2.16 *(E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4-(M-(4-methylpyrimidin-2-yl)sulfamoyl)phenyl)imino)methyl)benzoate (10p). White powder, yield: 50%. Mp 245–246 °C; ¹H NMR (DMSO-d6) δ ppm: 2.33, 2.48 (s, 6H, 2 × CH₃), 4.68–4.76 (t, 4H, 2 × CH₂), 6.91–8.34 (m, 11H, ArHs), 8.72 (s, 1H, CH=N), 11.72 (s, 1H, SO₂NH); anal. calcd for C₂₅H₂₃N₇O₆S (549.56 g mol⁻¹): C, 54.64; H, 4.22; N, 17.84 (%); found: C, 56.79; H, 4.12; N, 17.58 (%); MS (*m*/*z*): 549.1 (M⁺).

4.2.17 (*E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4-(*A*,6-dimethylpyrimidin-2-yl)sulfamoyl)phenyl)imino) methyl)benzoate (10q). White powder, yield: 54%. Mp 256–257 °C; ¹H NMR (DMSO-d6) δ ppm: 2.24, 2.26, 2.47 (s, 9H, 3 × CH₃), 4.67–4.75 (t, 4H, 2 × CH₂), 5.94–8.04 (m, 10H, ArHs), 8.71 (s, 1H, CH=N), 11.75 (s, 1H, SO₂NH); anal. calcd for C₂₆H₂₅N₇O₆S (563.59 g mol⁻¹): C, 55.41; H, 4.47; N, 17.40 (%); found: C, 55.31; H, 4.25; N, 17.63 (%); MS (*m*/*z*): 563.2 (M⁺).

4.2.18 *(E*)-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-(((4-(*N*-carbamimidoylsulfamoyl)phenyl)imino)methyl)benzoate (10r). White powder, yield: 51%. Mp 232–233 °C; ¹H NMR (DMSO-d6) δ ppm: 2.48 (s, 3H, CH₃), 4.69–4.76 (t, 4H, 2 × CH₂), 6.72–8.09 (m, 12H, ArHs + NH₂), 8.73 (s, 1H, CH=N), 11.73 (s, 1H, SO₂NH); anal. calcd for C₂₁H₂₁N₇O₆S (499.50 g mol⁻¹): C, 50.50; H, 4.24; N, 19.63 (%); found: C, 50.37; H, 4.06; N, 19.48 (%); MS (*m*/*z*): 499.1 (M⁺).

4.2.19 *(E)*-2-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)ethyl 4-((phenethylimino)methyl)benzoate (11s). White powder, yield: 80%. Mp 198–199 °C; ¹H NMR (DMSO-d6) δ ppm: 2.47 (s, 3H, CH₃), 2.95 (s, 2H, CH₂), 3.86 (s, 2H, CH₂), 4.65–4.76 (t, 4H, 2 × CH₂), 7.17–8.06 (m, 10H, ArHs), 8.35 (s, 1H, CH=N); anal. calcd for C₂₂H₂₂N₄O₄ (406.43 g mol⁻¹): C, 65.01; H, 5.46; N, 13.78 (%); found: C, 64.86; H, 5.64; N, 13.85 (%); MS (*m*/*z*): 406.2 (M⁺).

4.2.20 (*E*)-1-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)propan-2-yl 4-(((4-methoxyphenyl)imino)methyl)benzoate (12t). White powder, yield: 87%. Mp 204–205 °C; ¹H NMR (DMSO-d6) δ ppm: 1.57, 2.54 (s, 6H, 2 × CH₃), 3.89 (s, 3H, OCH₃), 4.48– 4.78 (d, 2H, CH₂), 5.59–5.64 (t, 1H, CH), 6.99–8.04 (m, 9H, ArHs), 8.58 (s, 1H, CH=N); anal. calcd for C₂₂H₂₂N₄O₅ (422.43 g mol⁻¹): C, 62.55; H, 5.25; N, 13.26 (%); found: C, 62.41; H, 5.04; N, 13.14 (%); MS (*m*/*z*): 422.2 (M⁺).

4.2.21 (*E*)-1-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)propan-2-yl 4-((*p*-tolylimino)methyl)benzoate (12u). White powder, yield: 86%. Mp 203–205 °C; ¹H NMR (DMSO-d6) δ ppm: 1.56, 2.43, 2.54 (s, 9H, 3 × CH₃), 4.48–4.78 (d, 2H, CH₂), 5.60–5.64 (t, 1H, CH), 7.21–8.05 (m, 9H, ArHs), 8.56 (s, 1H, CH=N); anal. calcd for C₂₂H₂₂N₄O₄ (406.43 g mol⁻¹): C, 65.01; H, 5.46; N, 13.78 (%); found: C, 65.13; H, 5.30; N, 13.83 (%); MS (*m*/*z*): 406.2 (M⁺).

4.2.22 (E)-1-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)propan-2-yl 4-(((4-(*N*-(4-methylpyrimidin-2-yl)sulfamoyl)phenyl)imino)methyl) **benzoate** (12v). White powder, yield: 45%. Mp 256–257 °C; ¹H NMR (DMSO-d6) δ ppm: 2.24, 2.26, 2.47 (s, 9H, 3 × CH₃), 4.67–4.75 (d, 2H, CH₂), 5.60–5.64 (t, 1H, CH), 5.94–8.04 (m, 11H, ArHs + NH₂), 8.71 (s, 1H, CH=N), 11.75 (s, 1H, SO₂NH); anal. calcd for C₂₆H₂₅N₇O₆S (563.59 g mol⁻¹): C, 55.41; H, 4.47; N, 17.40 (%); found: C, 55.31; H, 4.25; N, 17.63 (%); MS (*m*/*z*): 563.2 (M⁺).

4.2.23 *(E)*-1-(2-Methyl-5-nitro-1*H*-imidazol-1-yl)propan-2-yl 4-((((4-(*N*-carbamimidoylsulfamoyl)phenyl)imino)methyl)benzoate (12w). White powder, yield: 54%. Mp 240–241 °C; ¹H NMR (DMSO-d6) δ ppm: 1.46, 2.45 (s, 6H, 2 × CH₃), 4.57–4.73 (d, 2H, CH₂), 5.71 (t, 1H, CH), 7.37–8.08 (m, 11H, ArHs + NH₂), 8.74 (s, 1H, CH=N), 11.75 (s, 1H, SO₂NH); anal. calcd for C₂₂H₂₃N₇O₆S (513.53 g mol⁻¹): C, 51.46; H, 4.51; N, 19.09 (%); found: C, 51.52; H, 4.40; N, 19.20 (%); MS (*m*/*z*): 513.1 (M⁺).

4.3 Biological assays

4.3.1 Antibacterial activity assay. The antibacterial activities of the synthetic compounds were tested against two Gram-negative bacterial strains, *i.e.*, *E. coli* ATCC 35218 and *P. aeruginosa* ATCC 13525, and two Gram-positive bacterial strains, *i.e.*, *B. subtilis* ATCC 6633 and *S. aureus* ATCC 6538, using the method recommended by National Committee for Clinical Laboratory Standards (NCCLS).²² *In vitro* activities of the compounds were tested in nutrient broth (NB) for bacteria by the twofold serial dilution method.

Seeded broth (broth containing microbial spores) was prepared in NB from 24 h old bacterial cultures on nutrient agar (HiMedia) at 37 \pm 1 °C. The bacterial suspension was adjusted with sterile saline to a concentration of 1 \times 10⁴ to 10⁵ CFU. The tested compounds and reference drugs were prepared by twofold serial dilution to obtain the required concentrations of 100, 50, 25, 12.5, 6.25 and 3.13 µg mL⁻¹. The tubes were incubated in BOD incubators at 37 \pm 1 °C for bacterial growth. The MICs were recorded by visual observations after 24 h (for bacteria) of incubation. Kanamycin B and penicillin G were used as standards for antibacterial activity. The observed MICs are presented in Table 1.

4.3.2 E. coli FabH purification and activity assay. Fulllength E. coli acyl carrier protein (ACP), acyl carrier protein synthase (ACPS), and β -ketoacyl-ACP synthase III (FabH) were individually cloned into pET expression vectors with an N-terminal His-tag (ACP, ACPS in pET19; FabH in pET28). All proteins were expressed in E. coli strain BL21 (DE3). Transformed cells were grown on Luria-Bertani (LB) agar plates supplemented with kanamycin B (30 μ g mL⁻¹). Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) analysis was used to screen colonies for over expression of proteins. One such positive colony was used to inoculate 10 mL of LB medium with 30 µg mL⁻¹ of kanamycin B and grown overnight at 37 °C, 1 mL of which was used to inoculate 100 mL LB medium supplemented with 30 mg mL⁻¹ of kanamycin B. The culture was shaken for 4 h at 37 °C, and then induced with 0.5 mM isopropyl β -D-thiogalactopyranoside (IPTG). The culture was grown for 4 h, and harvested by centrifugation (30 min at 15 000 rpm).

Harvested cells containing His-tagged ACP, ACPS, and FabHs were lysed by sonication in 20 mM Tris, pH 7.6, 5 mM imidazole, 0.5 M NaCl and centrifuged at 20 000 rpm for 30 min. The

supernatant was applied to a Ni-NTA agarose column, washed, and eluted using a 5–500 mM imidazole gradient over 20 column volumes. Eluted protein was dialyzed against 20 mM Tris, pH 7.6, 1 mM DTT, and 100 mM NaCl. Purified FabHs were concentrated up to 2 mg mL⁻¹ and stored at -80 °C in 20 mM Tris, pH 7.6, 100 mM NaCl, 1 mM DTT, and 20% glycerol for enzymatic assays.

Purified ACP contains the apo-form that needs to be converted into the holo-form. The conversion reaction is catalyzed by acyl carrier protein synthase (ACPS). In the final volume of 50 mL, 50 mg ACP, 50 mM Tris, 2 mM DTT, 10 mM MgCl₂, 600 μ M CoA, and 0.2 μ M ACPS were incubated for 1 h at 37 °C. The pH of the reaction was then adjusted to approximately 7.0 using 1 M potassium phosphate. Holo-ACP was purified by fractionation of the reaction mixture by Source Q-15 ion exchange chromatography using a 0–500 mM NaCl gradient over 25 column volumes.

In a final 20 μ L reaction, 20 mM Na₂HPO₄/NaH₂PO₄, pH 7.0, 0.5 mM DTT, 0.25 mM MgCl₂, and 2.5 μ M holo-ACP were mixed with 1 nM FabH, and H₂O was added to 15 mL. After 1 min incubation, a 2 μ L mixture of 25 μ M acetyl-CoA and 0.75 μ Ci [3H] acetyl-CoA was added for FabH reaction for 25 min. The reaction was stopped by adding 20 mL of ice-cold 50% TCA, incubating for 5 min on ice, and centrifuging to pellet the protein. The pellet was washed with 10% ice-cold TCA and resuspended with 5 μ L of 0.5 M NaOH. The incorporation of the 3H signal in the final product was read by liquid scintillation. When determining the inhibition constant (IC₅₀), inhibitors were added from a concentrated DMSO stock such that the final concentration of DMSO did not exceed 2%.

4.3.3 Acute oral toxicity assay. Five thousand milligrams of the compounds (10b, 10f, 10q, 10r, 12v) per kilogram of bodyweight were administered to 25 healthy rats by oral gavage, respectively. The animals were observed for mortality, signs of gross toxicity and behavioral changes at least once daily for 14 days. Bodyweights were recorded prior to administration and again on days 7 and 14. All animals kept active and healthy during the entire study time. There were no signs of gross toxicity or abnormal behavior.

4.4 Docking simulations

The crystal structures of *E. coli* FabH (PDB code: 1HNJ) were obtained from the Protein Data Bank (http://www.rcsb.org). Molecular docking of compounds into the three-dimensional X-ray structure of FabH was carried out using Ligand Fit Dock protocol of Discovery Studio 3.5.

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