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Synthesis, biological activity and molecular modeling study of new Schiff bases incorporated with indole moiety

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Abstract: A new series of heterocyclic Schiff bases **2–9** containing indole moiety were synthesized by facile and efficient condensation of indole-3/2/5-carboxaldehyde (**1a/1b/1c**) with different aromatic and heterocyclic primary amines using conventional and/or microwave irradiation methods. The structures of the obtained compounds were assigned by sophisticated spectroscopic and spectrometric techniques (1D-NMR, 2D-NMR and MS). The synthesized compounds were screened for their cytotoxicity and antibacterial activities. In vitro cytotoxicity screening revealed that compound **5** exhibited moderate activity against KB-3-1 cell line ($IC_{50} = 57.7 \mu M$) while 5-indolylimino derivative **7** indicated close to the activity ($IC_{50} = 19.6 \mu M$) in comparison with the positive control (+)-Griseofulvin ($IC_{50} = 19.2 \mu M$), while the tested compounds **5**, **6b**, **7** and **9** revealed good or moderate antibacterial activity. In addition, molecular docking study of

Schiff bases **2–9** was performed by Molecular Operating Environment (MOE 2014.09) program on the matrix metalloproteinase-8 (MMP-8) (Protein Data Bank (PDB) ID: 1MNC) in an attempt to explore their mode of action as anticancer drugs.

Keywords: antibacterial activity; cytotoxicity activity; microwave irradiation; molecular docking; Schiff base; thermal synthesis.

1 Introduction

Indole derivatives are found in many natural products such as fungal metabolites, indole alkaloids and marine organisms [1–6]. The indole nucleus has been reported to have an important role in medicinal chemistry involving antimicrobial [7, 8], anti-inflammatory [9, 10], antioxidant [11–13], anticancer [14–17], antibiotic [2] and anti-HIV [18, 19] activities. Besides, C-3-substituted indoles are versatile intermediates for the synthesis of many pharmacologically active compounds [20–24]. Schiff bases are a vital class of organic molecules that have azomethine group and versatile applications such as polymer stabilizers, catalysts and intermediates in organic synthesis, ligands in coordination chemistry, and pigments or dyes [25–27]. Moreover, Schiff bases have attracted considerable attention due to their extensive biological activities, including antibacterial, antifungal, antimalarial, antiviral and antipyretic properties [28–30].

The aim of the present investigation was to design new Schiff bases incorporated with indole moiety and check their biological activity in a trial to obtain new derivatives with high activity and less toxicity. Additionally, we investigated the molecular docking of the synthesized compounds using an MOE module (MOE2014.09) to understand the mode of action of Schiff bases through their various interactions with active sites of MMP-8 (PDB ID: 1MNC).

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2 Results and discussion

2.1 Chemistry

In thermal or microwave-assisted synthesis, 1*H*-indole-3-carboxaldehyde (**1a**) and primary amines, namely, 2-amino-6-ethoxy/methoxybenzothiazole, 4-aminoacetanilide, 4,4'-diamino-3,3'-dimethoxybiphenyldihydrochloride, benzophenone hydrazone, 4-aminobenzoic acid and methyl 4-aminobenzoate, were refluxed and/or irradiated in the presence of a catalytic amount of acetic acid or triethylamine to afford the corresponding Schiff bases **2–6** as depicted in Scheme 1.

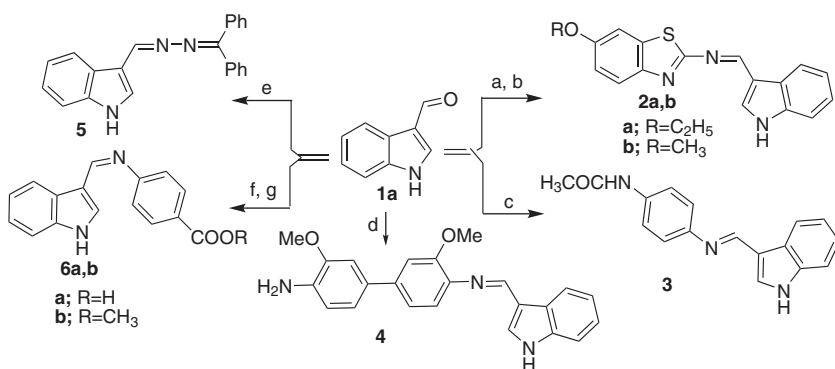
In a similar manner, the treatment of indole-carboxaldehydes (**1a–c**), namely, 1*H*-indole-3-carboxaldehyde (**1a**), 1*H*-indole-2-carboxaldehyde (**1b**) and 1*H*-indole-5-carboxaldehyde (**1c**), with 5-aminoindole affords the corresponding Schiff bases **7–9** as shown in Scheme 2.

The observed physical properties of the title compounds and comparison between the thermal and microwave methods are given in Tables S1 and S2 (see Supplementary information).

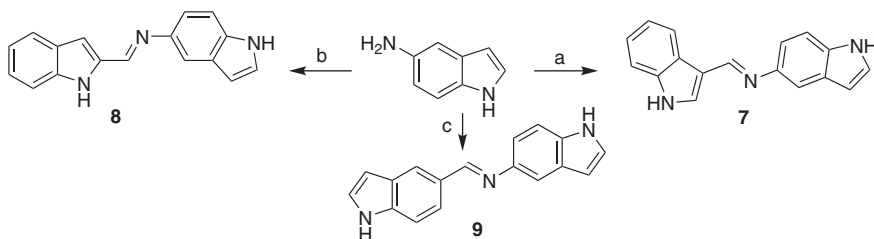
The results in Table S2 indicated that short reaction times, high purity of products, high yields, less side products, simplified synthetic procedure, economical with environmental technology, are all advantages offered by microwave irradiation method, which is better than thermal method.

The proton and carbon-13 nuclear magnetic resonance (¹H and ¹³C NMR) spectra of **2–6** revealed the presence of a broad ¹H singlet at δ 12.28–9.76 ppm due to the NH of indole moiety and a singlet at δ 9.94–8.72 ppm due to the proton of azomethine groups and the respective carbons at δ 160.8–154.6 ppm.

According to the heteronuclear multiple-quantum correlation spectroscopy (HMQC) experiment of **2a**, the proton resonance at δ 9.19 (H-8) ppm is directly connected to carbon at δ 160.8 (C-8) ppm and did not have any correlation with other protons according to the correlation spectroscopy (¹H,¹H-COSY) spectrum (Supplementary information, Table S3, Figures S3 and S4). The formation of Schiff base **2a** was further confirmed by HMBC correlation, as shown in the Supplementary information, Figures S5 and S6, where methine proton was coupled with C-3 (δ 114.8 ppm) in indole ring through two-bond



Scheme 1: Schematic representation for the synthesis of Schiff bases **2–6**. *Reagents:* (a) reflux or MW, MeOH, AcOH, 2-amino-6-ethoxybenzothiazole; (b) reflux or MW, MeOH, AcOH, 2-amino-6-methoxybenzothiazole; (c) reflux or MW, AcOH, 4-aminoacetanilide; (d) reflux or MW, MeOH, TEA, 4,4'-diamino-3,3'-dimethoxybiphenyldihydrochloride; (e) reflux or MW, MeOH, AcOH, benzophenone hydrazone; (f) reflux or MW, MeOH, AcOH, 4-aminobenzoic acid; (g) reflux or MW, MeOH, AcOH and methyl-4-aminobenzoate.



Scheme 2: Schematic representation for the synthesis of Schiff bases **7–9**. *Reagents:* (a) reflux or MW, MeOH, AcOH, 1*H*-indole-3-carboxaldehyde (**1a**); (b) reflux or MW, MeOH, AcOH, 1*H*-indole-2-carboxaldehyde (**1b**); (c) reflux or MW, MeOH, AcOH, 1*H*-indole-5-carboxaldehyde (**1c**).

correlation (2f) and with carbons C-2/3a/2' through three-bond correlation (3f), proving the formation of imine functional group between the reactants. In addition, the electrospray ionization mass spectrometry (ESI-MS) spectrum of compound **2a** shows the molecular ion peaks at m/z : 322 $[M+H]^+$ in the positive mode and 320 $[M-H]^-$ in the negative mode, respectively confirming the molecular weight of **2a** as 321 Dalton. Its high resolution electron ionization mass spectrometry (HR-EIMS) was compatible with the molecular formula $C_{18}H_{15}N_3OS$ (M^+ : 321.09200).

The formation of Schiff base **5** was confirmed by two-dimensional nuclear magnetic resonance spectroscopy (2D NMR) spectra (Supplementary information, Figures S25–S28), where the imine proton at δ 8.84 ppm was directly connected to the sp^2 carbon at δ 156.6 ppm according to the HMQC experiment. The mass spectrum of **5** provided additional evidence to confirm the structure, where the ESI-MS spectrum displays the molecular ion peak at m/z : 324 $[M+H]^+$. HR-EI-MS spectrum of **5** further established the structure, where it showed a molecular ion peak at m/z : 323.14164, which corresponds to the molecular formula $C_{22}H_{17}N_3$.

Besides, one-dimensional nuclear magnetic resonance spectroscopy (1D NMR) spectra of compounds **7–9** exhibit two broad signals at δ 11.70–11.39 and 11.16–11.08 ppm due to 2 NH of the indole moieties, also a singlet at δ 8.82–8.69 ppm due to the proton of imine groups and the respective carbons at δ 157.0–149.1 ppm.

The structure of compound **8** was further confirmed by 2D-NMR spectra (Supplementary information, Table S4, Figs S45–S48), where in the $^1H,^1H$ -COSY experiment, methine proton at δ 8.69 ppm did not have any correlation with other protons. In the HMQC spectrum, we saw that the proton with a chemical shift of δ 8.69 ppm was attached directly to the sp^2 carbon with resonance at δ 149.1 ppm. According to the heteronuclear multiple bond correlation spectroscopy (HMBC) experiment, the imine proton was coupled with three different carbons C-2/3/5', proving the formation of Schiff base **8**. MALDI-MS spectra exhibited the molecular ion peak at m/z : 260 $[M+H]^+$ for **7** and **8**, while the HR-EI-MS spectrum of **9** further confirmed the structure, where it showed the molecular ion peak at m/z : 259.10927, which corresponds to the molecular formula $C_{17}H_{13}N_3$.

2.2 Biological activities

2.2.1 Cytotoxic activity

Based on the reported cytotoxic and biological activities of the indole nucleus and Schiff base compounds [1–24,

Table 1: In vitro cytotoxicity of Schiff bases **2–9** against KB-3-1 cell line.

Compound	IC ₅₀ (μM)	Compound	IC ₅₀ (μM)
	KB-3-1		KB-3-1
2a	–	6b	>100
2b	–	7	19.6
3	–	8	–
4	–	9	–
5	57.7	(+)-Griseofulvin	19.2
6a	–	DMSO	–

28–30], new Schiff bases with indole moieties **2–9** were synthesized and selected to carry out a preliminary screening for their cytotoxic effect against human cervix carcinoma cell line KB-3-1 using the Resazurin assay [31, 32]. In vitro cytotoxicity activity of the synthesized Schiff bases **2–9** was evaluated against KB-3-1 cell line, and (+) Griseofulvin was used as reference cytotoxic compound. The IC₅₀ values for all tested compounds are shown in Table 1. The results indicate that 5-indolylimino derivative **7** exhibited excellent activity (IC₅₀ = 19.6 μM) and was very close to the reference [(+) Griseofulvin IC₅₀ = 19.2 μM], so it is the most potent one, while hydrazineylidene derivative **5** showed moderate activity (IC₅₀ = 57.7 μM). In contrast, the other compounds showed no activity against KB-3-1 cell line.

2.2.2 Antibacterial activity

Schiff bases **2–9** were screened to antibacterial assay by agar diffusion method [33] employing Gram-positive bacteria, namely, *Bacillus subtilis*, *Micrococcus luteus* and *Staphylococcus warneri* as well as Gram-negative bacteria, namely, *Escherichia coli* and *Pseudomonas agarici*. Activities were

Table 2: Inhibition zones of compounds **2–9** against bacterial strains (Ø: mm).

Compound	<i>E. coli</i>	<i>P. agarici</i>	<i>B. subtilis</i>	<i>M. luteus</i>	<i>S. warneri</i>
2a	–	–	–	–	–
2b	–	7	–	–	–
3	6.5	14	–	–	–
4	–	14	–	–	–
5	–	7	7	7	8
6a	–	10	7	–	–
6b	6.5	14	6.5	–	7
7	–	14	7	10	7
8	–	–	–	–	7
9	–	17	–	14	15
Gentamycin	18	23	20	18	16
DMSO	–	–	–	–	–

compared to gentamycin as positive control, while DMSO was used as negative control and tabulated in Table 2.

Interestingly, compounds **5**, **6b** and **7** showed moderate activity against all the bacterial strain except *Escherichia coli* with **5**, **7** and *Micrococcus luteus* with **6b**, which were not active. Compound **4** exhibited good activity against *Pseudomonas agarici* and did not show any activity against *Escherichia coli*, *Bacillus subtilis*, *Micrococcus luteus* and *Staphylococcus warneri*, while compound **9** showed activity against *Pseudomonas agarici*, *Micrococcus luteus* and *Staphylococcus warneri* close to the gentamycin and not active against *Escherichia coli* and *Bacillus subtilis*. In addition, the other compounds showed no activity mostly with all bacterial strains.

2.3 Molecular docking study

Docking study of Schiff bases **2–9** was performed by MOE 2014.09 program [34] on the matrix MMP-8 (PDB ID: 1MNC) [35, 36] in a trial to explore their mode of action as anticancer drugs. Based on the resulting data (see supplementary information, Table S5 and the score energy in Figure S57), compounds **3**, **9**, **6b**, **5** and **2b** showed maximum affinity with the active sites of the protein MMP-8, and the docking score energy for the tested compounds followed this order: **3** > **9** > **6b** > **5** > **2b** > **2a** > **8** > **7** > **6a** > **4** > (+)-Griseofulvin.

2.3.1 Docking of (+)-Griseofulvin into MMP-8 active site

Docking of (+)-Griseofulvin into MMP-8 active site showed the presence of several hydrophobic interactions involving methyl groups, oxygen atoms of carbonyl functions, chlorine atom and other atoms of the compound with the following amino acid residues: Gly 179, Ile 180, Leu 181, Ala 182, Glu 219, Pro 238, Asn 239 and Tyr 240 (see supplementary information Figure S58).

2.3.2 Docking of compound **2a** into MMP-8 active site

Docking of compound **2a** into MMP-8 active site revealed the interaction of sulfur atom as a hydrogen bond donor with the side chain residue Tyr 237 (1.42 Å) at a strength of 32.49%, as well as the presence of arene hydrogen interaction between the center of benzene ring of benzothiazole moiety and the side chain residue Ala 241. In addition, there were hydrophobic interactions between nitrogen atom and C-5,6,7 of indole moiety with various amino acid

residues: Gly 179, Ile 180, Leu 181, Ala 182, Leu 214, Val 215, His 218, Glu 219, Pro 232, Gly 233, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239, Tyr 240, Ala 241, Arg 243 and Zn 281 (see supplementary information Figure S59).

2.3.3 Docking of compound **2b** into MMP-8 active site

Docking of compound **2b** into MMP-8 active site exhibited the presence of hydrogen bond interaction between the sulfur atom and the side chain residue Tyr 237 (1.37 Å) at a strength of 26.14%, besides the presence of two arene hydrogen interactions between the center of benzene and thiazole rings in benzothiazole moiety with the side chain residues Ala 241 and Tyr 240, respectively. In addition, there were hydrophobic interactions involving C-5,6 of indole moiety and with various amino acid residues: Ile 180, Leu 181, Ala 182, Leu 214, Val 215, His 218, Glu 219, Pro 232, Gly 233, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239, Tyr 240, Ala 241, Arg 243 and Tyr 248 (see supplementary information Figure S60).

2.3.4 Docking of compound **3** into MMP-8 active site

Docking of compound **3** into MMP-8 active site displayed the presence of a hydrogen bond interaction between the nitrogen atom of NHCOCH_3 group and the side chain residue Ala 182 (1.14 Å) at a strength of 3.83%. Moreover, it revealed the presence of arene interaction between the phenyl ring of acetanilide moiety and the side chain residue His 218, also arene hydrogen interactions between the centers of indole moiety with the side chain residue Ala 241. In addition, there were hydrophobic interactions involving methyl group and other atoms of the compound with various amino acid residues: Ile 180, Leu 181, Ala 182, His 183, Leu 214, Val 215, His 218, Glu 219, His 228, Pro 232, Gly 233, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239, Tyr 240, Ala 241 and Arg 243 (see Supplementary information Figure S61).

2.3.5 Docking of compound **4** into MMP-8 active site

Docking of compound **4** into MMP-8 active site showed the presence of three arene hydrogen interactions between pyrrole ring of indole moiety and diphenyl rings of amine moiety with the side chain residues Ala 184, Leu 181 and Asn 239, respectively. Additionally, there were several hydrophobic interactions involving amino function,

C-4,5,6,7 of indole moiety, methyl groups and other atoms of the compound with various amino acid residues: Asn 178, Gly 179, Ile 180, Leu 181, Ala 182, His 183, Ala 184, Tyr 210, His 218, Glu 219, His 222, His 228, Pro 238, Asn 239 and Tyr 240 (see Supplementary information Figure S62).

2.3.6 Docking of compound 5 into MMP-8 active site

Docking of compound **5** into MMP-8 active site revealed the presence of arene hydrogen interaction between the center of benzene ring of indole moiety and the side chain residue Ala 241. In addition, there were several hydrophobic interactions involving other atoms of the compound with the following amino acid residues: Gly 179, Ile 180, Leu 181, Ala 182, His 183, Val 215, His 218, Glu 219, His 222, His 228, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239 and Tyr 240 (see Supplementary information Figure S63).

2.3.7 Docking of compound 6a into MMP-8 active site

Docking of compound **6a** into MMP-8 active site exhibited the presence of arene hydrogen interaction between the center of phenyl ring of benzoic acid moiety and the side chain residue Leu 181. Besides, there were several hydrophobic interactions involving other atoms of the molecule with the following amino acid residues: Asn 178, Gly 179, Ile 180, Leu 181, Ala 182, Tyr 210, His 218, Glu 219, His 222, His 228, Pro 238 and Tyr 240 (See supplementary information Figure S64).

2.3.8 Docking of compound 6b into MMP-8 active site

Docking of compound **6b** into MMP-8 active site displayed two arene hydrogen interactions between the centers of indole moiety with the side chain residue Ala 241. Furthermore, it revealed the presence of arene interaction between the phenyl ring of methyl benzoate moiety and amino acid residue His 218. In addition, there were hydrophobic interactions between methyl group and other atoms of the compound with the following amino acid residues: Ile 180, Ala 182, His 183, Val 215, His 218, Pro 232, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239, Tyr 240, Ala 241 and Arg 243 (see Supplementary information Figure S65).

2.3.9 Docking of compound 7 into MMP-8 active site

Docking of compound **7** into MMP-8 active site showed the presence of hydrogen bond interaction between nitrogen

atom of indole-3-carboxaldehyde moiety and the amino acid residue Glu 219 (0.96 Å) at a strength of 26.96%. Moreover, it revealed the presence of arene hydrogen interactions between two indole moieties with the side chain residues, Leu 181, Leu 235, Tyr 240 and Ala 241. In addition, there were hydrophobic interactions between C-4,5,6,7 with the following amino acid residues: Gly 179, Ile 180, Leu 181, Ala 182, Leu 214, Val 215, His 218, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239, Tyr 240, Ala 241, Arg 243 and Tyr 248 (see Supplementary information Figure S66).

2.3.10 Docking of compound 8 into MMP-8 active site

Docking of compound **8** into MMP-8 active site exhibited the presence of arene hydrogen interactions between two indole moieties with the side chain residues, Leu 181 and Leu 235. In addition, there were hydrophobic interactions between C-4,5,6,7 with the following amino acid residues: Ile 180, Leu 181, Ala 182, Leu 214, Val 215, His 218, Glu 219, Pro 232, Gly 233, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239, Tyr 240, Ala 241, Arg 243 and Tyr 248 (see Supplementary information Figure S67).

2.3.11 Docking of compound 9 into MMP-8 active site

Docking of compound **9** into MMP-8 active site revealed the presence of hydrogen bond interaction between nitrogen atom of indole moiety with the amino acid residue Ala 182 (0.69 Å) at a strength of 18.98%. Besides, it revealed the presence of arene hydrogen interactions in one indole moiety with the side chain residues Tyr 240 and Ala 241. In addition, there were hydrophobic interactions between C-2,3,4,7a with the following amino acid residues: Ile 180, Leu 181, Ala 182, Leu 214, Val 215, His 218, Glu 219, His 228, Ala 234, Leu 235, Tyr 237, Pro 238, Asn 239, Tyr 240, Ala 241 and Arg 243 (see Supplementary information Figure S68).

3 Experimental

3.1 General

Melting points were determined on a BÜCHI Melting Point B-540 apparatus (BÜCHI, Germany). NMR spectra (¹H NMR, ¹³C NMR, COSY, HMQC and HMBC) were measured on Bruker Avance DRX 500 MHz (125 MHz for ¹³C NMR) spectrometer (Bruker BioSpin, Billerica, MA, USA) with TMS as internal standard. Mass spectrometry experiments

were performed using a Fourier Transform Ion Cyclotron Resonance (FTICR 4.7T) mass spectrometer APEX II (Bruker Daltonik GmbH, Bremen, Germany) equipped with a 7.0-T, 160-mm bore superconducting magnet (Bruker Analytic GmbH-Magnetics, Karlsruhe, Germany) and infinity cell and interfaced to an external (Nano) ESI or MALDI ion source. EI-MS was recorded on a Finnigan MAT 95 spectrometer (70 eV) (Waters, Milford, MA, USA) with perfluorokerosene as the reference substance for HR-EI-MS. The microwave-assisted reactions (Matthews, NC, USA) were carried out in a CEM Discover, single-mode cavity with focused MW heating (MW power supply of 0–300 W, IR temperature sensor, open or closed vessel mode, pressure range of 0–20 bar, 10-ml or 80-ml vials). Starting materials, reagents and solvents were obtained from Sigma-Aldrich (St. Louis, MO, USA) and used without further purification. The purity of the synthesized compounds was investigated by TLC, performed on Merck precoated silica gel 60 F₂₅₄ aluminum sheets with solvent mixture of dichloromethane-methanol (95:5) as eluent. Spots were visualized under UV lamp at 254 and 366 nm and again after spraying with anisaldehyde/H₂SO₄ reagent and heating to accelerate the reaction.

3.2 Synthesis

Thermal method: A solution of indole-carboxaldehyde (**1a–c**) (1 mmol) in methanol (10 ml) containing two drops of acetic acid (triethylamine instead of acetic acid for compound **4**) was heated at 70 °C for 5 min. A solution of primary amine (2-amino-6-ethoxybenzothiazole, 2-amino-6-methoxybenzothiazole, 4-aminoacetanilide, 4,4'-diamino-3,3'-dimethoxybiphenyl-dihydrochloride, benzophenone hydrazone, 4-aminobenzoic acid, methyl-4-aminobenzoate and 5-aminoindole) (1 mmol) in methanol (5 ml) was added slowly and the reaction mixture was refluxed at 100 °C for a given time (Table S2). After completion (TLC), evaporation of the solvent under reduced pressure furnished crude solids, which were washed with DCM then warm methanol three times and dried to afford the target compounds **2–9** with 65–89% yield (Table S2).

Microwave synthesis: A mixture of indole-carboxaldehyde (**1a–c**) (1 mmol) and amine (1 mmol) in methanol (2 ml) in the presence of two drops of acetic acid (triethylamine instead of acetic acid for compound **4**) was placed into a 10-ml vial with a stirring bar then stirred at room temperature for 2 min and irradiated by microwave for a given time (Table S2) at 100 °C with power of 50 W. The

progress of the reaction was monitored by TLC. After completion of the reaction, the obtained solid was filtered, washed with DCM then warm methanol once time and dried to afford the title compound **2–9** with good purity (TLC) and excellent yield 79–99% yield (Table S2). The observed physical properties of title compounds **2–9** and the comparison between thermal method and microwave (MW) are given in Tables S1 and S2.

3.2.1 3-[(6-Ethoxybenzothiazol-2-imino)methyl]indole (**2a**)

¹H and ¹³C NMR data (see Table S3); MS ((+)-ESI) *m/z*: 322 [M+H]⁺; ((-)-ESI) *m/z*: 320 [M-H]⁻; MS (HR-EI) *m/z*: 321.09200 (Calcd. 321.09303 for C₁₈H₁₅N₃OS [M]⁺).

3.2.2 3-[(6-Methoxybenzothiazol-2-imino)methyl]indole (**2b**)

¹H NMR (DMSO-*d*₆, 500 MHz) δ (ppm): 12.23 (br s, 1H, NH), 9.20 (s, 1H, CH=N), 8.38–8.34 (m, 2H), 7.75 (d, *J*=8.9 Hz, 1H), 7.59 (d, *J*=2.6 Hz, 1H), 7.55 (d, 1H), 7.34–7.26 (m, 2H), 7.06 (dd, *J*=8.9, 2.6 Hz, 1H), 3.83 (s, 3H, OCH₃); ¹³C NMR (DMSO-*d*₆, 125 MHz) δ (ppm): 171.4 (C-2'), 160.8 (CH=N), 157.2 (C-6'), 146.3, 138.7, 138.0, 135.1, 125.01, 124.1, 122.8, 122.4, 122.4, 115.6, 114.8, 113.0, 105.6, 56.1(OCH₃); MS ((+)-ESI) *m/z* (%): 308 [M+H]⁺ (91), 330 [M+Na]⁺ (43); ((-)-ESI) *m/z*: 306 [M-H]⁻; MS (HR-EI) *m/z*: 307.07586 (Calcd. 307.07738 for C₁₇H₁₃N₃OS [M]⁺).

3.2.3 3-[(4-Acetylaminophenylimino)methyl]indole (**3**)

¹H NMR (DMSO-*d*₆, 500 MHz) δ (ppm): 11.74 (br d, *J*=3.1 Hz, 1H, NH-indole), 9.95 (d, *J*=1.7 Hz, 1H, NH-acetanilide), 8.72 (s, 1H, CH=N), 8.39 (d, *J*=7.7 Hz, 1H), 7.98 (d, *J*=2.8 Hz, 1H), 7.66–7.59 (m, 2H), 7.48 (d, *J*=8.0 Hz, 1H), 7.25–7.15 (m, 4H), 2.06 (s, 3H, COCH₃); ¹³C NMR (DMSO-*d*₆, 125 MHz) δ (ppm): 168.4 (C=O), 154.6 (CH=N), 148.6, 137.6, 136.8, 133.6, 125.2, 123.2, 122.3, 121.4, 121.2, 120.2, 115.6, 112.4, 24.4 (CH₃); MS ((+)-ESI) *m/z* (%): 278 [M+H]⁺ (100), 300 [M+Na]⁺ (99.5); ((-)-ESI) *m/z*: 276 [M-H]⁻; MS (HR-EI) *m/z*: 277.11976 (Calcd. 277.12096 for C₁₇H₁₅N₃O [M]⁺).

3.2.4 3-[[[4'-Amino-3,3'-dimethoxy-1,1'-biphenyl]-4-imino]methyl]indole (**4**)

¹H NMR (DMSO-*d*₆, 500 MHz) δ (ppm): 12.28 (br s, 1H, NH), 9.93 (s, 1H, CH=N), 9.34 (d, *J*=11.7 Hz, 1H), 9.22 (s,

1H), 8.35 (s, 1H), 8.29 (d, $J=3.1$ Hz, 1H), 8.11–8.06 (m, 1H), 7.55–7.49 (m, 1H), 7.49–7.39 (m, 4H), 7.32 (dd, $J=8.1, 1.9$ Hz, 1H), 7.29–7.18 (m, 2H), 4.09 (d, $J=18.2$ Hz, 3H, OCH₃), 4.00 (d, $J=14.2$ Hz, 3H, OCH₃); ¹³C NMR (DMSO-*d*₆, 125 MHz) δ (ppm): 158.1 (CH=N), 152.6, 152.1, 138.9, 137.5, 124.6, 124.2, 123.8, 122.6, 121.2, 120.0, 119.6, 118.6, 114.3, 112.9, 111.4, 111.1, 57.0 (OCH₃), 56.6 (OCH₃); MS ((+)-ESI) m/z : 372 [M+H]⁺; MS (HR-EI) m/z : 371.16153 (Calcd. 371.16283 for C₂₃H₂₁N₃O₂ [M]⁺).

3.2.5 3-[(Diphenylmethylene)hydrazineylidene]methyl]indole (5)

¹H NMR (acetonitrile-*d*₃, 500 MHz) δ (ppm): 9.76 (br s, 1H, NH), 8.84 (s, 1H, CH=N), 7.77–7.73 (m, 2H), 7.71 (dd, $J=6.9, 1.2$ Hz, 2H), 7.53 (dd, $J=5.6, 1.8$ Hz, 3H), 7.48–7.44 (m, 3H), 7.42 (ddd, $J=6.9, 4.4, 1.9$ Hz, 3H), 7.21 (ddd, $J=8.3, 7.1, 1.2$ Hz, 1H), 6.99 (td, $J=7.5, 7.0, 1.0$ Hz, 1H); ¹³C NMR (Acetonitrile-*d*₃, 125 MHz) δ (ppm): 165.3 (C=N), 156.6 (CH=N), 138.8, 137.6, 137.2, 132.2, 130.3, 129.9, 128.8, 128.7, 128.6, 128.1, 125.1, 123.5, 122.8, 121.2, 113.5, 112.0; MS ((+)-ESI) m/z : 324 [M+H]⁺; MS (HR-EI) m/z : 323.14164 (Calcd. 323.14170 for C₂₂H₁₇N₃ [M]⁺).

3.2.6 3-[(4-Carboxyphenylimino)methyl]indole (6a)

¹H NMR (DMSO-*d*₆, 500 MHz) δ (ppm): 13.22 (br s, 1H, COOH), 12.18 (br s, 1H, NH), 9.94 (s, 1H, CH=N), 8.29 (d, $J=3.1$ Hz, 1H), 7.68–7.65 (m, 1H), 7.65–7.63 (m, 2H), 7.52 (dt, $J=8.2, 1.0$ Hz, 1H), 7.29–7.19 (m, 2H), 6.61–6.56 (m, 2H); ¹³C NMR (DMSO-*d*₆, 125 MHz) δ (ppm): 165.8 (C=O), 156.6 (CH=N), 151.0, 136.8, 135.4, 129.6, 122.4, 121.8, 120.4, 119.2, 118.6, 116.5, 111.2, 110.8; MS ((+)-MALDI) m/z : 265 [M+H]⁺; MS (EI) m/z (%): 264 (M⁺; 100).

3.2.7 3-[(4-Methoxycarbonylphenylimino)methyl]indole (6b)

¹H NMR (DMSO-*d*₆, 500 MHz) δ (ppm): 12.19 (br s, 1H, NH), 9.94 (s, 1H, CH=N), 8.29 (d, $J=3.1$ Hz, 1H), 7.66–7.64 (m, 3H), 7.52 (dt, $J=8.1, 1.0$ Hz, 1H), 7.29–7.19 (m, 2H), 6.61–6.56 (m, 2H) 3.73 (s, 3H, OCH₃); ¹³C NMR (DMSO-*d*₆, 125 MHz) δ (ppm): 166.0 (C=O), 158.7 (CH=N), 153.7, 138.9, 137.5, 131.2, 123.8, 122.6, 121.2, 120.8, 118.6, 116.4, 114.0, 113.2, 52.6 (OCH₃); MS ((+)-MALDI) m/z : 279 [M+H]⁺; MS (HR-EI) m/z : 278.10429 (Calcd. 278.10498 for C₁₇H₁₄N₂O₂ [M]⁺).

3.2.8 3-[(5-Indolylimino)methyl]indole (7)

¹H NMR (DMSO-*d*₆, 500 MHz) δ (ppm): 11.70 (br s, 1H, NH), 11.08 (br s, 1H, NH), 8.82 (s, 1H, CH=N), 8.50–8.46 (m, 1H), 8.32 (s, 1H), 8.17–8.13 (m, 1H), 8.01–7.98 (m, 1H), 7.56 (dt, $J=8.0, 1.0$ Hz, 1H), 7.52 (dt, $J=8.1, 1.0$ Hz, 1H), 7.45–7.43 (m, 1H), 7.33–7.27 (m, 2H), 6.47 (ddd, $J=3.1, 2.1, 0.9$ Hz, 1H); ¹³C NMR (DMSO-*d*₆, 125 MHz) δ (ppm): 153.3 (CH=N), 145.9, 138.9, 137.6, 134.6, 132.7, 128.7, 126.3, 123.9, 121.2, 121.1, 118.6, 116.2, 112.8, 112.0, 111.2, 101.8; MS ((+)-MALDI) m/z : 260 [M+H]⁺; MS (EI) m/z (%): 259 (M⁺; 100).

3.2.9 2-[(5-Indolylimino)methyl]indole (8)

¹H and ¹³C NMR data (see Table S4); MS ((+)-MALDI) m/z : 260 [M+H]⁺; MS (EI) m/z (%): 259 (M⁺; 79), 258 (100).

3.2.10 5-[(5-Indolylimino)methyl]indole (9)

¹H NMR (DMSO-*d*₆, 500 MHz) δ (ppm): 11.39 (br s, 1H, NH), 11.11 (br s, 1H, NH), 8.72 (s, 1H, CH=N), 8.11–8.07 (m, 1H), 7.84 (dd, $J=8.5, 1.5$ Hz, 1H), 7.52 (d, $J=8.5$ Hz, 1H), 7.48 (d, $J=2.0$ Hz, 1H), 7.45–7.42 (m, 2H), 7.37 (t, $J=2.7$ Hz, 1H), 7.16 (dd, $J=8.5, 2.0$ Hz, 1H), 6.58 (ddd, $J=3.0, 1.8, 0.8$ Hz, 1H), 6.47 (ddd, $J=2.9, 1.8, 0.8$ Hz, 1H); ¹³C NMR (DMSO-*d*₆, 125 MHz) δ (ppm): 157.0 (CH=N), 142.6, 135.8, 132.8, 126.7, 126.5, 125.9, 124.8, 124.4, 121.1, 118.8, 114.2, 110.2, 110.0, 109.7, 100.6, 99.8; MS ((+)-ESI) m/z : 260 [M+H]⁺; ((-)-ESI) m/z : 258 [M-H]⁻; MS ((+)-MALDI) m/z : 260 [M+H]⁺; MS (HR-EI) m/z : 259.10927 (Calcd. 259.11040 for C₁₇H₁₃N₃ [M]⁺).

3.3 Biological assays

3.3.1 Resazurin-based cytotoxicity assay

KB 3-1 cells were cultivated as a monolayer in Dulbecco's modified Eagle medium (DMEM) with glucose (4.5 g/l), L-glutamine, sodium pyruvate and phenol red, supplemented with 10% of KB 3-1 and fetal bovine serum (FBS). Cells were maintained at 37 °C and 5.3% CO₂-humidified air. One day prior to the test, cells of 70% confluence were detached with 0.05%/0.02% of trypsin-ethylenediamine tetraacetic acid solution in Dulbecco's phosphate-buffered saline (DPBS) and placed in sterile 96-well plates in a density of 10,000 cells in 100- μ l medium per well. The dilution series of the compounds were prepared from stock solutions in DMSO of concentrations of 100 μ M, 50 μ M, or 25 μ M. The stock solutions were diluted with culture

medium (10% FBS [KB 3-1]) down to pM range and dilutions added to the wells. Each concentration was tested in six replicates. Dilution series were prepared by pipetting liquid from well to well, with the control containing the same concentration of DMSO as the first dilution. After incubation for 72 h at 37 °C and 5.3% CO₂-humidified air, 30 µl of aqueous resazurin solution (175 µM) was added to each well. The cells were incubated under the conditions mentioned above for further 5 h and fluorescence was measured (λ_{ex} = 530 nm, λ_{em} = 588 nm). Results are given as IC₅₀, calculated as average of two determinations by sigmoidal dose-response curve fitting model using Graph Pad Prism software version 4.03.

3.3.2 Antibacterial agar plate diffusion assay

By using a sterile pipette, 0.2 ml of the broth culture of each test bacterium was added to a sterile petri dish containing a nutrient broth agar or trypticase soy broth layer. Sterile paper disks with diameter of 6 mm were impregnated with 20 mg/ml of pure compounds dissolved in DMSO and dried under sterile conditions, and the disks were placed on agar plates pre-inoculated with broth cultures of Gram-positive bacteria *Bacillus subtilis*, *Micrococcus luteus*, or *Staphylococcus warneri* or Gram-negative bacteria *Escherichia coli* or *Pseudomonas agarici*. Plates were incubated for 24 h at 30–37 °C, and the diameter of inhibition zones was measured by a ruler in millimeter. Gentamycin at 20 mg/ml was used as positive control for each plate with test strain and DMSO as negative control.

3.4 Molecular docking study

Molecular modeling study of Schiff bases **2–9** was done using MOE module (MOE 2014.09; Chemical Computing Group, Montreal, Canada) as the computational software to understand the action mode of compounds through their various interactions with the active sites of MMP-8 (PDB ID: 1MNC). The program operated on an Intel Pentium 1.6-GHz processor, 512-MB memory with windows XP operating system. All the minimizations were performed with MOE until an RMSD gradient of 0.05 K Cal/mol Å with MMFF94X force field and the partial charges were automatically calculated.

Coordinates of X-ray crystal structure of (+)-Griseofulvin bound to matrix metalloproteinase (MMP-8) enzyme were obtained from the PDB (PDB ID: 1MNC). Enzyme structures were checked for missing atoms, bonds and contacts. Hydrogen atoms were added to the enzyme

structure. Water molecules and bound ligands were manually deleted. Ligand molecules were constructed using the builder molecule and were energy minimized. The active site was generated using the MOE-Alpha site finder. Dummy atoms were created from the obtained alpha spheres. Ligands were docked within MMP-8 active sites using the MOE-Dock with simulated annealing used as the search protocol and MMFF94X molecular mechanics force field for 8000 interactions. The lowest energy conformation was selected and subjected to an energy minimization using MMFF94X force field.

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