

## Molecular Design, Synthesis and Biological Evaluation of Heterocyclic Compounds as Potential Targeted Antimicrobial Agents

#### Thesis

Submitted in Partial Fulfillment of the Master's Degree in Pharmaceutical Sciences (Pharmaceutical Chemistry)

### Presented by

### Menna-Allah Wagih Anwar Mohamed Shalaby

B.Sc. in Pharmaceutical Sciences (May 2014) Teaching Assistant, Pharmaceutical Chemistry Faculty of Pharmacy, Ain Shams University

Under Supervision of

### Prof. Dr. Khaled Abouzid Mohamed Abouzid

Professor of Pharmaceutical Chemistry & Dean of Faculty of Pharmacy, Sadat City University

### Assoc. Prof. Dr. Rabah Ahmed Taha Serya

Associate Professor of Pharmaceutical Chemistry & Deputy Head of the Pharmaceutical Chemistry Department, Faculty of Pharmacy, Ain Shams University

### Dr. Eman Mahmoud Elawady Dokla

Lecturer of Pharmaceutical Chemistry, Faculty of Pharmacy, Ain Shams University

> Faculty of Pharmacy Ain Shams University 2019

## **Acknowledgments**

It's a pleasure to express my sincere appreciation to Professor Dr. Khaled Abouzid, Professor of Pharmaceutical Chemistry and Dean of Faculty of Pharmacy, Sadat City University, for his scientific supervision, innovative ideas, fruitful opinion, invaluable advices and continuous encouragement. I am indebted to him for his guidance and endless support throughout this work, which allowed this thesis to appear in its final form.

I owe my truthful gratitude to Assoc. Prof. Dr. Rabah Taha, Associate Professor of Pharmaceutical Chemistry and Deputy Head of the Pharmaceutical Chemistry Department, and Dr. Eman Dokla, Lecturer of Pharmaceutical Chemistry, for their continuous encouragement and tremendous support. I am heartily grateful to their indispensable opinion, real interest, trust, eminent guidance and untiring help throughout the whole work.

I acknowledge with thankfulness all my colleagues in the Pharmaceutical Chemistry Department, for their friendly cooperation, support and invaluable aid.

I express my appreciation to Professor Mohamed Seleem lab, Purdue University, USA for performing the antimicrobial screening.

I would like to express my thanks to the Center for Drug Discovery Research and Development, Ain Shams University, for performing the NMR spectroscopy analysis.

# List of Contents

Title	Page N
List of Tables	IV
List of Figures	V
List of Abbreviations	.VIII
Abstract	
1. Introduction	1
1.1. Overview	
1.2. Evolution of MRSA	
1.3. Resistance to β-lactam antibiotics	
1.4. Bacterial cell-wall biosynthesis and the role of Penicillin-Binding Proteins	
1.4.1 Cell wall biosynthesis	
1.4.2. Penicillin-binding proteins: the key players in bacterial cell w	
synthesis	
1.5. Understanding PBP2a resistance	
1.5.1. PBP2a resistance mechanism	
1.5.2. Structural information on PBP2a	
1.5.3. Structural and kinetic resistance to $\beta$ -lactam antibiotics by PBP2a	
1.6. Allosteric control of PBP2a physiological function	
1.7. Targeting PBP2a	
1.7.1. $\beta$ -lactam antibiotics	
1.7.2. Oxadiazoles derivatives	
1.7.2. Oxadiazoles derivatives	
1.7.4. Non-covalent Inhibitors	
1.7.4. Non-covatent inmotiors 1.7.5. Miscellaneous PBP2a inhibitors	
2. Rationale and Design	
2.1. Identification of key interactions between PBP2a enzyme allosteric bind	-
site and quinazolinone-based derivative 11.	
2.2. Rational modification of the lead compound (11)	
2.3. Preliminary evaluation of the designed compounds using Computer-Aio	
Molecular Modeling.	
2.3.1. Molecular Field Alignment	
2.3.2. Docking study	
2.4. Synthetic Schemes of the designed compounds	
2.4.1. Scheme 1 for synthesis of 1-phenylpyrazole derivatives	
2.4.2. Scheme 2 for synthesis of chromen-4-one derivatives	
2.4.3. Scheme 3 for the synthesis of benzimidazole derivatives	
3. Results and Discussion	
3.1. Chemistry	
3.1.1. Scheme 1	
3.1.2. Scheme 2	
3.1.3. Scheme 3	
3.2. Biological Evaluation	
3.2.1. Evaluation of antimicrobial activity	75

3.2.2. In vitro cytotoxicity analysis	85
3.3. Molecular Modeling	83
3.3.1. Validation of the docking protocol	89
3.3.2. Results of docking of the target compounds into PBP2a-allost	eric site 89
4. Conclusion	98
5. Experimental	100
5.1. Chemistry	100
5.1.1. Materials and instrumentation	
5.1.2. Synthesis	101
5.2. Biological evaluation	
5.2.1. Determination of the minimum inhibitory concentration (	(MIC) and
minimum bactericidal concentration (MBC) against Gram-positiv	e bacterial
pathogens	126
5.2.2. Intracellular infection of J774 cells with MRSA and trea	tment with
XIVa, XIVb and XIVc	126
5.2.3. MRSA biofilm eradication assessment	126
5.2.4. Evaluation of XIIIb, and XIVa-c combination with $\beta$ -lactam as	ntibiotics 126
5.2.5. In vitro cytotoxicity analysis	126
5.3. Molecular Modelling study	129
5.3.1. Preparation of the enzyme	129
5.3.2. Identifying the binding pocket	130
5.3.3. Display lead- protein interactions	130
5.3.3. Docking of the test set	
6. Supplementary Data	132
7. References	156
Arabic Summary	

# List of Tables

Table No.	. Title P	age No.
Table 1:	Docking energy and amino acids involved in the binding interactions of some of the designed compounds.	
Table 2:	The minimum inhibitory concentration (MIC in μg/mL) of phenylpyrazole derivatives screened against <i>Staphylococc</i> .	1- us
Table 3:	aureus strains cultivated on tryptone soya broth medium	of us
Table 4:	The minimum inhibitory concentration (MIC in µg/mL) benzimidazole derivatives screened against <i>Staphylococci</i>	of
Table 5:	aureus strains cultivated on tryptone soya broth medium	nd
Table 6:	most active compounds against methicillin-sensiting Staphylococcus aureus (MSSA), methicillin-resistate Staphylococcus aureus (MRSA), vancomycin-resistate Staphylococcus aureus (VRSA), Staphylococcus epidermidis The minimum inhibitory concentration (MIC in µg/mL) and minimum bactericidal concentration (MBC in µg/mL) of the most active compounds against clinically relevant Gram-positive bacterial pathogens including multi-drug resistant Streptococcus pneumoniae, vancomycin-resistant Enterococcus faecal.	nt nt 81 nd he ve us
Table 7:	vancomycin-resistant Enterococcus faecium, and Lister monocytogens	<i>ia</i> 81 th 00

# List of Figures

Fig. No.	Title Pa	ge No.
Figure 1. Figure 2.	PBP2a and β-lactamase expression regulation	1
Figure 3.	Synthesis.  Classification of PBPs by molecular mass and by domain composition	n
Figure 4.	β-lactam antibiotics interaction with PBPs.	7
Figure 5.	Ribbon representation of the x-ray crystal structure of PBP2a (PDB: <b>1VQQ</b> )	
Figure 6.	The active site of PBP2a from <i>Staphylococcus aureus</i> in uncomplexed (purple) and complexed (green) forms reveals that drug resistance may be related to active site distortion and domain movement	t 1
Figure 7.	Three-steps reaction scheme for interactions of PBP with $\beta$ lactam antibiotics	
Figure 8.	Diagrammatic representation of the allosteric activation of PBP2a to carry out its physiological function in cell wal crosslinking.	1
Figure 9.	Inhibition of the <i>S. aureus</i> PBP2a by ceftaroline (1)	14
Figure 10.	Superimposition of the active sites of the unbound (PDB ID <b>1VQQ</b> ) and ceftaroline bound <i>S. aureus</i> PBP2a (PDB: <b>3ZG0</b> )	:
Figure 11.	Allosteric site mutations confer low-level ceftaroline resistance to the mutant MRSA strains	
Figure 12.	Inhibition of the S. aureus PBP2a by ceftobiprole (2)	19
Figure 13.	View of ceftobiprole within the active site of PBP2a showing the R1 group in both its proposed conformations (PDB ID 4DKI).	:
Figure 14.	Comparison of the binding mode and interactions of ceftaroline (green, PDB: <b>3ZG0</b> ) and ceftobiprole (magenta, PDB: <b>4DKI</b> within the PBP2a active site	)
Figure 15.	Chemical structures of two investigational β-lactam antibiotics ME1036 and L-695,256.	
Figure 16.	1,2,4-oxadiazole derivatives that exhibit good MIC activity against various MRSA strains.	
Figure 17.	General structure–activity relationship (SAR) for the newly discovered oxadiazole class of antibiotics	
Figure 18.	Initial hit and optimized 4(3 <i>H</i> )-quinazolinone antibacterials	26
Figure 19.	Inhibition of the <i>S. aureus</i> PBP2a by quinazolinone derivative compound <b>11</b>	

Figure 20.	General structure-activity relationship (SAR) for the newly	
rigure 20.	discovered quinazolinone class of antibiotics.	28
Figure 21.	Structural comparison of the ceftaroline and compound 11 interaction with the PBP2a allosteric site	
Figure 22.	Non-covalent inhibitors of PBP2a.	30
Figure 23.	2D interaction diagram the postulated binding mode for non-covalent inhibitor; compound 13, into the PBP2a active site (PDB: 1VQQ)	31
Figure 24.	Miscellaneous PBP2a inhibitors	34
Figure 25.	Detailed view of compound <b>11</b> binding at the allosteric binding site of the PBP2a enzyme (PDB code: <b>4CJN</b> )	36
Figure 26.	Rescaffolding and optimization strategy of the quinazolinone-based lead compound 11.	37
Figure 27.	Representative designed compounds (pink:chromen-4-one; green: 1-phenylpyrazole; blue: benzimidazole) aligned to compound 11 (grey) using FieldAlign	40
Figure 28.	Classification of active centers	50
Figure 29.	Hydrazone formation mechanism	50
Figure 30.	The proposed mechanism for Vilsmeier-Haack reaction	52
Figure 31.	Wittig reaction mechanism.	54
Figure 32.	Béchamp Reduction, mechanism of metal-catalyzed nitro reduction. (M= Metal)	56
Figure 33.	Perkin reaction.	58
Figure 34.	Cinnamic acid synthesis from acetic acid esters	58
Figure 35.	Cinnamic acid synthesis from benzal chloride.	59
Figure 36.	Cinnamic acid synthesis from cinnamaldehyde	59
Figure 37.	Baker-Venkataraman rearrangement mechanism	61
Figure 38.	Proposed mechanism for cyclization	62
Figure 39.	Suzuki-Miyaura Reaction	64
Figure 40.	Mechanism of Suzuki-Miyaura coupling reaction	65
Figure 41.	Mechanism of Amide formation through TBTU/DMAP-assisted coupling	71
Figure 42.	Synthesis of benzimidazole by condensation of aryl diamine with suitable aldehyde	73
Figure 43.	Mechanism of benzimidazole ring closure	73
Figure 44.	Examination of the activity of the tested compounds on the clearance of intracellular MRSA present in murine macrophage (J774) cells.	89
Figure 45.	Combination effects of <b>XIIIb</b> , and <b>XIVa-c</b> with piperacillin against MRSA NRS123 using a standard checkerboard assay	
Figure 46.	Analyzing the toxicity of chromen-4-one compounds, XIIb, XIVa, XIVb, and XIVc.	

List	of	Fig	gur	es	2
-150	Ο.		~·	-	$\sim$

Figure 47.	The alignment between the co-crystallized bioactive conformer	
	of lead compound (11) (green) and the pose of (11) retrieved	
	from docking using CDOCKER.	89

# List of Abbreviations

Abb.	Full term
<sup>13</sup> C NMR	
<sup>1</sup> H NMR	Proton Nuclear Magnetic Resonance
	Antimicrobial resistance
BOP	Benzotriazol-1-yloxytris(dimethylamino)phosphonium
	hexafluorophosphate
<i>CAMHB</i>	Cation adjusted Mueller Hinton Broth
	Center for disease control and prevention
	based docker CHARMm-
CHARMm	Chemistry at Harvard Macromolecular Mechanics
	N,N'-Dicyclohexylcarbodiimide
	Deuterium oxide
	dichloromethane
DMAP	4-(Dimethylamino)pyridine
	Dimethylformamide
	Dimethyl sulfoxide
	Electron Ionization Mass Spectrometry
	Ethyl acetate
	Food and Drug Administration
	Fractional inhibitory concentration
	Glycosyl transferase
	hydrogen bond
	High Molecular Mass
hr	
	Hexafluorophosphate Azabenzotriazole Tetramethyl Uronium
<i>Hz</i>	
	Half-maximal inhibitory concentration
	Liquid chromatography–mass spectrometry
	Low Molecular Mass
<i>MS</i>	Mass spectroscopy
	mass-to-charge ratio
	Melting point
	Molecular ion
	Molecular Dynamics
	Monofunctional glycosyl transferase
	Mega hertz
	Micromole
΄μl	
•	Minimum inhibitory concentration
mmol	· · · · · · · · · · · · · · · · · · ·
	Multiple drug resistance
	Minimum bactericidal concentration
	Methicillin resistance staphylococcus aureus.



MCCA	M-41: -:11:
MSSA	Methicillin sensitive staphylococcus aureus
<i>Mwt</i>	
<i>NAG</i>	.N-acetylglucosamine
<i>NAM</i>	.N-acetylmuramic acid
<i>PBP</i>	Penicillin binding protein.
<i>PDB</i>	.Protein data bank
<i>Ppm</i>	.Part per million
QSAR	.Quantitative structure activity relationship
$R_f$	.Retention factor
<i>RMSD</i>	Root mean square deviation
rt	.Room temperature
S.aureus	.Staphylococcus aureus
S.epidermidis	.Staphylococcus epidermidis
S.pneumoniae	.Streptococcus pneumoniae
<i>SAR</i>	.Structure activity relationship
<i>T3P</i>	.Propanephosphonic acid anhydride
	.2-(1H-Benzotriazole-1-yl)-1,1,3,3-tetramethylaminium
	tetrafluoroborate
<i>TEA</i>	.Triethylamine
<i>THF</i>	.Tetrahydrofuran
<i>TLC</i>	.Thin layer Chromatography
<i>TMS</i>	.Tetramethylsilane
<i>TP</i>	.Transpeptidation
<i>TSA</i>	.Tryptic Soy Agar
<i>UDP</i>	
	-

### **Abstract**

The rapid and continuous spread of antimicrobial resistance poses an enormous burden and threat to the global public health, where infections caused by multidrug resistant bacteria are associated with serious morbidity and mortality. The Gram-positive bacterium Staphylococcus aureus is a major cause of both nosocomial and community-acquired infections worldwide. The first methicillin-resistant S. aureus (MRSA) strain was isolated in the United Kingdom in 1961. This resistance phenotype arose through the acquisition of a gene cassette containing mecA, which encoded an altered transpeptidase, penicillin binding protein 2a (PBP2a), that demonstrated low binding affinity to most commercially available β-lactam antibiotics and was capable of cross-linking the peptidoglycan chains of the cell wall when other transpeptidases were inhibited by  $\beta$ -lactams. Since 1990 and up till today, MRSA infections presented a stressing global problem and the development of new antimicrobial agents to combat MRSA infections is of utmost importance. Targeting the key resistance enzyme, penicillin binding protein 2a, with small molecules is a promising therapeutic approach to tackle MRSA infections and was proved successful by the approval of the  $\beta$ -lactam antibiotics, ceftobiprole and ceftaroline.

Our research objectives were to design, synthesize and biologically evaluate new inhibitors targeting MRSA infections via inhibition of the mutant PBP2a. The design process aimed to target PBP2a allosteric site and started by identification of the key interactions between PBP2a enzyme allosteric binding site and a recently reported quinazolinone-based PBP2a inhibitor [(E)-3-(2-(4-cyanostyryl)-4-oxoquinazolin-3(4H)-yl)benzoic acid], following, rational modification of the lead compound was proposed and three series of derivatives were suggested (1-phenylpyrazole, chromen-4-one, and benzimidazole) and finally molecular modeling studies including field alignment and docking were performed to investigate the predicted binding modes and binding affinities of the designed compounds.

The designed compounds were synthesized, purified and structurally confirmed by different analytical and spectral techniques.

### The study involved the synthesis of the following unavailable reported intermediates:

- 1) 3-Nitroacetophenone (**Ia**)
- 2) (E)-1-(1-(3-Nitrophenyl)ethylidene)-2-phenylhydrazine (**IIa**).
- 3) 3-(3-Nitrophenyl)-1-phenyl-1*H*-pyrazole-4-carbaldehyde (**IIIa**)
- 4) (E)-3-(4-Cyanophenyl)acrylic acid (**VIc**).
- 5) 2-Acetylphenyl (*E*)-3-phenylacrylate (**VIIIa**).
- 6) 2-Acetylphenyl (*E*)-3-(4-fluorophenyl)acrylate (**VIIIb**).
- 7) (E)-1-(2-Hydroxyphenyl)-5-phenylpent-4-ene-1,3-dione (**IXa**).
- 8) (E)-5-(4-Fluorophenyl)-1-(2-hydroxyphenyl)pent-4-ene-1,3-dione (**IXb**).
- 9) (E)-2-Styryl-4H-chromen-4-one ( $\mathbf{Xa}$ ).
- 10) (E)-2-(4-Fluorostyryl)-4H-chromen-4-one (**Xb**).
- 11) (E)-4-(2-(4-Oxo-4H-chromen-2-yl)vinyl)benzonitrile ( $\mathbf{Xc}$ )
- 12) (E)-3-Bromo-2-styryl-4H-chromen-4-one (XIa).
- 13) 2-Acetylphenyl 1-naphthoate (XIX)
- 14) 1-(2-Hydroxyphenyl)-3-(naphthalen-2-yl)propane-1,3-dione (XX).
- 15) 2-(Naphthalen-2-yl)-4*H*-chromen-4-one (**XXI**).
- 16) N-(3-Aminophenyl) methanesulfonamide (**XXIV**).

#### Also, it comprised the synthesis of the following new intermediates:

- 1) (E)-3-(1-(2-Phenylhydrazono)ethyl)benzonitrile (IIb).
- 3-(4-Formyl-1-phenyl-1*H*-pyrazol-3-yl)benzonitrile (**IIIb**).
- (E)-3-(3-Nitrophenyl)-1-phenyl-4-styryl-1*H*-pyrazole (**IVa**)
- (E)-4-(4-Fluorostyryl)-3-(3-nitrophenyl)-1-phenyl-1*H*-pyrazole (**IVb**)
- 2-Acetylphenyl (*E*)-3-(4-cyanophenyl)acrylate (**VIIIc**).
- (E)-4-(5-(2-Hydroxyphenyl)-3,5-dioxopent-1-en-1-yl)benzonitrile (**IXc**).
- (E)-3-Bromo-2-(4-fluorostyryl)-4H-chromen-4-one (**XIb**).
- (E)-4-(2-(3-Bromo-4-oxo-4H-chromen-2-yl)vinyl)benzonitrile (**XIc**).
- 9) (E)-4-(2-(3-(3-Aminophenyl)-4-oxo-4H-chromen-2-yl)vinyl)benzonitrile (XIIj).
- 10) (E)-3-(3-Aminophenyl)-2-styryl-4H-chromen-4-one (XIIIa).
- 11) 3-Bromo-2-(naphthalen-2-yl)-4*H*-chromen-4-one (**XXII**).
- 12) N-(3-((2-Nitrophenyl)amino)phenyl)methanesulfonamide (**XXV**).

### Furthermore, the study involved the synthesis and characterization of the following new final compounds:

- 1) (E)-4-(2-(3-(3-Nitrophenyl)-1-phenyl-1H-pyrazol-4-yl)vinyl)benzonitrile (**IVc**).
- 2) (E)-3-(4-(4-Methylstyryl)-1-phenyl-1H-pyrazol-3-yl)benzonitrile (**IVd**).
- 3)  $(E)-N-(3-(1-\text{Phenyl-}4-\text{styryl-}1H-\text{pyrazol-}3-\text{yl})\text{phenyl})\text{methanesulfonamide }(\mathbf{Va}).$
- 4) (E)-N-(3-(4-(4-Fluorostyryl)-1-phenyl-1H-pyrazol-3yl)phenyl)methanesulfonamide (Vb).
- 5) (E)-N-(3-(4-(4-Cyanostyryl)-1-phenyl-1H-pyrazol-3yl)phenyl)methanesulfonamide (Vc).
- 6) (E)-3-(4-Hydroxyphenyl)-2-styryl-4H-chromen-4-one (**XIIa**).
- 7) (E)-3-(4-Oxo-2-styryl-4H-chromen-3-yl)benzonitrile (**XIIb**).
- 8) (E)-3-(3-Nitrophenyl)-2-styryl-4H-chromen-4-one (XIIc).
- 9) (*E*)-3-(4-(Hydroxymethyl)phenyl)-2-styryl-4*H*-chromen-4-one (**XIId**).
- 10) (E)-3-(4-Hydroxy-3-methoxyphenyl)-2-styryl-4H-chromen-4-one (**XIIe**).
- 11) (E)-2-(4-Fluorostyryl)-3-(pyridin-3-yl)-4H-chromen-4-one (**XIIf**).
- 12) (E)-3-(2-(4-Fluorostyryl)-4-oxo-4H-chromen-3-yl)benzonitrile (**XIIg**).
- 13) (E)-2-(4-Fluorostyryl)-3-(3-methoxyphenyl)-4H-chromen-4-one (**XIIIh**).
- 14) (*E*)-2-(4-Fluorostyryl)-3-(3-nitrophenyl)-4*H*-chromen-4-one (**XIIi**).
- 15) (E)-3-(3-Aminophenyl)-2-(4-fluorostyryl)-4*H*-chromen-4-one (**XIIIb**).
- 16) (E)-N-(3-(4-Oxo-2-styryl-4H-chromen-3-yl)phenyl)methanesulfonamide (XIVa).
- 17) (E)-N-(3-(2-(4-Fluorostyryl)-4-oxo-4H-chromen-3-yl)phenyl)methanesulfonamide (XIVb).
- 18) (E)-N-(3-(2-(4-Cyanostyryl)-4-oxo-4*H*-chromen-3-yl)phenyl)methanesulfonamide (XIVc).
- 19) (E)-N-(3-(4-Oxo-2-styryl-4H-chromen-3-yl)phenyl)benzenesulfonamide (**XV**).
- 20) (E)-N-(3-(4-Oxo-2-styryl-4H-chromen-3-yl)phenyl)acetamide (**XVI**).
- 21) (E)-N-(3-(4-Oxo-2-styryl-4H-chromen-3-yl)phenyl)cyclopropanecarboxamide (XVII).
- 22) 3-(2-(Naphthalen-2-yl)-4-oxo-4*H*-chromen-3-yl)**benzonitrile** (**XXIII**).
- 23) (E)-N-(3-(2-Styryl-1H-benzo[d]imidazol-1-yl)phenyl)methanesulfonamide (XXVI).



24) N-(3-(2-(Naphthalen-2-yl)-1H-benzo[d]imidazol-1-yl)phenyl)methanesulfonamide (XXVII).

Initial antimicrobial screening identified five chromen-4-one derivatives (XIIIb, XIVa-c and XV) with modest to potent antimicrobial activity (MIC values between 0.008-16 µg/mL) against MRSA USA300 strain, while the 1-phenylpyrazole and benzimidazole derivatives failed to demonstrate any antibacterial activity. Further screening of the chromen-4-one derivatives (XIIIb, XIVa-c) established them as promising bacteriostatic agents against several Gram-positive bacterial strains, with compounds XIVa, XIVc demonstrating nano-range activity (MIC values between 0.008-0.5 µg/mL) particularly against methicillin-sensitive, methicillin-resistant and vancomycin-resistant S. aureus strains. Compound XIVa outperformed vancomycin in passing into the MRSA infected macrophages cells and reducing the intracellular MRSA burden by 0.066-log<sub>10</sub>-reduction. Additionally, two compounds (**XIVb**, **XIVc**) exhibited a synergistic activity when combined with piperacillin against MRSA clinical isolate in vitro using the checkerboard assay. All of the tested chromen-4-one derivatives manifested great selectivity for bacterial over mammalian cells (Caco-2, Vero, and J774 cells) and demonstrated an excellent safety profile (non-toxic up to 32 µg/mL). Further mechanistic investigations and pharmacokinetic studies will follow to validate the mode of action of the reported chromen-4-one derivatives and to establish them as a novel class of antibacterial agents with promising activity against MRSA strains.



### 1. Introduction

#### 1.1. Overview

ntimicrobial resistance (AMR) is a current threat worldwide with an alarming increase in infection-related morbidity and mortality rates. One of the major causes of hospital and community acquired infections is the methicillin-resistant Staphylococcus aureus (MRSA). 2,3 According to the Centers for Disease Control and Prevention (CDC) antibiotic resistance threats report in 2013, MRSA was ranked as a serious threat with more than 80,461 infections and 11,285 deaths per year in USA.<sup>4</sup> Standard treatment options as \beta-lactam antibiotics are out of use, as the microorganism developed several mutations rendering this class almost inactive against several S. aureus strains including MRSA. 5,6 Production of a homologous of penicillin binding protein 2 named PBP2a is the major mechanism employed by MRSA to exhibit a broad clinical resistance to the β-lactam antibiotics.<sup>7</sup> The emergence of such resistance is mediated through the acquisition of a gene cassette containing mecA, which encodes an altered, low-affinity transpeptidase; PBP2a.8 Consequently, an urgent need to develop effective antibiotics to meet the emerging threats of MRSA resistance, is greater than ever.

#### 1.2. Evolution of MRSA

S. aureus is a Gram-positive organism, first discovered by Sir Alexander Ogston in 1880. Since its discovery, it has been regarded as a serious threat to human health, capable of causing a wide spectrum of infections, ranging from acute to life threatening infections such as boils, deep tissue abscesses, enterocolitis, bacteriuria, osteomyelitis, pneumonia, carditis, meningitis and septicemia. 9,10 The prognosis for patients with severe staphylococcal infections was extremely poor until the introduction of penicillin into clinical use in the early 1940s. However, few years later, the first penicillin-resistant strain of S. aureus was reported, and by 1946 it was estimated that 60% of hospital isolates in the UK were resistant to this antibiotic. 11 Albeit several antibiotics were introduced later as streptomycin, tetracycline, chloramphenicol and erythromycin, tolerant or resistant strains emerged rapidly. 12,13