

## Supplementary Materials

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# 1 Abbreviations

**AMK**= amikacin,

**ATM**= aztreonam,

**AVI**= avibactam

**AZM**= azithromycin,

**CAZ**=ceftazidime,

**CFS**= cefoperazone/sulbactam,

**CHBD**= checkerboard assay

**CHL**= chloramphenicol,

**CIP**= ciprofloxacin,

**CRO**= ceftriaxone,

**CST**= colistin,

**CZA**= ceftazidime/avibactam,

**DAP**= daptomycin,

**DDST**= double-disk synergy test,

**DOR**= doripenem,

**ERV**= eravacycline,

**FA**= fusidic acid, **FEP**= cefepime,

**FICI**= fractional inhibitory concentration index,

**FOF**= fosfomycin,

**GEN**= gentamicin,

**HFIM**= hollow-fiber infection model,

**IMP**= imipenem,

**LVX**=levofloxacin,

**LZD**= linezolid,

**MCBT**= multiple-combination bactericidal test,

**MIN**= minocycline,  
**MEM**= meropenem,  
**MXF**= moxifloxacin,  
**NR**= not reported,  
**PK/PD**= pharmacokinetic/pharmacodynamic study,  
**PLZ**= plazomicin,  
**PMB**= polymyxin-B,  
**RFB**= rifabutin,  
**RIF**= rifampicin,  
**SAM**= ampicillin/sulbactam,  
**SUL**= sulbactam,  
**SXT**= trimethoprim/sulfamethoxazole,  
**TEC**= teicoplanin,  
**TIM**= ticarcillin-clavulanic acid,  
**TGC**= tigecycline,  
**TKA**= time-kill assay,  
**TMP**= trimethoprim,  
**TOB**= tobramycin,  
**TZB**= tazobactam,  
**TZP**= piperacillin/tazobactam,  
**VAN**= vancomycin

## 2 Summary of reviewed studies

### 2.1 Summary and characteristics of reviewed studies

Author-Year	Country (number of institutions from which the isolates were collected)	Methods for evaluation of synergy	Antimicrobial combinations tested (synergy present/number of eligible <sup>1</sup> strains)
Cebrero-Cangueiro T, 2021 [1] and Nordmann P, 2020 [2]	Barhein, Brazil, Colombia, France, Saudi Arabia, Switzerland, and Turkey (Unclear number of institutions)	CHBD, intraperitoneal infection mouse model	MEM/IMP (CHBD 6/21, animal model 2/2)
Cheng J 2021 [3]	USA (NR)	CHBD	CST/RIF (2/2), CST/RBT (3/3)
Nwabor OF 2021 [4]	Thailand (4)	CHBD, TKA	FOF/IMP (CHBD 0/2), FOF/MEM (CHBD 0/1), FOF/DOR (CHBD 3/3, TKA 0/1), FOF/GEN (CHBD 2/2), FOF/TOB (CHBD 1/2), FOF/CIP (CHBD 1/2, TKA 0/1), FOF/LVX (CHBD 0/1), FOF/TGC (CHBD 3/4, TKA 1/1)
Armengol E, 2020 [5]	Spain (1)	CHBD	RIF/LZD (0/3)
Li J, 2020 [6]	China (1)	CHBD, TKA	CST/MEM (CHBD 4/5, TKA 1/1), CST/LVX (CHBD 1/1, TKA 1/1)
Limsrivanichakorn S, 2020 [7]	Thailand (1)	CHBD, E-test	CFS/MXF (CHBD 4/80, E-test 2/80)
Mohd Sazlly Lim S 2020 [8], 2021 [9], 2021 [10]	Saudi Arabia, United Arab Emirates, Oman, Kuwait, Qatar, Bahrain (7)	CHBD, TKA, semi-mechanistic PK/PD, Monte-Carlo simulation	<u>CHBD</u> : FOF/SUL (37/50), MEM/SUL (28/50), FOF/MEM (14/50), FOF/RIF (12/50), MEM/RIF (10/50), RIF/SUL (10/50). <u>TKA</u> : FOF/SUL (3/4) <u>semi-mechanistic PK/PD</u> : FOF/SUL (based on TKA for 2 isolates synergy was achievable at clinically relevant concentration). <u>PK/PD modelling and Monte-Carlo simulations</u> : FOF/MEM (proposed breakpoints: MEM 8 mg/L, FOF 128 mg/L)
Rodriguez CH, 2020 [11]	South America (6 countries, 15 hospitals)	Agar dilution, TKA	SUL/AVI (agar dilution 35/38, TKA 1/1)
Gaudereto JJ, 2019	Brazil (1)	DDST, TKA	CZA/MEM (DDST 2/11,

Author-Year	Country (number of institutions from which the isolates were collected)	Methods for evaluation of synergy	Antimicrobial combinations tested (synergy present/number of eligible <sup>1</sup> strains)
[12]			TKA 0/11)
Ghaith D, 2019 [13]	Egypt (NR)	CHBD	CST/RIF (14/23)
Mataraci Kara E, 2019 [14]	Turkey (1)	TKA	CST/CZA (2/2), CZA/LVX (3/4), CZA/TGC (3/4), CZA/TOB (1/2), CZA/MEM (3/4)
Mengucci TC 2019 [15], 2016 [16]	Brazil (2)	CHBD	PMB/MEM (3/3), PMB/SUL (2/3), PMB/FOF (0/3), MEM/FOF (1/6), MEM/SUL (6), PMB/MEM/FOF (3), PMB/MEM/SUL (3/3)
Oliva A, 2019 [17]	Italy (1)	CHBD, TKA	CST/VAN (CHBD 2/2, TKA 2/2), CST/RIF (CHBD 2/2, TKA 2/2), CST/MEM (CHBD 1/2, TKA 2/2s)
Ozger HS, 2019 [18]	Turkey (NR)	CHBD	CST/ERV (1/3)
Phee LM, 2015 [19] and 2019 [20]	UK (1)	CHBD, TKA, PK/PD modelling	CST/FA (CHBD 3/3, TKA 1/1)
Poulakou G, 2019 [21]	Greece (1)	TKA, Intraperitoneal infection mouse model	CST/DAP (1/1)
Shinohara DR, 2019 [22]	Brazil (2)	CHBD, TKA, agar/disk, agar/gradient	PMB/VAN (CHBD 3/3, TKA 2/3, agar/disk 2/3, agar/gradient 3/3)
Wang J, 2019 [23]	China (4)	CHBD, TKA	CHBD: MEM/VAN (3/5), MEM/SAM (2/5), MEM/TZB (2/5), MEM/CST (4/5) TKA: MEM/CST (2/2)
Chen F, 2018 [24]	China (1)	CHBD	AMK/CIP (4/34), AMK/MEM (12/34), MEM/CIP (3/34)
Singham-In U, 2018 [25]	Thailand (1)	CHBD, TKA	MEM/AMK (CHBD 2/2), MEM/FOF (CHBD 0/22), IMP/AMK (CHBD 1/2), IMP/FOF (CHBD 15/23, TKA 8/9)
Zhu W, 2018 [26]	China (1)	CHBD	CST/IMP (2/3), CST/DOR (0/2), CST/FOF (0/3), CST/CFS (0/3), IMP/CFS (11/16), IMP/FOF (11/20)
Lenhard JR, 2017 [27,28]	Thailand (1)	TKA, HFIM	TKA: PMB/MEM (0/2), PMB/SAM (0/2), MEM/SAM (0/2), PMB/MEM/SAM (2/2) HFIM: PMB/MEM (0/1), PMB/SAM (0/1), MEM/SAM (0/1), PMB/MEM/SAM (1/1)
Madadi-Goli N,	Iran (1)	Fixed ratio E-test	LVX/SAM (7/7), LVX/TGC (0/7), TGC/SAM

Author-Year	Country (number of institutions from which the isolates were collected)	Methods for evaluation of synergy	Antimicrobial combinations tested (synergy present/number of eligible <sup>1</sup> strains)
2017 [29]		method	(0/7)
Wei W, 2017 [30]	China (1)	CHBD, TKA, G. mellonella model	CST/LVX (CHBD 0/1, TKA 0/1, G. mellonella 0/1)
Wei WJ, 2017 [31]	China (unclear)	CHBD, TKA	CST/CHL (CHBD 2/2, TKA 0/1)
Bae S, 2016 [32]	South Korea (1)	MCBT, CHBD (only the CST-based combinations)	MCBT for all possible combinations of: CST, SAM, AMK, AZM, ATM, MEM, RIF, TGC, SXT, VAN, TEC. Synergy shown only for the following: SAM/RIF (1/8), SAM/SXT (1/7), SAM/TEC (1/8), AMK/CAZ (1/6), AMK/SXT (1/6), AZM/CAZ (1/9), AZM/SXT (1/7), AZM/TEC (1/8), ATM/CAZ (1/9), ATM/SXT (1/7), ATM/TEC (1/9), CAZ/MEM (1/9), CAZ/RIF (1/9), CAZ/TGC (1/9), CAZ/SXT (1/7), CAZ/VAN (1/9), MEM/RIF (1/9), MEM/SXT (1/7), MEM/TEC (1/9), RIF/SXT (1/7), SXT/VAN (1/7), AMK/RIF (2/6), CAZ/TEC (2/9), CST/RIF (9/9), CST/TEC (9/9), CST/VAN (8/9), CST/MEM (8/9), CST/ATM (8/9), CST/CAZ (6/9), CST/SAM (5/8), CST/SXT (3/7), CST/AMK (4/6), CST/AZM (4/8), CST/TGC (0/9) CHBD: CST/RIF (9/9), CST/TEC (4/9), CST/VAN (7/9), CST/MEM (3/9), CST/ATM (4/9), CST/CAZ (4/9), CST/SAM (0/8), CST/SXT (1/7), CST/AMK (2/6), CST/AZM (1/8), CST/TGC (0/9)
Bowler SL, 2016 [33]	USA (1)	CHBD, TKA	CHBD: CST/FA (3/3), TKA: CST/FA (1/3), CST/VAN (1/3), CST/DOR (1/3)
Hong DJ, 2016 [34]	South Korea (1)	Fixed ratio E-test method	CST/MEM (41), CST/IMP (41), CST/RIF (41)
Laishram S, 2016 [35]	India (1)	CHBD, TKA	MEM/SUL (CHBD: 16/50, TKA: 29/50)
Leite GC, 2016 [36]	Brazil (unclear)	CHBD, (TKA data were excluded because reported data were not	CST/RIF (4/4), CST/VAN (7/7), CST/MEM (7/7), CST/IMP (7/7), CST/TGC (0/1), CST/FOF (0/6), CST/GEN (0/1), FOF/GEN (10/11), FOF/AMK (26/27)

Author-Year	Country (number of institutions from which the isolates were collected)	Methods for evaluation of synergy	Antimicrobial combinations tested (synergy present/number of eligible <sup>1</sup> strains)
		sufficient to allow accurate extraction)	
Park GC, 2016 [37]	South Korea (1***)	TKA	CST/DOR (10/17), CST/TGC (7/12), TGC/DOR (5/45)
Yang H, 2016 [38]	China (1)	CHBD, TKA, G. mellonella model	CST/VAN (1/1)
Yang YS, 2016 [39]	Taiwan (3)	CHBD, TKA	MEM/MIN (0/3), MEM/CFS (CHBD 0/2, TKA 1/2)
Yavaş S, 2016 [40]	Turkey (1)	Fixed ratio E-test method	MEM/SUL (1/7)
Córdoba J, 2015 [41]	Spain (2)	Dynamic in-vitro PK/PD model	IMP/ETP (0/3), CST/DAP (1/1), CST/IMP (0/1)
García-Salguero C, 2015 [42]	Spain (1)	Disk diffusion, CHBD, TKA	AMK/IMP (CHBD 2/2), AMK/MEM (CHBD 2/2), AMK/FOF (CHBD 0/2), PLZ/IMP (CHBD 6/8), PLZ/MEM (CHBD 2/4), PLZ/FOF (CHBD 1/9, TKA 1/2)
Marie MA, 2015 [43]	Saudi Arabia (1)	CHBD, E-test/agar method	MEM/SUL (CHBD 24/54, E-test 22/54), MEM/TZB (CHBD 22/54, E-test 19/54)
Rodriguez CH, 2015 [44]	Argentina (1)	TKA	IMP/MIN (0/1), MIN/RIF (0/1)
Vourli S, 2015 [45]	Greece (1)	CHBD	CST/MEM (2/2), CST/SAM (0/2), MEM/SAM (0/5)
Galani I, 2014 [46]	Greece (2)	E-test/agar dilution. TKA	CST/DAP (0/4)
Majewski P, 2014 [47]	Poland (1)	CHBD	IMP/RIF (4/10)
Nastro M, 2014 [48]	Argentina (unclear)	E-test/agar, TKA	CST/RIF (E-test/agar 4/4, TKA 4/4)
Oleksium LM, 2014 [49]	USA (1)	TKA	CST/DOR (5/6), CST/SUL (2/6), CST/DOR/SUL (6/6), DOR/SUL (4/17)
Percin D, 2014 [50]	Turkey (3)	CHBD, TKA	CST/VAN (CHBD 9/10, TKA 10/10)
Sun Y, 2014 [51]	China (1)	CHBD	MEM/CFS (0/11), MEM/AMK (0/9), MEM/CIP (1/11), MEM/AZM (0/12)
Wang Y, 2014 [52]	China (9)	CHBD, disk diffusion combination	IMP/RIF (12/18)
Cetin ES, 2013 [53]	Turkey (1)	CHBD, Perpendicular E-	RIF/SAM (7/7), RIF/CFS (2/7)

Author-Year	Country (number of institutions from which the isolates were collected)	Methods for evaluation of synergy	Antimicrobial combinations tested (synergy present/number of eligible <sup>1</sup> strains)
		test method	
Housman ST, 2013 [54]	USA (1)	Dynamic in-vitro PK/PD model	<b>DOR/SAM</b> (0/3), <b>DOR/TGC</b> (0/2), <b>SAM/TGC</b> (0/1)
Lee HJ, 2013 [55]	USA (1)	Dynamic in-vitro PK/PD model	<b>CST/RIF</b> (1/1)
O'Hara JA, 2013 [56]	USA (1)	CHBD, TKA, <i>G. mellonella</i> infection model	<b>CST/DOR</b> (CHBD 2/3, TKA 3/3, <i>G. mellonella</i> 0/3), <b>CST/VAN</b> (CHBD 3/3, TKA 2/3, <i>G. mellonella</i> 0/3), <b>VAN/DOR</b> (CHBD 0/3, TKA 0/3, <i>G. mellonella</i> 3/3), <b>CST/DOR/VAN</b> (TKA 3/3, <i>G. mellonella</i> 3/3)
Principe L, 2013 [57]	Italy (7)	CHBD, (TKA also conducted, but no eligible isolates)	<b>DOR/TGC</b> (3/3), <b>DOR/AMK</b> (1/4), <b>DOR/CST</b> (0/1), <b>DOR/SAM</b> (0/1), <b>DOR/RIF</b> (0/1)
Queenan AM, 2013 [58]	USA (1)	TKA, intraperitoneal infection mouse model	<b>DOR/CIP</b> (TKA 0/1, mouse model 0/1), <b>DOR/ LVX</b> (TKA 0/1, mouse model 1/1)
Deveci A, 2012 [59]	Turkey (1)	CHBD	<b>SUL/CAZ</b> (7/10), <b>SUL/MEM</b> (0/9), <b>SUL/CRO</b> (4/10), <b>SUL/CIP</b> (8/10), <b>SUL/GEN</b> (8/10), <b>SUL/FEP</b> (4/10)
Peck KR, 2012 [60]	South Korea (4)	TKA	<b>CST/RIF</b> (1/1), <b>CST/IMP</b> (0/2), <b>IMP/SAM</b> (6/6)
Vidaillac C, 2012 [61]	France (1)	CHBD, TKA	<b>CST/VAN</b> (CHBD 1/1, TKA 0.25xMIC 1/1, TKA 0.5xMIC 1/1), <b>CST/TMP</b> (CHBD 1/1, TKA 0.25xMIC 0/1, TKA 0.5xMIC 1/1), <b>CST/SXT</b> (CHBD 1/1, TKA 0.25xMIC 0/1, TKA 0.5xMIC 1/1)
Santimaleeworagun W, 2011 [62]	Thailand (1)	CHBD, TKA	<b>SUL/FOF</b> (CHBD 5/6, TKA 5/6), <b>SUL/IMP</b> (CHBD 0/6)
Pachón-Ibáñez ME, 2011 [63]	Spain (1)	TKA, pneumonia mouse models	<b>RIF/IMP</b> (TKA 2/2, animal model 0/2), <b>RIF/SUL</b> (TKA 2/2, animal model 1/2)
Tan TY, 2011 [64]	Singapore (4)	CHBD, perpendicular E-test method, TKA	<b>PMB/RIF</b> (CHBD 3/3, E-test 1/3, TKA 1/3), <b>PMB/TGC</b> (CHBD 3/4, E-test 0/4, TKA 0/4), <b>TGC/RIF</b> (CHBD 1/3, E-test 1/3, TKA 0/3)
Kiratisin P, 2010 [65]	Thailand (1)	Perpendicular E-test method	<b>DOR/CFS</b> (4/19), <b>DOR/DOX</b> (0/21), <b>DOR/RIF</b> (0/17), <b>DOR/NET</b> (0/21), <b>DOR/MXF</b> (0/21), <b>IMP/CFS</b> (9/19), <b>IMP/DOX</b> (0/21), <b>IMP/RIF</b> (0/17), <b>IMP/NET</b>

Author-Year	Country (number of institutions from which the isolates were collected)	Methods for evaluation of synergy	Antimicrobial combinations tested (synergy present/number of eligible <sup>1</sup> strains)
			(0/21), IMP/MXF (1/21), MEM/CFS (10/19), MEM/DOX (0/21), MEM/RIF (0/17), MEM/NET (0/21), MEM/MXF (0/21)
Pachón-Ibáñez ME, 2010 [66]	Spain (1)	TKA, mouse pneumonia and meningitis model	SUL/IMP (TKA: 2/4, model 1/1), RIF/IMP (TKA 2/4, model 0/1), RIF/SUL (TKA 1/4, model 0/1)
Pankuch GA, 2010 [67]	Germany (1)	TKA	DOR/LVX (3/5), DOR/AMK (2/2), DOR/CST (4/4)
Rodríguez CH, 2010 [68]	Argentina (1)	TKA	IMP/RIF (0/4), IMP/GEN (0/2)
Urban C, 2010 [69]	USA (1)	TKA	DOR/RIF (2/5)
Yuan Z, 2010 [70] and Lim TP, 2008 [71]	USA (1)	TKA (interactive index method), HFIM, mouse pneumonia model	AMK/FEP (TKA 1/1, HFIM 0/1, mouse model 0/1), FEP/LVX (TKA 1/1, mouse model 1/1), AMK/LVX (TKA 0/1, HFIM 0/1, mouse model 0/1)
Lim TP, 2009 [72]	Singapore (1)	TKA	MEM/RIF (2/2), TGC/MEM (0/1), TGC/RIF (1/1)
Principe L, 2009 [73]	Italy (5)	CHBD, TKA	TGC/LVX (CHBD 4/18, TKA 0/2), TGC/TZP (CHBD 0/18), TGC/AMK (CHBD 2/14, TKA 1/1), TGC/IMP (CHBD 1/12, TKA 0/1), TGC/RIF (CHBD 0/13), TGC/SAM (CHBD 0/6)
Song YC, 2009 [74]	South Korea (1)	Pneumonia mouse model	IMP/RIF (3/3), RIF/AMK (0/1), IMP/AMK (0/1)
Lee CH, 2008 [75]	Taiwan (1)	TKA	MEM/SUL (1/2)
Lee NY, 2007 [76]	Taiwan (3)	Agar dilution, CHBD	IMP/SUL (agar 4/4, CHBD 0/4), MEM/SUL (agar 4/4, CHBD 0/4)
Sader HS, 2005 [77]	USA (unclear)	CHBD	FEP/SUL (2/2)
Sader HS, 2005 [78]	USA (unclear)	TKA	ATM/FEP (0/3), ATM/CAZ (0/3), ATM/MEM (0/1), ATM/SAM (0/1)
Choi JY, 2004 [79]	South Korea (1)	TKA	IMP/SUL (1/1)
Jung R, 2004 [80]	USA (1)	TKA	FEP/MXF (2/2)
Montero A, 2004 [81]	Spain (1)	TKA, mouse pneumonia model	IMP/RIF (TKA 2/2, mouse model 1/2), IMP/SUL (TKA 0/1)
Yoon J, 2004 [82]	USA (1)	TKA	PMB/IMP (1/1)
Fernández-Cuenca F, 2003 [83]	Spain (3)	CHBD	AZM/IMP (0/2), AZM/CAZ (1/3), AZM/AMK (0/2), AZM/CIP (0/3)

Author-Year	Country (number of institutions from which the isolates were collected)	Methods for evaluation of synergy	Antimicrobial combinations tested (synergy present/number of eligible <sup>1</sup> strains)
Roussel-Delvallez M, 1996 [84]	France (1)	TKA	IMP/SUL/AMK (0/8), IMP/TIM/AMK (0/8), TZP/SUL/AMK (0/8), TZP/TIM/AMK (0/8)

Studies with overlapping isolates are grouped together (same row).

<sup>1</sup> Eligible= non-susceptible to the tested antimicrobial combinations. The number of eligible isolates can be different for each combination.

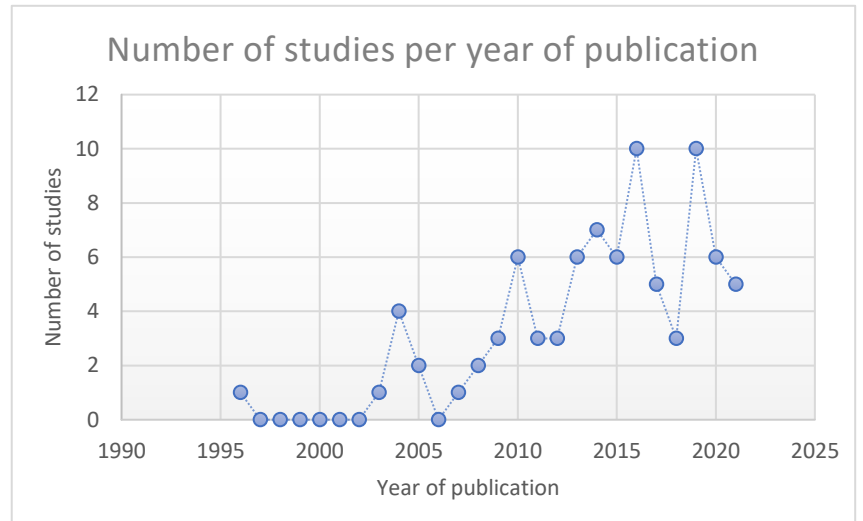
<sup>2</sup> See “Methods” for interpretation of clinical relevance

\*\* 50 isolates randomly selected from a pool of 117 isolates, 107 of which were from diverse clonal lineages [9]

\*\*\* 64 of 69 isolates from a single hospital. 5 of 69 from the Korean Antimicrobial Resistance Monitoring System

## 2.2 Distribution of studies by year of publication

Year of publication	Number of studies (%)
<b>2017-2021</b>	<b>29 (35%)</b>
2021	5 (6%)
2020	6 (7%)
2019	10 (12%)
2018	3 (4%)
2017	5 (6%)
<b>2012-2016</b>	<b>32 (38%)</b>
2016	10 (12%)
2015	6 (7%)
2014	7 (8%)
2013	6 (7%)
2012	3 (4%)
<b>2007-2011</b>	<b>15 (18%)</b>
2011	3 (4%)
2010	6 (7%)
2009	3 (4%)
2008	2 (2%)
2007	1 (1%)
<b>2002-2006</b>	<b>7 (8%)</b>
2005	2 (2%)
2004	4 (5%)
2003	1 (1%)
<b>1995-2001</b>	<b>1 (1%)</b>
1996	1 (1%)



## 2.3 Distribution of studies by country and WHO regions

WHO regions	Number of studies per region (%)
<b>Americas</b>	<b>24 (29%)</b>
Brazil	6 (7%)
USA	12 (14%)
Argentina	3 (4%)
Colombia	1 (1%)
<b>South-East Asia Region</b>	<b>7 (8%)</b>
India	1 (1%)
Thailand	6 (7%)
<b>European Region</b>	<b>28 (33%)</b>
France	3 (4%)
Germany	1 (1%)
Greece	3 (4%)
Italy	3 (4%)
Spain	7 (8%)
Turkey	7 (8%)
Switzerland	1 (1%)
United Kingdom	1 (1%)
<b>Eastern Mediterranean Region</b>	<b>5 (6%)</b>
Iran	1 (1%)
Saudi Arabia	4 (5%)
United Arab Emirates	2 (2%)
Oman	2 (2%)
Kuwait	2 (2%)
Qatar	2 (2%)
Bahrain	3 (4%)
<b>Western Pacific Region</b>	<b>20 (24%)</b>
China	9 (11%)
South Korea	6 (7%)
Taiwan	3 (3%)

## 2.4 Number of eligible isolates per study

Number of eligible isolates	Number of studies (%)
1-5	51 (61%)
6-10	13 (16%)
11-15	2 (2%)
16-20	3 (4%)
21-25	4 (5%)
26-30	1 (1%)
31-35	1 (1%)
36-40	1 (1%)
41-45	1 (1%)
46-50	4 (5%)
51-55	2 (2%)
> 55 (80)	1 (1%)

## 2.5 Number of studies with single-centre vs multicentre design

Single-centre, n (%)	54 (64%)
Multicentre, n (%)	26 (31%)
• 2 centres	6 (7%)
• 3 centres	4 (5%)
• 4 centres	4 (5%)
• 5 centres	1 (1%)
• 7 centres	5 (6%)
• 9 centres	1 (1%)
• 15 centres	1 (1%)
• Unclear	4 (5%)
Unclear, n (%)	4 (5%)

### 3 Overview of number of studies and eligible isolate for each combinations evaluated

#### 3.1 Summary table; Number of studies and eligible isolates per combination and method used

Antimicrobial combinations	Total		CHBD		TKA		Gradient-based methods		Disk-based methods		Agar dilution		Dynamic in vitro PK/PD modelling		Animal models	
	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates
<b>AZM-based</b>																
AZM/CAZ	2	11	1	3												
AZM/CIP	1	3	1	3												
AZM/IMP	1	2	1	2												
AZM/MEM	1	12	1	12												
AZM/AMK	1	2	1	2												
AZM/CST	1	8	1	8												
AZM/SXT	1	6														
AZM/TEC	1	8														
<b>ATM-based</b>																
ATM/SAM	1	1			1	1										
ATM/CAZ	2	13			1	3										
ATM/FEP	1	3			1	3										
ATM/MEM	1	3			1	1										
ATM/CST	1	9	1	9												
ATM/SXT	1	7														
ATM/TEC	1	9														
<b>SUL-based</b>																
SUL/CRO	1	10	1	10												
SUL/CAZ	1	10	1	10												
SUL/FEP	1	9	1	9												
SUL/CIP	1	10	1	10												
SUL/IMP	5	16	2	10	3	6					1	4			1	1

Antimicrobial combinations	Total		CHBD		TKA		Gradient-based methods		Disk-based methods		Agar dilution		Dynamic in vitro PK/PD modelling		Animal models	
	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates
SUL/MEM	8	181	6	173	3	54	2	61			1	4				
SUL/DOR	1	17			1	17										
SUL/AVI	1	38			1	1					1	38				
SUL/GEN	1	10	1	10												
SUL/CST	1	6			1	6										
SUL/PMB	1	3	1	3												
SUL/RIF	3	56	1	50	2	6									2	3
SUL/FOF	2	56	2	56	2	10										
<b>SAM-based</b>																
SAM/ATM	1	1			1	1										
SAM/FEP	1	2	1	2												
SAM/LVX	1	7	1	7												
SAM/IMP	1	6			1	6										
SAM/MEM	3	12	2	10	1	2							1	1		
SAM/DOR	2	7	1	1									1	3		
SAM/CST	2	10	2	10												
SAM/PMB	1	2			1	2							1	1		
SAM/TGC	3	14	2	13									1	1		
SAM/RIF	2	15	1	7			1	7								
SAM/SXT	1	7														
SAM/TEC	1	8														
<b>CSF-based</b>																
CFS/MXF	1	80	1	80			1	80								
CFS/IMP	2	35	1	16			1	19								
CFS/MEM	2	30	1	11			1	19								
CFS/DOR	1	19					1	19								

[illegible]

Antimicrobial combinations	Total		CHBD		TKA		Gradient-based methods		Disk-based methods		Agar dilution		Dynamic in vitro PK/PD modelling		Animal models	
	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates
FEP/MXF	1	2			1	2										
FEP/AMK	1	1			1	1							1	1	1	1
<b>CIP-based</b>																
CIP/AZM	1	3	1	3												
CIP/SUL	1	10	1	10												
CIP/MEM	2	45	2	45												
CIP/DOR	1	1			1	1									1	1
CIP/AMK	1	34	1	34												
CIP/FOF	1	2	1	2	1	1										
<b>LVX-based</b>																
LVX/SAM	1	7	1	7												
LVX/FEP	1	1			1	1									1	1
LVX/DOR	2	6			2	6									1	1
LVX/CZA	1	4			1	4										
LVX/AMK	1	1			1	1							1	1	1	1
LVX/CST	2	2	2	2	2	2									1	1
LVX/TGC	2	25	2	25	1	2										
LVX-FOF	1	1	1	1												
<b>MXF-based</b>																
MXF/CFS	1	80	1	80			1	80								
MXF/FEP	1	2			1	2										
MXF/IMP	1	21					1	21								
MXF/MEM	1	21					1	21								
MXF/DOR	1	21					1	21								
<b>ETP-based</b>																
ETP/IMP	1	3											1	3		

Antimicrobial combinations	Total		CHBD		TKA		Gradient-based methods		Disk-based methods		Agar dilution		Dynamic in vitro PK/PD modelling		Animal models	
	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates
<b>IMP-based</b>																
IMP/AZM	1	2	1	2												
IMP/SUL	5	16	2	10	3	6					1	4			1	1
IMP/SAM	1	6			1	6										
IMP/CFS	2	35	1	16			1	19								
IMP/MXF	1	21					1	21								
IMP/ETP	1	3											1	3		
IMP/MEM	1	21	1	21											1	2
IMP/AMK	3	6	2	4											1	1
IMP/GEN	1	2			1	2										
IMP/NET	1	21					1	21								
IMP/PLZ	1	8	1	8												
IMP/CST	5	54	2	10	1	2	1	41					1	1		
IMP/PMB	1	1			1	1										
IMP/DOX	1	21					1	21								
IMP/TGC	1	12	1	12	1	1										
IMP/MIN	1	1			1	1										
IMP/RIF	9	61	2	28	5	13	1	17	1	1					4	8
IMP/FOF	3	45	3	45	1	9										
<b>MEM-based</b>																
MEM/AZM	1	12	1	12												
MEM/ATM	1	3			1	1										
MEM/SUL	8	181	6	173	3	54	2	61			1	4				
MEM/SAM	3	12	2	10	1	2							1	1		
MEM/CFS	2	30	1	11			1	19								
MEM/TZB	2	59	2	59			1	54								

[illegible]

[illegible]



Antimicrobial combinations	Total		CHBD		TKA		Gradient-based methods		Disk-based methods		Agar dilution		Dynamic in vitro PK/PD modelling		Animal models	
	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates
CST/LVX	2	2	2	2	2	2									1	1
CST/IMP	5	54	2	10	1	2	1	41					1	1		
CST/MEM	7	70	6	29	3	4	1	41								
CST/DOR	7	37	3	6	5	33									1	3
CST/CZA	1	2			1	2										
CST/AMK	1	6	1	6												
CST/GEN	1	1	1	1												
CST/TGC	3	22	2	10	1	12										
CST/ERV	1	3	1	3												
CST/RIF	9	87	5	40	3	7	2	45					1	1		
CST/RFB	1	3	1	3												
CST/FOF	2	9	2	9												
CST/TMP	1	1	1	1	1	1										
CST/SXT	2	9	2	8	1	1										
CST/CHL	1	2	1	2	1	2										
CST/FA	2	6	2	6	2	4			1	3						
CST/VAN	8	36	7	33	6	20									2	4
CST/TEC	1	9	1	9												
CST/DAP	3	6			2	5	1	4					1	1	1	1
<b>PMB-based</b>																
PMB/SUL	1	3	1	3												
PMB/SAM	1	2	0	0	1	2							1	1		
PMB/IMP	1	1	0	0	1	1										
PMB/MEM	2	5	1	3	1	2							1	1		
PMB/TGC	1	4	1	4	1	4	1	4								
PMB/RIF	1	3	1	3	1	3	1	3								





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Antimicrobial combinations	Total		CHBD		TKA		Gradient-based methods		Disk-based methods		Agar dilution		Dynamic in vitro PK/PD modelling		Animal models	
	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates	Studies	Isolates
VAN/CST	8	36	7	33	6	20									2	4
VAN/PMB	1	3	1	3	1	3	1	3	1	3						
VAN/SXT	1	7														
<b>TEC-based</b>																
TEC/AZM	1	8														
TEC/ATM	1	9														
TEC/SAM	1	8														
TEC/CAZ	1	9														
TEC/MEM	1	9														
TEC/CST	1	9	1	9												
<b>DAP-based</b>																
DAP/CST	3	6			2	5	1	4					1	1	1	1
<b>LZD-based</b>																
LZD/RIF	1	3	1	3												
<b>Triple combinations</b>																
PMB/FOF/MEM	1	3	1	3												
PMB/SUL/MEM	1	3	1	3												
PMB/SAM/MEM	2	2			2	2							1	1		
CST/DOR/SUL	1	6			1	6										
CST/VAN/DOR	1	3			1	3									1	3
IMP/SUL/AMK	1	8			1	8										
IMP/TIM/AMK	1	8			1	8										
TZP/SUL/AMK	1	8			1	8										
TZP/TIM/AMK	1	8			1	8										

MCBT assay was used in only 1 study and is not shown in the Table. See Section 4.5 (Bae S, 2016 [32])

### 3.2 Few studies available for each combination

Number of studies	Number of combinations
1	98
2	22
3	11
4	2
5	2
6	0
7	2
8	2
9	2

I.e. there were; only 1 study available for 98 of the 141 double combinations evaluated, 2 studies for 22 of the combinations, 3 studies for 11 of the combinations, 4 studies for 2 of the combinations, 5 studies for 2 of the combinations, 7 studies for 2 of the combinations, 8 studies for 2 of the combinations and 9 studies for 2 of the combinations.

### 3.3 Number of studies per combination (only double combinations shown)

	AZM	ATM	SUL	SAM	CFS	TZB	TZP	CRO	CAZ	FEP	CIP	LVX	MXF	ETP	IMP	MEM	DOR	CZA	AVI	AMK	GEN	TOB	NET	PLZ	CST	PMB	DOX	TGC	MIN	ERV	RIF	RFB	FOF	TMP	SXT	CHL	FA	VAN		
AZM		0	0	0	0	0	0	0	2	0	1	0	0	0	1	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		
ATM	0		0	1	0	0	0	0	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		
SUL	0	0				0	0	1	1	1	1	0	0	0	5	8	1	0	1	0	1	0	0	0	1	1	0	0	0	0	0	3	0	2	0	0	0	0		
SAM	0	1				0	0	0	0	0	1	0	1	0	1	0	0	1	3	2	0	0	0	0	0	0	2	1	0	3	0	0	2	0	0	0	1	0	0	0
CFS	0	0				0	0	0	0	0	0	0	0	0	1	0	2	2	1	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0
TZB	0	0	0	0	0		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
TZP	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	
CRO	0	0	1	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CAZ	2	2	1	0	0	0	0	0		0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	1	0	0	1	0	0	0	1	0	0	1		
FEP	0	1	1	1	0	0	0	0	0		0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CIP	1	0	1	0	0	0	0	0	0	0		0	0	0	0	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	
LVX	0	0	0	1	0	0	0	0	0	1	0		0	0	0	0	2	1	0	1	0	0	0	0	2	0	0	2	0	0	0	0	1	0	0	0	0	0	0	
MXF	0	0	0	0	1	0	0	0	0	1	0	0		0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ETP	0	0	0	0	0	0	0	0	0	0	0	0	0		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
IMP	1	0	5	1	2	0	0	0	0	0	0	0	1	1		1	0	0	0	3	1	0	1	1	5	1	1	1	1	0	9	0	3	0	0	0	0	0	0	
MEM	1	1	8	3	2	2	0	0	1	0	2	0	1	1	1		0	2	0	3	0	0	1	1	7	2	1	1	1	0	4	0	4	0	1	0	0	1	0	0
DOR	0	0	1	2	1	0	0	0	0	0	1	2	1	0	0	0		0	0	2	0	0	1	0	7	0	1	3	0	0	3	0	1	0	0	0	0	0	1	
CZA	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0		0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	
AVI	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
AMK	1	0	0	0	0	0	0	0	1	1	1	1	0	0	3	3	2	0	0		0	0	0	0	1	0	0	1	0	0	2	0	2	0	1	0	0	0	0	
GEN	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	
TOB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	
NET	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PLZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
CST	1	1	1	2	1	0	0	0	1	0	0	2	0	0	5	7	7	1	0	1	1	0	0				0	3	0	1	9	1	2	1	2	1	2		8	
PMB	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0				0	1	0	0	1	0	1	0	0	0	0	0	1	
DOX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0		0			0	0	0	0	0	0	0	0	0	0	0	0
TGC	0	0	0	3	0	0	1	0	1	0	0	2	0	0	1	1	3	1	0	1	0	0	0	0	3	1	0				3	0	1	0	0	0	0	0	0	0
MIN	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0					0	0	0	0	0	0	0	0	0	
ERV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					0	0	0	0	0	0	0	0	0	0
RIF	0	0	3	2	1	0	0	0	1	0	0	0	0	0	9	4	3	0	0	2	0	0	0	0	9	1	0	3	0	0				1	0	1	0	0	0	0

	AZM	ATM	SUL	SAM	CFS	TZB	TZP	CRO	CAZ	FEP	CIP	LVX	MXF	ETP	IMP	MEM	DOR	CZA	AVI	AMK	GEN	TOB	NET	PLZ	CST	PMB	DOX	TGC	MIN	ERV	RIF	RFB	FOF	TMP	SXT	CHL	FA	VAN		
RFB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0			0	0	0	0	0	0		
FOF	0	0	2	0	0	0	0	0	0	0	1	1	0	0	3	4	1	0	0	2	2	1	0	1	2	1	0	1	0	0	1	0		0	0	0	0	0	0	
TMP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					0	0	0	
SXT	1	1	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	2	0	0	0	0	0	1	0	0					0	0	1
CHL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	
FA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0		0	0
VAN	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	8	1	0	0	0	0	0	0	0	0	0	1	0	0		
TEC	1	1	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DAP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LZD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	

	1 study		6 studies
	2 studies		7 studies
	3 studies		8 studies
	4 studies		9 studies

### 3.4 Number of eligible isolates per combination (only double combinations shown)

	AZM	ATM	SUL	SAM	CFS	TZB	TZP	CRO	CAZ	FEP	CIP	LVX	MXF	ETP	IMP	MEM	DOR	CZA	AVI	AMK	GEN	TOB	NET	PLZ	CST	PMB	DOX	TGC	MIN	ERV	RIF	RFB	FOF	TMP	SXT	CHL	FA	VAN	
AZM		0	0	0	0	0	0	0	11	0	3	0	0	0	2	12	0	0	0	2	0	0	0	0	8	0	0	0	0	0	0	0	0	0	6	0	0	0	
ATM	0		0	1	0	0	0	0	13	3	0	0	0	0	0	3	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	7	0	0	0	
SUL	0	0				0	0	10	10	9	10	0	0	0	16	181	17	0	38	0	10	0	0	0	6	3	0	0	0	0	56	0	56	0	0	0	0	0	
SAM	0	1				0	0	0	0	2	0	7	0	0	6	12	7	0	0	0	0	0	0	10	2	0	14	0	0	15	0	0	0	0	7	0	0	0	
CFS	0	0				0	0	0	0	0	0	0	80	0	35	30	19	0	0	0	0	0	0	3	0	0	0	2	0	7	0	0	0	0	0	0	0	0	
TZB	0	0	0	0	0		0	0	0	0	0	0	0	0	0	59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
TZP	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18	0	0	0	0	0	0	0	0	0	0	
CRO	0	0	10	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CAZ	11	13	10	0	0	0	0	0		0	0	0	0	0	0	9	0	0	0	6	0	0	0	0	9	0	0	9	0	0	9	0	0	0	7	0	0	9	
FEP	0	3	9	2	0	0	0	0	0		0	1	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CIP	3	0	10	0	0	0	0	0	0	0		0	0	0	0	45	1	0	0	34	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	
LVX	0	0	0	7	0	0	0	0	0	1	0		0	0	0	0	6	4	0	1	0	0	0	0	2	0	0	25	0	0	0	0	0	1	0	0	0	0	
MXF	0	0	0	0	80	0	0	0	0	2	0	0		0	21	21	21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ETP	0	0	0	0	0	0	0	0	0	0	0	0	0		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
IMP	2	0	16	6	35	0	0	0	0	0	0	0	21	3		21	0	0	0	6	2	0	21	8	54	1	21	12	1	0	61	0	45	0	0	0	0	0	
MEM	12	3	181	12	30	59	0	0	9	0	45	0	21	0	21		0	15	0	45	0	0	21	4	70	5	21	1	3	0	78	0	79	0	7	0	0	5	
DOR	0	0	17	7	19	0	0	0	0	0	1	6	21	0	0	0		0	0	6	0	0	21	0	37	0	21	50	0	0	23	0	3	0	0	0	0	3	
CZA	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	15	0		0	0	0	2	0	0	2	0	0	4	0	0	0	0	0	0	0	0	0	0	
AVI	0	0	38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
AMK	2	0	0	0	0	0	0	0	6	1	34	1	0	0	6	45	6	0	0		0	0	0	0	6	0	0	14	0	0	8	0	29	0	6	0	0	0	
GEN	0	0	10	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0		0	0	0	1	0	0	0	0	0	0	0	13	0	0	0	0	0	
TOB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	
NET	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21	21	21	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PLZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	9	0	0	0	0	0	
CST	8	9	6	10	3	0	0	0	9	0	0	2	0	0	54	70	37	2	0	6	1	0	0	0			0	22	0	3	87	3	9	1	9	2	6	36	
PMB	0	0	3	2	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	0	0	0	0	0			0	4	0	0	3	0	3	0	0	0	0	0	3
DOX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21	21	21	0	0	0	0	0	0	0			0	0	0	0	0	0	0	0	0	0	0	0	0
TGC	0	0	0	14	0	0	18	0	9	0	0	25	0	0	12	1	50	4	0	14	0	0	0	0	22	4					17	0	4	0	0	0	0	0	0
MIN	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0	0						0	0	0	0	0	0	0	
ERV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0					0	0	0	0	0	0	0	0	0
RIF	0	0	56	15	7	0	0	0	9	0	0	0	0	0	61	78	23	0	0	8	0	0	0	0	87	3	0	17	0	0			50	0	7	0	0	0	0
RFB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0			0	0	0	0	0	0	0

	AZM	ATM	SUL	SAM	CFS	TZB	TZP	CRO	CAZ	FEP	CIP	LVX	MXF	ETP	IMP	MEM	DOR	CZA	AVI	AMK	GEN	TOB	NET	PLZ	CST	PMB	DOX	TGC	MIN	ERV	RIF	RFB	FOF	TMP	SXT	CHL	FA	VAN
FOF	0	0	56	0	0	0	0	0	0	0	2	1	0	0	45	79	3	0	0	29	13	2	0	9	9	3	0	4	0	0	50	0		0	0	0	0	0
TMP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0				0	0	0
SXT	6	7	0	7	0	0	0	0	7	0	0	0	0	0	0	7	0	0	0	6	0	0	0	0	9	0	0	0	0	0	7	0	0			0	0	7
CHL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VAN	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	5	3	0	0	0	0	0	0	36	3	0	0	0	0	0	0	0	0	0	7	0	0	
TEC	8	9	0	8	0	0	0	0	9	0	0	0	0	0	0	9	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DAP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LZD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0

	1-5	21-30
	6-10	31-40
	11-15	41-50
	16-20	51-60
		>60

### 3.5 Number of studies per combinations (only double combinations shown) tested by checkerboard method

	AZM	ATM	SUL	SAM	CFS	TZB	TZP	CRO	CAZ	FEP	CIP	LVX	MXF	IMP	MEM	DOR	AMK	GEN	TOB	PLZ	CST	PMB	TGC	MIN	ERV	RIF	RFB	FOF	TMP	SXT	CHL	FA		
AZM		0	0	0	0	0	0	0	1	0	1	0	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		
ATM	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		
SUL	0	0				0	0	1	1	1	1	0	0	2	6	0	0	1	0	0	0	1	0	0	0	1	0	2	0	0	0	0		
SAM	0	0				0	0	0	0	1	0	1	0	0	0	2	1	0	0	0	0	0	2	0	2	0	0	1	0	0	0	0	0	0
CFS	0	0				0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0
TZB	0	0	0	0	0		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
TZP	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0		
CRO	0	0	1	0	0	0			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
CAZ	1	0	1	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		
FEP	0	0	1	1	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
CIP	1	0	1	0	0	0	0	0	0	0		0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0		
LVX	0	0	0	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	1	0	0	0	0		
MXF	0	0	0	0	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
IMP	1	0	2	0	1	0	0	0	0	0	0	0	0		1	0	2	0	0	1	2	0	1	0	0	2	0	3	0	0	0	0		
MEM	1	0	6	2	1	2	0	0	0	0	2	0	0	1		0	3	0	0	1	6	1	0	1	0	1	0	4	0	0	0	0		
DOR	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		1	0	0	0	3	0	1	0	0	1	0	1	0	0	0	0		
AMK	1	0	0	0	0	0	0	0	0	0	1	0	0	2	3	1		0	0	0	1	0	1	0	0	0	0	2	0	0	0	0		
GEN	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	1	0	0	0	0	0	0	2	0	0	0	0		
TOB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	1	0	0	0	0		
PLZ	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0		0	0	0	0	0	0	0	1	0	0	0	0		
CST	1	1	0	2	1	0	0	0	1	0	0	2	0	2	6	3	1	1	0	0			2	0	1	5	1	2	1	2	1	2		
PMB	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					1	0	0	1	0	1	0	0	0	0	
TGC	0	0	0	2	0	0	1	0	0	0	0	2	0	1	0	1	1	0	0	2			1				2	0	1	0	0	0	0	
MIN	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							0	0	0	0	0	0	0
ERV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							0	0	0	0	0	0
RIF	0	0	1	1	1	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	5	1	2	0	0			1	0	0	0	0		
RFB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					0	0	0	0	0	
FOF	0	0	2	0	0	0	0	0	0	0	1	1	0	3	4	1	2	2	1	1	2	1	1	0	0			1	0		0	0	0	0
TMP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0				0	0	
SXT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0				0	0	
CHL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0		0	0	
FA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0		0	
VAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	7	1	0	0	0	0	0	0	0	0	0	0	0	
TEC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
LZD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	

	1 study		6 studies
	2 studies		7 studies
	3 studies		8 studies
	4 studies		9 studies

3.6 Number of eligible isolates per combination (only double combinations are shown) tested by checkerboard method

	AZM	ATM	SUL	SAM	CFS	TZB	TZP	CRO	CAZ	FEP	CIP	LVX	MXF	IMP	MEM	DOR	AMK	GEN	TOB	PLZ	CST	PMB	TGC	MIN	ERV	RIF	RFB	FOF	TMP	SXT	CHL	FA	VAN	
AZM		0	0	0	0	0	0	0	3	0	3	0	0	2	12	0	2	0	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	
ATM	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	
SUL	0	0				0	0	10	10	9	10	0	0	10	173	0	0	10	0	0	0	3	0	0	0	50	0	56	0	0	0	0	0	
SAM	0	0				0	0	2	0	7	0	0	10	1	0	0	0	0	10	0	13	0	0	7	0	0	0	0	0	0	0	0	0	0
CFS	0	0				0	0	0	0	0	0	0	80	16	11	0	0	0	0	0	3	0	0	2	0	7	0	0	0	0	0	0	0	0
TZB	0	0	0	0	0		0	0	0	0	0	0	0	0	59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
TZP	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18	0	0	0	0	0	0	0	0	0	0	
CRO	0	0	10	0	0	0			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CAZ	3	0	10	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	
FEP	0	0	9	2	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CIP	3	0	10	0	0	0	0	0	0	0		0	0	0	45	0	34	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	
LVX	0	0	0	7	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	2	0	25	0	0	0	0	1	0	0	0	0	0	
MXF	0	0	0	0	80	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
IMP	2	0	10	0	16	0	0	0	0	0	0	0	0		21	0	4	0	0	8	10	0	12	0	0	28	0	45	0	0	0	0	0	
MEM	12	0	173	10	11	59	0	0	0	0	45	0	0	21		0	45	0	0	4	29	3	0	3	0	50	0	79	0	0	0	0	5	
DOR	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		4	0	0	0	6	0	3	0	0	1	0	3	0	0	0	0	3	
AMK	2	0	0	0	0	0	0	0	0	0	34	0	0	4	45	4		0	0	0	6	0	14	0	0	0	0	29	0	0	0	0	0	
GEN	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	1	0	0	0	0	0	0	13	0	0	0	0	0	
TOB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	2	0	0	0	0	0	
PLZ	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4	0	0	0	0	0		0	0	0	0	0	0	9	0	0	0	0	0	
CST	8	9	0	10	3	0	0	0	9	0	0	2	0	10	29	6	6	1	0	0			10	0	3	40	3	9	1	8	2	6	33	
PMB	0	0	3	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0			4	0	0	3	0	3	0	0	0	0	3	
TGC	0	0	0	13	0	0	18	0	0	0	0	25	0	12	0	3	14	0	0	0	10	4				16	0	4	0	0	0	0	0	
MIN	0	0	0	0	2	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0				0	0	0	0	0	0	0	0	
ERV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0				0	0	0	0	0	0	0	0	
RIF	0	0	50	7	7	0	0	0	0	0	0	0	0	28	50	1	0	0	0	0	40	3	16	0	0			50	0	0	0	0	0	
RFB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0			0	0	0	0	0	0	
FOF	0	0	56	0	0	0	0	0	0	0	2	1	0	45	79	3	29	13	2	9	9	3	4	0	0	50	0		0	0	0	0	0	
TMP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0			0	0	0	
SXT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0			0	0	0	
CHL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0		0	0	
FA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0		0	
VAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	3	0	0	0	0	33	3	0	0	0	0	0	0	0	0	0	0		0
TEC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LZD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0

	1-5		21-30
	6-10		31-40
	11-15		41-50
	16-20		51-60
			>60

### 3.7 Number of eligible studies (only double combinations shown) tested by TKA

	ATM	SUL	SAM	CFS	CAZ	FEP	CIP	LVX	MXF	IMP	MEM	DOR	CZA	AVI	AMK	GEN	TOB	PLZ	CST	PMB	TGC	MIN	RIF	FOF	TMP	SXT	CHL		
ATM		0	1	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
SUL	0				0	0	0	0	0	3	3	1	0	1	0	0	0	0	1	0	0	0	2	2	0	0	0		
SAM	1				0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	
CFS	0				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
CAZ	1				0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FEP	1	0	0	0	0		0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		
CIP	0	0	0	0	0	0		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		
LVX	0	0	0	0	0	1	0		0	0	0	2	1	0	1	0	0	0	2	0	1	0	0	0	0	0	0		
MXF	0	0	0	0	0	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
IMP	0	3	1	0	0	0	0	0	0		0	0	0	0	0	1	0	0	1	1	1	1	5	1	0	0	0		
MEM	1	3	1	0	0	0	0	0	0	0		0	2	0	0	0	0	0	3	1	1	1	1	0	0	0	0		
DOR	0	1	0	0	0	0	1	2	0	0	0		0	0	1	0	0	0	5	0	1	0	1	1	0	0	0		
CZA	0	0	0	0	0	0	0	1	0	0	2	0		0	0	0	1	0	1	0	1	0	0	0	0	0	0		
AVI	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0		
AMK	0	0	0	0	0	1	0	1	0	0	0	1	0	0		0	0	0	0	0	1	0	0	0	0	0	0		
GEN	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0		
TOB	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0	0	0	0	0	0	0		
PLZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	1	0	0	0		
CST	0	1	0	0	0	0	0	2	0	1	3	5	1	0	0	0	0	0			1	0	3	0	1	1	1		
PMB	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				1	0	1	0	0	0	0	
TGC	0	0	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	1	1			2	1	0	0	0		
MIN	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0					0	0	0	0	0
RIF	0	2	0	0	0	0	0	0	0	5	1	1	0	0	0	0	0	0	3	1	2	0		0	0	0	0		
FOF	0	2	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	1	0	0	1	0	0		0	0	0		
TMP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				0		
SXT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					0	
CHL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0			
FA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0		
VAN	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	6	1	0	0	0	0	0	0	0		
DAP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0		

	1 study		6 studies
	2 studies		7 studies
	3 studies		8 studies
	4 studies		9 studies

### 3.8 Number of eligible isolates (only double combinations shown) tested by TKA

	ATM	SUL	SAM	CFS	CAZ	FEP	CIP	LVX	MXF	IMP	MEM	DOR	CZA	AVI	AMK	GEN	TOB	PLZ	CST	PMB	TGC	MIN	RIF	FOF	TMP	SXT	CHL		
ATM		0	1	0	3	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
SUL	0				0	0	0	0	0	6	54	17	0	1	0	0	0	0	0	6	0	0	0	6	10	0	0	0	
SAM	1				0	0	0	0	0	0	6	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
CFS	0				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
CAZ	3	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
FEP	3	0	0	0	0		0	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		
CIP	0	0	0	0	0	0		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		
LVX	0	0	0	0	0	1	0		0	0	0	6	4	0	1	0	0	0	2	0	2	0	0	0	0	0	0		
MXF	0	0	0	0	0	2	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
IMP	0	6	6	0	0	0	0	0	0		0	0	0	0	0	2	0	0	2	1	1	1	13	9	0	0	0		
MEM	1	54	2	0	0	0	0	0	0	0		0	15	0	0	0	0	0	4	2	1	3	2	0	0	0	0		
DOR	0	17	0	0	0	0	1	6	0	0	0		0	0	2	0	0	0	33	0	45	0	5	1	0	0	0		
CZA	0	0	0	0	0	0	0	4	0	0	15	0		0	0	0	2	0	2	0	4	0	0	0	0	0	0		
AVI	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0		
AMK	0	0	0	0	0	1	0	1	0	0	0	2	0	0		0	0	0	0	0	0	1	0	0	0	0	0		
GEN	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0		
TOB	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0		0	0	0	0	0	0	0	0	0	0		
PLZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	2	0	0	0		
CST	0	6	0	0	0	0	0	2	0	2	4	33	2	0	0	0	0	0				12	0	7	0	1	1	2	
PMB	0	0	2	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0		4		0	3	0	0	0		
TGC	0	0	0	0	0	0	0	2	0	1	1	45	4	0	1	0	0	0	12	4			4	1	0	0	0		
MIN	0	0	0	2	0	0	0	0	0	1	3	0	0	0	0	0	0	0	0	0			0	0	0	0	0		
RIF	0	6	0	0	0	0	0	0	0	13	2	5	0	0	0	0	0	0	7	3	4	0		0	0	0	0		
FOF	0	10	0	0	0	0	1	0	0	9	0	1	0	0	0	0	0	2	0	0	1	0	0		0	0	0		
TMP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0			0		
SXT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0			0		
CHL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0			
FA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0		
VAN	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	20	3	0	0	0	0	0	0	0		
DAP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0		

	1-5		21-30
	6-10		31-40
	11-15		41-50
	16-20		51-60
			>60

### 3.9 Number of eligible studies tested by gradient methods

	SUL	SAM	CFS	TZB	MXF	IMP	MEM	DOR	NET	CST	PMB	DOX	TGC	RIF	VAN
SUL				0	0	0	2	0	0	0	0	0	0	0	0
SAM				0	0	0	0	0	0	0	0	0	0	1	0
CFS				0	1	1	1	1	0	0	0	0	0	1	0
TZB	0	0	0		0	0	1	0	0	0	0	0	0	0	0
MXF	0	0	1	0		1	1	1	0	0	0	0	0	0	0
IMP	0	0	1	0	1		0	0	1	1	0	1	0	1	0
MEM	2	0	1	1	1	0		0	1	1	0	1	0	1	0
DOR	0	0	1	0	1	0	0		1	0	0	1	0	1	0
NET	0	0	0	0	0	1	1	1		0	0	0	0	0	0
CST	0	0	0	0	0	1	1	0	0			0	0	2	0
PMB	0	0	0	0	0	0	0	0	0			0	1	1	1
DOX	0	0	0	0	0	1	1	1	0	0	0		0	0	0
TGC	0	0	0	0	0	0	0	0	0	0	1	0		1	0
RIF	0	1	1	0	0	1	1	1	0	2	1	0	1		0
VAN	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
DAP	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

	1 study		6 studies
	2 studies		7 studies
	3 studies		8 studies
	4 studies		9 studies

### 3.10 Number of eligible isolates tested by gradient methods

	SUL	SAM	CFS	TZB	MXF	IMP	MEM	DOR	CST	PMB	DOX	TGC	RIF	VAN	DAP
SUL				0	0	0	61	0	0	0	0	0	0	0	0
SAM				0	0	0	0	0	0	0	0	0	7	0	0
CFS				0	80	19	19	19	0	0	0	0	7	0	0
TZB	0	0	0		0	0	54	0	0	0	0	0	0	0	0
MXF	0	0	80	0		21	21	21	0	0	0	0	0	0	0
IMP	0	0	19	0	21		0	0	41	0	21	0	17	0	0
MEM	61	0	19	54	21	0		0	41	0	21	0	17	0	0
DOR	0	0	19	0	21	0	0		0	0	21	0	17	0	0
CST	0	0	0	0	0	41	41	0			0	0	45	0	4
PMB	0	0	0	0	0	0	0	0			0	4	3	3	0
DOX	0	0	0	0	0	21	21	21	0	0		0	0	0	0
TGC	0	0	0	0	0	0	0	0	0	4	0		3	0	0
RIF	0	7	7	0	0	17	17	17	45	3	0	3		0	0
VAN	0	0	0	0	0	0	0	0	0	3	0	0	0		0
DAP	0	0	0	0	0	0	0	0	4	0	0	0	0	0	

	1-5		21-30
	6-10		31-40
	11-15		41-50
	16-20		51-60
			>60

### 3.11 Number of eligible studies tested by disk methods

	IMP	MEM	CZA	CST	PMB	RIF	FA	VAN
IMP		0	0	0	0	1	0	0
MEM	0		1	0	0	0	0	0
CZA	0	1		0	0	0	0	0
CST	0	0	0			0	1	0
PMB	0	0	0			0	0	1
RIF	1	0	0	0	0		0	0
FA	0	0	0	1	0	0		0
VAN	0	0	0	0	1	0	0	

	1 study		6 studies
	2 studies		7 studies
	3 studies		8 studies
	4 studies		9 studies

### 3.12 Number of eligible isolates tested by disk methods

	IMP	MEM	CZA	CST	PMB	RIF	FA	VAN
IMP		0	0	0	0	1	0	0
MEM	0		11	0	0	0	0	0
CZA	0	11		0	0	0	0	0
CST	0	0	0			0	3	0
PMB	0	0	0			0	0	3
RIF	1	0	0	0	0		0	0
FA	0	0	0	3	0	0		0
VAN	0	0	0	0	3	0	0	

	1-5		21-30
	6-10		31-40
	11-15		41-50
	16-20		51-60
			>60

### 3.13 Number of eligible studies tested by agar dilution method

	SUL	IMP	MEM	AVI
SUL		1	1	1
IMP	1		0	0
MEM	1	0		0
AVI	1	0	0	

1 study	6 studies
2 studies	7 studies
3 studies	8 studies
4 studies	9 studies

### 3.14 Number of eligible isolates tested by agar dilution method

	SUL	IMP	MEM	AVI
SUL		4	4	38
IMP	4		0	0
MEM	4	0		0
AVI	38	0	0	

1-5	21-30
6-10	31-40
11-15	41-50
16-20	51-60
	>60

### 3.15 Number of eligible studies (only double combinations shown) tested by dynamic in vitro PK/PD models

	SAM	FEP	LVX	ETP	IMP	MEM	DOR	AMK	CST	PMB	TGC	RIF	DAP
SAM		0	0	0	0	1	1	0	0	1	1	0	0
FEP	0		0	0	0	0	0	1	0	0	0	0	0
LVX	0	0		0	0	0	0	1	0	0	0	0	0
ETP	0	0	0		1	0	0	0	0	0	0	0	0
IMP	0	0	0	1		0	0	0	1	0	0	0	0
MEM	1	0	0	0	0		0	0	0	1	0	0	0
DOR	1	0	0	0	0	0		0	0	0	1	0	0
AMK	0	1	1	0	0	0	0		0	0	0	0	0
CST	0	0	0	0	1	0	0	0			0	1	1
PMB	1	0	0	0	0	1	0	0			0	0	0
TGC	1	0	0	0	0	0	1	0	0	0		0	0
MIN	0	0	0	0	0	0	0	0	0	0		0	0
ERV	0	0	0	0	0	0	0	0	0	0		0	0
RIF	0	0	0	0	0	0	0	0	1	0	0		0
DAP	0	0	0	0	0	0	0	0	1	0	0	0	

	1 study		6 studies
	2 studies		7 studies
	3 studies		8 studies
	4 studies		9 studies

### 3.16 Number of eligible isolates (only double combinations shown) tested by dynamic in vitro PK/PD models

	SAM	FEP	LVX	ETP	IMP	MEM	DOR	AMK	CST	PMB	TGC	RIF	DAP
SAM		0	0	0	0	1	3	0	0	1	1	0	0
FEP	0		0	0	0	0	0	1	0	0	0	0	0
LVX	0	0		0	0	0	0	1	0	0	0	0	0
ETP	0	0	0		3	0	0	0	0	0	0	0	0
IMP	0	0	0	3		0	0	0	1	0	0	0	0
MEM	1	0	0	0	0		0	0	0	1	0	0	0
DOR	3	0	0	0	0	0		0	0	0	2	0	0
AMK	0	1	1	0	0	0	0		0	0	0	0	0
CST	0	0	0	0	1	0	0	0			0	1	1
PMB	1	0	0	0	0	1	0	0			0	0	0
TGC	1	0	0	0	0	0	2	0	0	0		0	0
RIF	0	0	0	0	0	0	0	0	1	0	0		0
DAP	0	0	0	0	0	0	0	0	1	0	0	0	

	1-5		21-30
	6-10		31-40
	11-15		41-50
	16-20		51-60
			>60

### 3.17 Number of eligible studies (only double combinations shown) tested by animal models

	SUL	FEP	CIP	LVX	IMP	MEM	DOR	AMK	CST	RIF	VAN	DAP
SUL		0	0	0	1	0	0	0	0	2	0	0
FEP	0		0	1	0	0	0	1	0	0	0	0
CIP	0	0		0	0	0	1	0	0	0	0	0
LVX	0	1	0		0	0	1	1	1	0	0	0
IMP	1	0	0	0		1	0	1	0	4	0	0
MEM	0	0	0	0	1		0	0	0	0	0	0
DOR	0	0	1	1	0	0		0	1	0	1	0
AMK	0	1	0	1	1	0	0		0	1	0	0
CST	0	0	0	1	0	0	1	0		0	2	1
RIF	2	0	0	0	4	0	0	1	0		0	0
VAN	0	0	0	0	0	0	1	0	2	0		0
DAP	0	0	0	0	0	0	0	0	1	0	0	

	1 study		6 studies
	2 studies		7 studies
	3 studies		8 studies
	4 studies		9 studies

### 3.18 Number of eligible isolates (only double combinations shown) tested by animal models

	SU L	FEP	CIP	LV X	IM P	ME M	DO R	AM K	CST	RIF	VA N	DA P
SU L		0	0	0	1	0	0	0	0	3	0	0
FEP	0		0	1	0	0	0	1	0	0	0	0
CIP	0	0		0	0	0	1	0	0	0	0	0
LV X	0	1	0		0	0	1	1	1	0	0	0
IM P	1	0	0	0		2	0	1	0	8	0	0
ME M	0	0	0	0	2		0	0	0	0	0	0
DO R	0	0	1	1	0	0		0	3	0	3	0
AM K	0	1	0	1	1	0	0		0	1	0	0
CST	0	0	0	1	0	0	3	0		0	4	1
RIF	3	0	0	0	8	0	0	1	0		0	0
VA N	0	0	0	0	0	0	3	0	4	0		0

DA												
P	0	0	0	0	0	0	0	0	1	0	0	

	1-5		21-30
	6-10		31-40
	11-15		41-50
	16-20		51-60
			>60

## 4 Assessment of clinical relevance of observed synergy

### 4.1 Summary Table (sum of all studies): Proportion of synergy and clinically relevant synergy in checkerboard (CHBD) and time-kill assay (TKA)

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
<b>AZM-based</b>												
AZM/CAZ	1	3	1 (33%)	0 (0%)	1 (33%)	0 (0%)						
AZM/CIP	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
AZM/IMP	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
AZM/MEM	1	12	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
AZM/AMK	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
AZM/CST	1	8	1 (13%)	0 (0%)	0 (0%)	1 (13%)						
<b>ATM-based</b>												
ATM/SAM							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
ATM/CAZ							1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)
ATM/FEP							1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)
ATM/MEM							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
ATM/CST	1	9	4 (44%)	0 (0%)	0 (0%)	4 (44%)						
<b>SUL-based</b>												
SUL/CRO	1	10	4 (40%)	0 (0%)	4 (40%)	0 (0%)						
SUL/CAZ	1	10	7 (70%)	1 (10%)	6 (60%)	0 (0%)						
SUL/FEP	1	9	4 (44%)	0 (0%)	4 (44%)	0 (0%)						
SUL/CIP	1	10	8 (80%)	2 (20%)	6 (60%)	0 (0%)						
SUL/IMP	2	10	0 (0%)	0 (0%)	0 (0%)	0 (0%)	3	6	3 (50%)	0 (0%)	3(50%)	0 (0%)

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
SUL/MEM	6	173	72 (42%)	2 (1%)	2 (1%)	68 (39%)	3	54	32 (59%)	0 (0%)	7 (13%)	25 (46%)
SUL/DOR							1	17	4 (24%)	4 (24%)	0 (0%)	0 (0%)
SUL/AVI							1	1	1 (100%)	1 (100%)	0 (0%)	0 (0%)
SUL/GEN	1	10	8 (80%)	2 (20%)	6 (60%)	0 (0%)						
SUL/CST							1	6	2 (33%)	2 (33%)	0 (0%)	0 (0%)
SUL/PMB	1	3	2 (67%)	2 (67%)	0 (0%)	0 (0%)						
SUL/RIF	1	50	10 (20%)	0 (0%)	0 (0%)	10 (20%)	2	6	3 (50%)	0 (0%)	3 (50%)	0 (0%)
SUL/FOF	2	56	41 (73%)	3 (5%)	37 (66%)	1 (2%)	2	10	7 (70%)	0 (0%)	7 (70%)	0 (0%)
<b>SAM-based</b>												
SAM/ATM							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
SAM/FEP	1	2	2 (100%)	1 (50%)	1 (50%)	0 (0%)						
SAM/LVX	1	7	7 (100%)	5 (71%)	2 (29%)	0 (0%)						
SAM/IMP							1	6	6 (100%)	0 (0%)	0 (0%)	6 (100%)
SAM/MEM	2	10	2 (100%)	2 (100%)	0 (0%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
SAM/DOR	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
SAM/CST	2	10	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
SAM/PMB							1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
SAM/TGC	2	13	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
SAM/RIF	1	7	7 (100%)	4 (57%)	1 (14%)	2 (29%)						
<b>CSF-based</b>												
CFS/MXF	1	80	4 (5%)	0 (0%)	0 (0%)	4 (5%)						
CFS/IMP	1	16	11 (69%)	9 (56%)	2 (13%)	0 (0%)						
CFS/MEM	1	11	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
CFS/CST	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)						

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
CFS/MIN	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)
CFS/RIF	1	7	2 (29%)	1 (14%)	0 (0%)	1 (14%)						
<b>TZB-based</b>												
TZB/MEM	2	59	24 (41%)	0 (0%)	0 (0%)	24 (41%)						
<b>TZP-based</b>												
TZP/TGC	1	18	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>CRO-based</b>												
CRO/SUL	1	10	4 (40%)	0 (0%)	4 (40%)	0 (0%)						
<b>CAZ-based</b>												
CAZ/AZM	1	3	1 (33%)	0 (0%)	1 (33%)	0 (0%)						
CAZ/ATM							1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)
CAZ/SUL	1	10	7 (70%)	1 (10%)	6 (60%)	0 (0%)						
CAZ/CST	1	9	4 (44%)	0 (0%)	0 (0%)	4 (44%)						
<b>FEP-based</b>												
FEP/ATM							1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)
FEP/SUL	1	9	4 (44%)	0 (0%)	4 (44%)	0 (0%)						
FEP/SAM	1	2	2 (100%)	1 (50%)	1 (50%)	0 (0%)						
FEP/LVX							1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
FEP/MXF							1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
FEP/AMK							1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
<b>CIP-based</b>												
CIP/AZM	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
CIP/SUL	1	10	8 (80%)	2 (20%)	6 (70%)	0 (0%)						
CIP/MEM	2	45	4 (9%)	0 (0%)	1 (2%)	3 (7%)						

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
CIP/DOR							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
CIP/AMK	1	34	4 (12%)	0 (0%)	0 (0%)	4 (12%)						
CIP/FOF	1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<b>LVX-based</b>												
LVX/SAM	1	7	7 (100%)	5 (71%)	2 (29%)	0 (0%)						
LVX/FEP							1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
LVX/DOR							2	6	3 (50%)	0 (0%)	3 (50%)	0 (0%)
LVX/CZA							1	4	3 (75%)	0 (0%)	3 (75%)	0 (0%)
LVX/AMK							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
LVX/CST	2	2	1 (50%)	1 (50%)	0 (0%)	0 (0%)	2	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)
LVX/TGC	2	25	4 (16%)	0 (0%)	4 (16%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
LVX/FOF	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>MXF-based</b>												
MXF/CFS	1	80	4 (5%)	0 (0%)	0 (0%)	4 (5%)						
MXF/FEP							1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
<b>IMP-based</b>												
IMP/AZM	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
IMP/SUL	2	10	0 (0%)	0 (0%)	0 (0%)	0 (0%)	3	6	3 (50%)	0 (0%)	3 (50%)	0 (0%)
IMP/SAM							1	6	6 (100%)	0 (0%)	0 (0%)	6 (100%)
IMP/CFS	1	16	11 (69%)	9 (56%)	2 (13%)	0 (0%)						
IMP/MEM	1	21	6 (29%)	0 (0%)	6 (29%)	0 (0%)						
IMP/AMK	2	4	3 (75%)	0 (0%)	2 (50%)	1 (25%)						
IMP/GEN							1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
IMP/PLZ	1	8	6 (75%)	0 (0%)	5 (63%)	1 (13%)						

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
IMP/CST	2	10	9 (90%)	2 (20%)	7 (70%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
IMP/PMB							1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
IMP/TGC	1	12	1 (8%)	0 (0%)	1 (8%)	0 (0%)	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
IMP/MIN							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
IMP/RIF	2	28	16 (57%)	11 (39%)	3 (11%)	2 (7%)	5	13	6 (46%)	0 (0%)	6 (46%)	0 (0%)
IMP/FOF	3	45	26 (58%)	9 (20%)	10 (22%)	7 (16%)	1	9	8 (89%)	0 (0%)	8 (89%)	0 (0%)
MEM-based												
MEM/AZM	1	12	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
MEM/ATM							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
MEM/SUL	6	173	72 (42%)	2 (1%)	2 (1%)	68 (39%)	3	54	32 (59%)	0 (0%)	7 (13%)	25 (46%)
MEM/SAM	2	10	2 (20%)	2 (20%)	0 (0%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
MEM/CFS	1	11	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
MEM/TZB	2	59	24 (41%)	0 (0%)	0 (0%)	24 (41%)						
MEM/CIP	2	45	4 (9%)	0 (0%)	1 (2%)	3 (7%)						
MEM/IMP	1	21	6 (29%)	0 (0%)	6 (29%)	0 (0%)						
MEM/CZA							2	15	3 (20%)	0 (0%)	3 (20%)	0 (0%)
MEM/AMK	4	47	16 (34%)	1 (2%)	2 (4%)	13 (28%)						
MEM/PLZ	1	4	2 (50%)	0 (0%)	2 (50%)	0 (0%)						
MEM/CST	6	29	21 (72%)	5 (17%)	11 (38%)	5 (17%)	3	4	4 (100%)	0 (0%)	4 (100%)	0 (0%)
MEM/PMB	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
MEM/TGC							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
MEM/MIN	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)
MEM/RIF	1	50	10 (20%)	0 (0%)	0 (0%)	10 (20%)	1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
MEM/FOF	4	79	15 (19%)	1 (1%)	14 (18%)	0 (0%)						

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
MEM/VAN	1	5	3 (60%)	1 (20%)	0 (0%)	2 (40%)						
<b>DOR-based</b>												
DOR/SUL							1	17	4 (24%)	4 (24%)	0 (0%)	0 (0%)
DOR/SAM	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
DOR/CIP							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
DOR/LVX							2	6	3 (50%)	0 (0%)	3 (50%)	0 (0%)
DOR/AMK	1	4	1 (25%)	0 (0%)	0 (0%)	1 (25%)	1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
DOR/CST	3	6	2 (33%)	1 (17%)	1 (17%)	0 (0%)	5	33	23 (70%)	19 (58%)	4 (12%)	0 (0%)
DOR/TGC	1	3	3 (100%)	1 (33%)	0 (0%)	2 (67%)	1	45	5 (11%)	5 (11%)	0 (0%)	0 (0%)
DOR/RIF	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	5	2 (40%)	1 (20%)	1 (20%)	0 (0%)
DOR/FOF	1	3	3	3 (100%)	3	3 (100%)	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
DOR/VAN	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<b>CZA- or AVI-based</b>												
AVI/SUL							1	1	1 (100%)	1 (100%)	0 (0%)	0 (0%)
CZA/LVX							1	4	3 (75%)	0 (0%)	3 (75%)	0 (0%)
CZA/MEM							2	15	3 (20%)	0 (0%)	3 (20%)	0 (0%)
CZA/TOB							1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)
CZA/CST							1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
CZA/TGC							1	4	3 (75%)	0 (0%)	3 (75%)	0 (0%)
<b>AMK-based</b>												
AMK/AZM	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
AMK/FEP							1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
AMK/CIP	1	34	4 (12%)	0 (0%)	0 (0%)	4 (12%)						
AMK/LVX							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
AMK/IMP	2	4	3 (75%)	0 (0%)	2 (50%)	1 (25%)						
AMK/MEM	4	47	16 (34%)	1 (2%)	2 (4%)	13 (28%)						
AMK/DOR	1	4	1 (25%)	0 (0%)	0 (0%)	1 (25%)	1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
AMK/CST	1	6	2 (33%)	0 (0%)	0 (0%)	2 (33%)						
AMK/TGC	1	14	2 (14%)	1 (7%)	1 (7%)	0	1	1	1 (100%)	1 (100%)	0 (0%)	0 (0%)
AMK/FOF	2	29	26 (90%)	11 (38%)	15 (52%)	0 (0%)						
GEN-based												
GEN/SUL	1	10	8 (80%)	2 (20%)	6 (60%)	0 (0%)						
GEN/IMP							1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
GEN/CST	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
GEN/FOF	2	13	12 (92%)	3 (23%)	9 (69%)	0 (0%)						
TOB-based												
TOB/CZA							1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)
TOB/FOF	1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)						
PLZ-based												
PLZ/IMP	1	8	6 (75%)	0 (0%)	5 (63%)	1 (13%)						
PLZ/MEM	1	4	2 (50%)	0 (0%)	2 (50%)	0 (0%)						
PLZ/FOF	1	9	1 (11%)	0 (0%)	1 (11%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
CST-based												
CST/AZM	1	8	1 (13%)	0 (0%)	0 (0%)	1(13%)						
CST/ATM	1	9	4 (44%)	0 (0%)	0 (0%)	4 (44%)						
CST/SUL							1	6	2 (33%)	2 (33%)	0 (0%)	0 (0%)
CST/SAM	2	10	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
CST/CFS	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)						

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
CST/CAZ	1	9	4 (44%)	0 (0%)	0 (0%)	4 (44%)						
CST/LVX	2	2	1 (50%)	1 (50%)	0 (0%)	0 (0%)	2	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)
CST/IMP	2	10	9 (90%)	2 (20%)	7 (70%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
CST/MEM	6	29	21 (72%)	5 (17%)	11 (38%)	5 (17%)	3	4	4 (100%)	0 (0%)	4 (100%)	0 (0%)
CST/DOR	3	6	2 (33%)	1 (17%)	1 (17%)	0 (0%)	5	33	23 (70%)	19 (58%)	4 (12%)	0 (0%)
CST/CZA							1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
CST/AMK	1	6	2 (33%)	0 (0%)	0 (0%)	2 (33%)						
CST/GEN	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
CST/TGC	2	10	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	12	7 (58%)	7 (58%)	0 (0%)	0 (0%)
CST/ERV	1	3	1 (33%)	0 (0%)	1 (33%)	0 (0%)						
CST/RIF	5	40	31 (78%)	10 (25%)	10 (25%)	11 (28%)	3	7	7 (100%)	0 (0%)	6 (86%)	1 (14%)
CST/RFB	1	3	3 (100%)	0 (0%)	0 (0%)	3 (100%)						
CST/FOF	2	9	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
CST/TMP	1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)	1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
CST/SXT	2	8	2 (25%)	1 (13%)	0 (0%)	1 (13%)	1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
CST/CHL	1	2	2 (100%)	1 (50%)	1 (50%)	0 (0%)	1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
CST/FA	2	6	6 (100%)	1 (17%)	2 (33%)	3 (50%)	2	4	3 (75%)	0 (0%)	3 (75%)	0 (0%)
CST/VAN	7	33	29 (88%)	2 (6%)	2 (6%)	25 (76%)	6	20	16 (80%)	13 (65%)	3 (15%)	0 (0%)
CST/TEC	1	9	4 (44%)	0 (0%)	0 (0%)	4 (44%)						
CST/DAP							2	5	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<b>PMB-based</b>												
PMB/SUL	1	3	2 (67%)	2 (67%)	0 (0%)	0 (0%)						
PMB/SAM							1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
PMB/IMP							1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
PMB/MEM	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
PMB/TGC	1	4	3 (75%)	0 (0%)	2 (50%)	1 (25%)	1	4	0 (0%)	0 (0%)	0 (0%)	0 (0%)
PMB/RIF	1	3	3 (100%)	1 (33%)	1 (33%)	1 (33%)	1	3	1 (33%)	1 (33%)	0 (0%)	0 (0%)
PMB/FOF	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
PMB/VAN	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)	1	3	2 (67%)	0 (0%)	2 (67%)	0 (0%)
TGC-based												
TGC/SAM	2	13	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
TGC/TZP	1	18	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
TGC/LVX	2	25	4 (16%)	0 (0%)	4 (16%)	0 (0%)	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)
TGC/IMP	1	12	1 (8%)	0 (0%)	1 (8%)	0 (0%)	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
TGC/MEM							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
TGC/DOR	1	3	3 (100%)	1 (33%)	0 (0%)	2 (67%)	1	45	5 (11%)	5 (11%)	0 (0%)	0 (0%)
TGC/CZA							1	4	3 (75%)	0 (0%)	3 (75%)	0 (0%)
TGC/AMK	1	14	2 (14%)	1 (7%)	1 (7%)	0 (0%)	1	1	1 (100%)	1 (100%)	0 (0%)	0 (0%)
TGC/CST	2	10	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	12	7 (58%)	7 (58%)	0 (0%)	0 (0%)
TGC/PMB	1	4	3 (75%)	0 (0%)	2 (50%)	1 (25%)	1	4	0 (0%)	0 (0%)	0 (0%)	0 (0%)
TGC/RIF	2	16	1 (6%)	0 (0%)	1 (6%)	0 (0%)	2	4	1 (25%)	1 (25%)	0 (0%)	0 (0%)
TGC/FOF	1	4	3 (75%)	1 (25%)	2 (50%)	0 (0%)	1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
MIN-based												
MIN/CFS	1	2	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)
MIN/IMP							1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
MIN/MEM	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)
ERV-based												
ERV/CST	1	3	1 (33%)	0 (0%)	1 (33%)	0 (0%)						

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
<b>RIF-based</b>												
RIF/SUL	1	50	10 (20%)	0 (0%)	0 (0%)	10 (20%)	2	6	3 (50%)	0 (0%)	3 (50%)	0 (0%)
RIF/SAM	1	7	7 (100%)	4 (57%)	1 (14%)	2 (29%)						
RIF/CFS	1	7	2 (29%)	1 (14%)	0 (0%)	1 (14%)						
RIF/IMP	2	28	16 (57%)	11 (39%)	3 (11%)	2 (7%)	5	13	6 (46%)	0 (0%)	6 (46%)	0 (0%)
RIF/MEM	1	50	10 (20%)	0 (0%)	0 (0%)	10 (20%)	1	2	2 (100%)	0 (0%)	2 (100%)	0 (0%)
RIF/DOR	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	5	2 (40%)	0 (0%)	1 (20%)	0 (0%)
RIF/CST	5	40	31 (78%)	10 (25%)	10 (25%)	11 (28%)	3	7	7 (100%)	0 (0%)	6 (86%)	1 (14%)
RIF/PMB	1	3	3 (100%)	1 (33%)	1 (33%)	1 (33%)	1	3	1 (33%)	1 (33%)	0 (0%)	0 (0%)
RIF/TGC	2	16	1 (6%)	0 (0%)	1 (6%)	0 (0%)	2	4	1 (25%)	1 (25%)	0 (0%)	0 (0%)
RIF/FOF	1	50	12 (24%)	0 (0%)	0 (0%)	12 (24%)						
RIF/LZD	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>RFB-based</b>												
RFB/CST	1	3	3 (100%)	0 (0%)	0 (0%)	3 (100%)						
<b>FOF-based</b>												
FOF/SUL	2	56	41 (73%)	3 (5%)	37 (66%)	1 (2%)	2	10	7 (70%)	0 (0%)	7 (70%)	0 (0%)
FOF/CIP	1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
FOF/LVX	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
FOF/IMP	3	45	26 (58%)	9 (20%)	10 (22%)	7 (16%)	1	9	8 (89%)	0 (0%)	8 (89%)	0 (0%)
FOF/MEM	4	79	15 (19%)	1 (1%)	14 (18%)	0 (0%)						
FOF/DOR	1	3	3 (100%)	0 (0%)	3 (100%)	0 (0%)	1	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
FOF/AMK	2	29	26 (90%)	11 (38%)	15 (52%)	0 (0%)						
FOF/GEN	2	13	12 (92%)	3 (23%)	9 (69%)	0 (0%)						
FOF/TOB	1	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)						

[illegible]

Antimicrobial combinations	CHBD			CHBD: concentration at which synergy was present			TKA			TKA: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
LZD/RIF	1	3	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>Triple combinations</b>												
PMB/FOF/MEM	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)						
PMB/SUL/MEM	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)						
PMB/SAM/MEM							2	2	1 (50%)	0 (0%)	1 (50%)	0 (0%)
CST/DOR/SUL							1	6	6 (100%)	6 (100%)	0 (0%)	0 (0%)
CST/VAN/DOR							1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)
IMP/SUL/AMK							1	8	0 (0%)	0 (0%)	0 (0%)	0 (0%)
IMP/TIM/AMK							1	8	0 (0%)	0 (0%)	0 (0%)	0 (0%)
TZP/SUL/AMK							1	8	0 (0%)	0 (0%)	0 (0%)	0 (0%)
TZP/TIM/AMK							1	8	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<b>Sum</b>	139	1402	539 (39%)	112 (8%)	194 (14%)	233 (17%)	99	407	185 (46%)	65 (16%)	88 (22%)	32 (8%)

%= 100\*n/N

MCBT assay was used in only 1 study and is not shown in the Table. See Section 4.5 (Bae S, 2016 [32])

Highlighted in green= combinations shown to be synergistic at concentrations equal to or lower than established breakpoints of resistance.

## 4.2 Summary Table (sum of all studies): Proportion of synergy and clinically relevant synergy in gradient- and disk-based methods

Antimicrobial combinations	Gradient methods*			Gradient methods*: concentration at which synergy was present			Disk methods*			Disk methods*: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
<b>SUL-based</b>												
SUL/MEM	2	61	23 (38%)	0 (0%)	0 (0%)	23 (38%)						
<b>SAM-based</b>												
SAM/RIF	1	7	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>CSF-based</b>												
CFS/MXF	1	80	2 (3%)	0 (0%)	0 (0%)	2 (3%)						
CFS/IMP	1	19	9 (47%)	0 (0%)	0 (0%)	9 (47%)						
CFS/MEM	1	19	10 (53%)	0 (0%)	0 (0%)	10 (53%)						
CFS/DOR	1	19	4 (21%)	0 (0%)	0 (0%)	4 (21%)						
CFS/RIF	1	7	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>TZB-based</b>												
TZB/MEM	1	54	19 (35%)	0 (0%)	0 (0%)	19 (35%)						
<b>MXF-based</b>												
MXF/CFS	1	80	2 (3%)	0 (0%)	0 (0%)	2 (3%)						
MXF/IMP	1	21	1 (5%)	0 (0%)	0 (0%)	1 (5%)						
MXF/MEM	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
MXF/DOR	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>IMP-based</b>												
IMP/CFS	1	19	9 (47%)	0 (0%)	0 (0%)	9 (47%)						
IMP/MXF	1	21	1 (5%)	0 (0%)	0 (0%)	1 (5%)						

Antimicrobial combinations	Gradient methods*			Gradient methods*: concentration at which synergy was present			Disk methods*			Disk methods*: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
IMP/NET	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
IMP/CST	1	41	19 (46%)	0 (0%)	0 (0%)	19 (46%)						
IMP/DOX	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
IMP/RIF	1	17	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	1	1 (100%)	0 (0%)	1(100%)	0 (0%)
<b>MEM-based</b>												
MEM/SUL	2	61	23 (38%)	0 (0%)	0 (0%)	23 (38%)						
MEM/CFS	1	19	10 (53%)	0 (0%)	0 (0%)	10 (53%)						
MEM/TZB	1	54	19 (35%)	0 (0%)	0 (0%)	19 (35%)						
MEM/MXF	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
MEM/CZA							1	11	2 (18%)	0 (0%)	0 (0%)	2 (18%)
MEM/NET	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
MEM/CST	1	41	35 (85%)	2 (5%)	0 (0%)	33 (81%)						
MEM/DOX	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
MEM/RIF	1	17	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>DOR-based</b>												
DOR/CFS	1	19	4 (21%)	0 (0%)	0 (0%)	4 (21%)						
DOR/MXF	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
DOR/NET	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
DOR/DOX	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
DOR/RIF	1	17	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>CZA- or AVI-based</b>												
CZA/MEM							1	11	2 (18%)	0 (0%)	0 (0%)	2 (18%)
<b>NET-based</b>												
NET/IMP	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						

Antimicrobial combinations	Gradient methods*			Gradient methods*: concentration at which synergy was present			Disk methods*			Disk methods*: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
NET/MEM	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
NET/DOR	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>CST-based</b>												
CST/IMP	1	41	19 (46%)	0 (0%)	0 (0%)	19 (46%)						
CST/MEM	1	41	35 (85%)	2 (5%)	0 (0%)	33 (81%)						
CST/RIF	2	45	37 (82%)	0 (0%)	0 (0%)	37 (82%)						
CST/FA							1	3	3 (100%)	0 (0%)	3 (100%)	0 (0%)
CST/DAP	1	4	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>PMB-based</b>												
PMB/TGC	1	4	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
PMB/RIF	1	3	1 (33%)	0 (0%)	0 (0%)	1 (33%)						
PMB/VAN	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)
<b>DOX-based</b>												
DOX/IMP	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
DOX/MEM	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
DOX/DOR	1	21	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>TGC-based</b>												
TGC/PMB	1	4	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
TGC/RIF	1	3	1 (33%)	0 (0%)	0 (0%)	1 (33%)						
<b>RIF-based</b>												
RIF/SAM	1	7	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
RIF/CFS	1	7	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
RIF/IMP	1	17	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1	1	1 (100%)	0 (0%)	1 (100%)	0 (0%)
RIF/MEM	1	17	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
RIF/DOR	1	17	0 (0%)	0 (0%)	0 (0%)	0 (0%)						

Antimicrobial combinations	Gradient methods*			Gradient methods*: concentration at which synergy was present			Disk methods*			Disk methods*: concentration at which synergy was present		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)
RIF/CST	2	45	37 (82%)	0 (0%)	0 (0%)	37 (82%)						
RIF/PMB	1	3	1 (33%)	0 (0%)	0 (0%)	1 (33%)						
RIF/TGC	1	3	1 (33%)	0 (0%)	0 (0%)	1 (33%)						
<b>FA-based</b>												
FA/CST							1	3	3 (100%)	0 (0%)	3 (100%)	0 (0%)
<b>VAN-based</b>												
VAN/PMB	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)	1	3	3 (100%)	3 (100%)	0 (0%)	0 (0%)
<b>DAP-based</b>												
DAP/CST	1	4	0 (0%)	0 (0%)	0 (0%)	0 (0%)						
<b>Sum</b>	30	650	164 (25%)	5 (1%)	0 (0%)	159 (24%)	4	18	9 (50%)	3 (17%)	4 (22%)	2 (11%)

%= 100\*n/N

\* Including gradient/agar and disk/agar methods

Highlighted in green= combinations shown to be synergistic at concentrations equal to or lower than established breakpoints of resistance.

### 4.3 Summary Table (sum of all studies): Proportion of synergy and clinically relevant synergy in agar dilution and dynamic in vitro PK/PD models

Antimicrobial combinations	Agar dilution			Agar dilution: concentration at which synergy was present			Dynamic in vitro PK/PD studies		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)
<b>SUL-based</b>									
SUL/IMP	1	4	4 (100%)	4 (100%)	0 (0%)	0 (0%)			
SUL/MEM	1	4	4 (100%)	4 (100%)	0 (0%)	0 (0%)			
SUL/AVI	1	38	35 (92%)	35 (92%)	0 (0%)	0 (0%)			
<b>SAM-based</b>									
SAM/MEM							1	1	0 (0%)
SAM/DOR							1	3	0 (0%)
SAM/PMB							1	1	0 (0%)
SAM/TGC							1	1	0 (0%)
<b>FEP-based</b>									
FEP/AMK							1	1	0 (0%)
<b>LVX-based</b>									
LVX/AMK							1	1	0 (0%)
<b>ETP-based</b>									
ETP/IMP							1	3	0 (0%)
<b>IMP-based</b>									
IMP/SUL	1	4	4 (100%)	4 (100%)	0 (0%)	0 (0%)			
IMP/ETP							1	3	0 (0%)
IMP/CST							1	1	0 (0%)
<b>MEM-based</b>									
MEM/SUL	1	4	4 (100%)	4 (100%)	0 (0%)	0 (0%)			

Antimicrobial combinations	Agar dilution			Agar dilution: concentration at which synergy was present			Dynamic in vitro PK/PD studies		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)
MEM/SAM							1	1	0 (0%)
MEM/PMB							1	1	0 (0%)
<b>DOR-based</b>									
DOR/SAM							1	3	0 (0%)
DOR/TGC							1	2	0 (0%)
<b>CZA- or AVI-based</b>									
AVI/SUL	1	38	35 (92%)	35 (92%)	0 (0%)	0 (0%)			
<b>AMK-based</b>									
AMK/FEP							1	1	0 (0%)
AMK/LVX							1	1	0 (0%)
<b>CST-based</b>									
CST/IMP							1	1	0 (0%)
CST/RIF							1	1	1 (100%)
CST/DAP							1	1	0 (0%)
<b>PMB-based</b>									
PMB/SAM							1	1	0 (0%)
PMB/MEM							1	1	0 (0%)
<b>TGC-based</b>									
TGC/SAM							1	1	0 (0%)
TGC/DOR							1	2	0 (0%)
<b>RIF-based</b>									
RIF/CST							1	1	1 (100%)
<b>DAP-based</b>									
DAP/CST							1	1	0 (0%)

Antimicrobial combinations	Agar dilution			Agar dilution: concentration at which synergy was present			Dynamic in vitro PK/PD studies		
	Studies N	Isolates n	Synergy n (%)	≤ breakpoints n (%)	> breakpoints n (%)	Unclear n (%)	Studies N	Isolates n	Synergy n (%)
Triple combinations									
PMB/SAM/MEM							1	1	1 (100%)
Sum	3	46	43 (94%)	43 (94%)	0 (0%)	0 (0%)	13	18	2 (11%)

%= 100\*n/N

Highlighted in green= combinations shown to be synergistic at concentrations equal to or lower than established breakpoints of resistance, or active in dynamic in vitro PK/PD models.

#### 4.4 Proportion of synergy and assessment of clinical relevance of observed synergy in checkerboard assays (study level data)

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
Cebrero-Cangueiro T, 2021 [1] and Nordmann P, 2020 [2]					
MEM/IMP	29 (6/21)	0 (0/21)	29 (6/21)	0 (0/21)	Checkerboard: Based on reported FICIs synergy was present at the following MEM/IMP concentrations: 32/16, 16/8, 16/8, 32/32, 16/8, 16/4 mg/L Animal model: Similar mortality and bacterial clearance comparing meropenem monotherapy to combination therapy. Decreased bacterial loads with combination vs monotherapy.
Cheng J 2021 [3]					
CST/RFB	100 (3/3)	0 (0/3)	0 (0/3)	100 (3/3)	Concentrations at which synergy was observed are not reported
CST/RIF	100 (2/2)	0 (0/2)	0 (0/2)	100 (2/2)	
Nwabor OF 2021 [4]					
FOF/IMP	0 (0/2)	NA	NA	NA	No synergy
FOF/MEM	0 (0/1)	NA	NA	NA	No synergy
FOF/DOR	100 (3/3)	0 (0/3)	100 (3/3)	0 (0/3)	Synergy at: 128/2, 128/4 and 512/4 mg/L.
FOF/TOB	50 (1/2)	0 (0/2)	50 (1/2)	0 (0/2)	Synergy at 128/2 mg/L.
FOF/GEN	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at 128/8 and 128/64 mg/L.
FOF/CIP	50 (1/2)	0 (0/2)	50 (1/2)	0 (0/2)	Synergy at 128/2 or 64/8 mg/L (2 possible MIC combinations based on the reported FICI).

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
FOF/LVX	0 (0/1)	NA	NA	NA	No synergy
FOF/TGC	75 (3/4)	25 (1/3)	50 (2/3)	0 (0/3)	Synergy at 128/0.5, 32/1 and 128/0.5 mg/L).
<b>Armengol E, 2020 [5]</b>					
RIF/LZD	0 (0/3)	NA	NA	NA	No synergy
<b>Li J, 2020 [6]</b>					
CST/MEM	80 (4/5)	40 (2/5)	20 (1/5)	20 (1/5)	Based on reported MICs and FICIs synergy at: AB075: 1/8 or 0.5/16 mg/L, AB084: 0.58 mg/L, AB118: 1/2 or 0.5/4 mg/L, AB133: 1/36 mg/L.
CST/LVX	100 (1/1)	100 (1/1)	0 (0/1)	0 (0/1)	Based on reported MICs and FICIs synergy at: AB075: 1/2 or 0.5/4 mg/L.
<b>Limsrivanichakorn S, 2020 [7]</b>					
CFS/MXF	5 (4/80)	0 (0/80)	0 (0/80)	5 (4/80)	Unclear at which concentration synergy was present
<b>Mohd Sazlly Lim S 2020 [8], 2021 [9], 2021 [10,85]</b>					
SUL/FOF	74 (37/50)	2 (1/50)	72 (36/50)	0 (0/50)	Synergy at: 0.5/256 (n=1), 4/128 (n=1), 8/32 (n=3), 8/64 (n=1), 8/128 (n=3), 16/32 (n=7), 16/64 (n=6), 16/128 (n=1), 32/8 (n=3), 32/32 (n=2), 32/64 (n=6), 32/128 (n=1), 64/8 (n=1), 64/64 (n= 1) mg/L.
SUL/MEM	56 (28/50)	0 (0/50)	56 (28/50)	0 (0/50)	Synergy at: 4/16 (n=1), 16/8 (n=2), 16/16 (n=1), 32/1 (n=1), 32/4 (n=1), 32/8 (n=2), 32/16 (n=4), 32/32 (n=5), 32/128 (n=1), 64/1 (n=2), 64/4 (n=1), 64/8 (n=2), 64/16

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
FOF/MEM	28 (14/50)	0 (0/50)	28 (14/50)	0 (0/50)	(n=2), 64/32 (n=2), 64/128 (n=1). Synergy at: 8/128 (n=2), 32/16 (n=2), 64/4 (n=1), 64/8 (n=1), 128/1 (n=1), 128/8 (n=2), 128/16 (n=1), 256/4 (n=1), 256/8 (n=2), 512/1 (n=1) mg/L.
FOF/RIF	24 (12/50)	0 (0/50)	0 (0/50)	24 (12/50)	Data not available. Combination MIC50 and MIC90 64/2 and 256/8 mg/L
MEM/RIF	20 (10/50)	0 (0/50)	0 (0/50)	20 (10/50)	Data not available. Combination MIC50 and MIC90 32/2 and 64/4mg/L
RIF/SUL	20 (10/50)	0 (0/50)	0 (0/50)	20 (10/50)	Data not available. Combination MIC50 and MIC90 2/32 and 4/64 mg/L
<b>Ghaith D, 2019 [13]</b>					
CST/RIF	61 (14/23)	22 (5/23)	39 (9/23)	0 (0/23)	Synergy at the following concentrations: 4/2, 16/1, 1/0.5, 0.5/0.5, 16/1, 0.5/0.5, 0.5/0.5, 2/16, 8/2, 2/0.5, 0.5/16, 0.5/16, 0.5/8, and 4/2 mg/L
<b>Mengucci TC 2019 [15], 2016 [16]</b>					
PMB/MEM	100 (3/3)	100 (3/3)	0 (0/3)	0 (0/3)	Synergy at; 0.5/0.5, 0.5/0.5 and 0.5/4 mg/L
PMB/SUL	67 (2/3)	67 (2/3)	0 (0/3)	0 (0/3)	Synergy at; 2/2 and 0.5/4 mg/L
PMB/FOF	0 (0/3)	NA	NA	NA	No synergy
FOF/MEM	17 (1/6)	17 (1/6)	0 (0/6)	0 (0/6)	Synergy at 32/2 mg/L
SUL/MEM	67 (4/6)	33 (2/6)	33 (2/6)	0 (0/6)	Synergy at 8/16, 4/8, 8/32 and 2/8 mg/L
PMB/FOF/MEM	100 (3/3)	100 (3/3)	0 (0/3)	0 (0/3)	Synergy at; 0.125/0.25/2, 0.125/4/8 and 0.125/1/16 mg/L
PMB/SUL/MEM	100 (3/3)	100 (3/3)	0 (0/3)	0 (0/3)	Synergy at; 0.5/2/2, 0.5/2/8 and 0.5/2/4 mg/L

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
<b>Oliva A, 2019 [17]</b>					
CST/MEM	100 (1/1)	100 (1/1)	0 (0/1)	0 (0/1)	Synergy at 0.5/16mg/L
CST/RIF	100 (2/2)	50 (1/2)	50 (1/2)	0 (0/2)	Synergy at 0.5/0.5 and 0.5/64mg/L.
CST/VAN	50 (1/2)	50 (1/2)	50 (1/2)	0 (0/2)	Synergy at 0.5/8 mg/L
<b>Ozger HS, 2019 [18]</b>					
CST/ERV	33 (1/3)	0 (0/3)	33 (1/3)	0 (0/3)	Synergy at 32/1 mg/L
<b>Phee LM, 2015 [19] and 2019 [20]</b>					
CST/FA	100 (3/3)	33 (1/3)	67 (1/3)	0 (0/3)	Synergy against all 3 isolates: against 2 of the 3 isolates at CST concentration >2mg/l (growth inhibition probability was <20% in PK/PD modelling against 1 of these isolates) and at 0.0625/4 mg/L against the other isolate.
<b>Shinohara DR, 2019 [22]</b>					
PMB/VAN	100 (3/3)	100 (3/3)	0 (3/3)	0 (3/3)	Synergy at 0.5/16, 4/2 and 0.5/8 mg/L
<b>Wang J, 2019 [23]</b>					
MEM/VAN	60 (3/5)	20 (1/5)	0 (0/5)	40 (2/5)	Synergy present against 3 of 5 isolates, against 1 isolate at concentrations ≤ breakpoints, while against the other 2 isolates it was not possible to confirm whether synergy was present at concentrations ≤ breakpoints. Based on reported FICIs and MICs synergy was
SAM/MEM	40 (2/5)	40 (2/5)	0 (0/5)	0 (0/5)	

Study-combinations	Synergy % (n/N)	Synergy at concentrations $\leq$ breakpoints % (n/N)	Synergy at concentrations $>$ breakpoints % (n/N)	Synergy but unclear if at concentration $\leq$ breakpoints % (n/N)	Notes
MEM/TZB	40 (2/5)	0 (0/5)	0 (0/5)	40 (2/5)	present at concentrations below breakpoints (exact concentrations not available). Not possible to extract whether synergy was present at concentrations $\leq$ breakpoints.
CST/MEM	80 (4/5)	40 (2/5)	0 (0/5)	40 (2/5)	Synergy in checkerboard against 4 of 5 isolates, against 2 isolates at concentrations $\leq$ breakpoints, while against the other 2 isolates it was not possible to confirm whether synergy was present at concentrations $\leq$ breakpoints.
Chen F, 2018 [24]					
MEM/AMK	35 (12/34)	0 (0/34)	0 (0/34)	35 (12/34)	Concentrations at which synergy was present are not reported
MEM/CIP	9 (3/34)	0 (0/34)	0 (0/34)	9 (3/34)	
AMK/CIP	12 (4/34)	0 (0/34)	0 (0/34)	12 (4/34)	
Singham-In U, 2018 [25]					
MEM/FOF	0 (0/22)	NA	NA	NA	No synergy
MEM/AMK	100 (2/2)	50 (1/2)	0 (0/2)	50 (1/2)	Synergy against both isolates, against one at concentrations $\leq$ breakpoints, against the other unclear if $\leq$ breakpoints
IMP/FOF	65 (15/23)	0 (0/23)	0 (0/23)	65 (15/23)	Concentrations at which synergy was present are not reported.
IMP/AMK	50 (1/2)	0 (0/2)	0 (0/2)	50 (1/2)	Unclear if synergy was present at concetrations $\leq$ breakpoints
Zhu W, 2018 [26]					

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
CST/IMP	67 (2/3)	67 (2/3)	0 (0/2)	0 (0/2)	Based on FICIs <0.5 and reported MICs synergy was present at <1/4 mg/L
CST/DOR	0 (0/2)	NA	NA	NA	No synergy
CST/FOF	0 (0/3)	NA	NA	NA	No synergy
CST/CFS	0 (0/3)	NA	NA	NA	No synergy
CFS/IMP	69 (11/16)	56 (9/16)	12.5 (2/16)	0 (0/16)	Based on reported FICIs and MICs synergy was present at: 14A: 64/4, 14B: <32/4, 14D: <8/4, 14F: 8/4, 14G: <32/4, 14H: 64/4, 14I: 16/4, 14J: <16/4, 14L: 16/4, 14N: <16/4, 14O: 32/4 mg/L.
IMP/FOF	55 (11/20)	25 (5/20)	25 (5/20)	5 (1/20)	Based on reported FICIs and MICs synergy was present at: 14B: <32/4, 14C: 64/4, 14D: 64/4, 14E: <64/4, 14G: 32/4, 14H: 32/4, 14I: 32/4, 14K: 32/4, 14L: 64/4, 14M: 64/4, 14O: 64/4 mg/L.
<b>Wei W, 2017 [30]</b>					
CST/LVX	0 (0/1)	NA	NA	NA	No synergy
<b>Wei WJ, 2017 [31]</b>					
CST/CHL	100 (2/2)	50 (1/2)	50 (1/2)	0 (0/2)	Synergy at 0.5/64 and 0.5/2 mg/L
<b>Bae S, 2016 [32]</b>					
CST/RIF	100 (9/9)	22 (2/9)	0 (0/9)	78 (7/9)	Only presence (FICI≤0.5) or not of synergy is reported. Based on the available data it was possible to confirm synergy at concentrations below breakpoints in only few cases (CST/RIF 2/9, CST/MEM 1/9)
CST/TEC	44 (4/9)	0 (0/9)	0 (0/9)	44 (4/9)	
CST/VAN	78 (7/9)	0 (0/9)	0 (0/9)	78 (7/9)	
CST/MEM	33 (3/9)	11 (1/9)	0 (0/9)	22 (2/9)	
CST/ATM	44 (4/9)	0 (0/9)	0 (0/9)	44 (4/9)	
CST/CAZ	44 (4/9)	0 (0/9)	0 (0/9)	44 (4/9)	
CST/SAM	0 (0/8)	0 (0/8)	0 (0/8)	0 (0/8)	

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
CST/SXT	13 (1/7)	0 (0/7)	0 (0/7)	13 (1/7)	
CST/AMK	33 (3/6)	0 (0/6)	0 (0/6)	33 (3/6)	
CST/AZM	13 (1/8)	0 (0/8)	0 (0/8)	13 (1/8)	
CST/TGC	0 (0/9)	NA	NA	NA	
Bowler SL, 2016 [33]					
CST/FA	100 (3/3)	0 (0/3)	0 (0/3)	100 (3/3)	Only FICI range and MIC range are reported and it was not possible to extract if synergy was present at concentrations below breakpoints
Laishram S, 2016 [35]					
SUL/MEM	32 (16/50)	0 (0/50)	0 (0/50)	32 (16/50)	Only FICI range and MIC range are reported and it was not possible to extract if synergy was present at concentrations below breakpoints
Leite GC, 2016 [36]					
CST/RIF	100 (4/4)	50 (2/4)	0 (0/4)	50 (2/4)	
CST/VAN	100 (7/7)	0 (0/7)	0 (0/7)	100 (7/7)	
CST/TGC	0 (0/1)	NA	NA	NA	
CST/FOF	0 (0/6)	NA	NA	NA	
CST/GEN	0 (0/1)	NA	NA	NA	Based on reported MICs and FICIs
CST/MEM	100 (7/7)	0 (0/7)	100 (7/7)	0 (0/7)	
CST/IMP	100 (7/7)	0 (0/7)	100 (7/7)	0 (0/7)	
FOF/GEN	91 (10/11)	27 (3/11)	64 (7/11)	0 (0/11)	
FOF/AMK	96 (26/27)	41 (11/27)	55 (15/27)	0 (0/27)	
Yang H, 2016 [38]					
CST/VAN	100 (1/1)	0 (0/1)	0 (0/1)	100 (1/1)	Based on a reported FICI of 0.188 synergy was

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
					present at either 0.5/16 or 1/32 mg/L
<b>Yang YS, 2016 [39]</b>					
MEM/MIN	0 (0/3)	NA	NA	NA	No synergy
CFS/MIN	0 (0/2)	NA	NA	NA	No synergy
<b>García-Salguero C, 2015 [42]</b>					
AMK/IMP	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at: Ab26: 64/32 or 16/128 mg/L, Ab66: 128/128 mg/L
AMK/MEM	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at: Ab26: 64/32 or 32/64 mg/L, Ab66: 128/16 mg/L
AMK/FOF	0 (0/2)	NA	NA	NA	No synergy
PLZ/IMP	75 (6/8)	0 (0/8)	63 (5/8)	13 (1/8)	Synergy at: Ab2: 2/16 mg/L, AB26: 4/128 mg/L, Ab66: 4/64 or 2/128 mg/L, AB80: 8/2 or 2/8 mg/L, AB102: 2/16 mg/L, AB 113: 2/4 or 1/8 mg/L
PLZ/MEM	50 (2/4)	0 (0/4)	50 (2/4)	0 (0/4)	Synergy at: Ab26: 4/64 mg/L, Ab125: 16/32 mg/L
PLZ/FOF	11 (1/9)	0 (0/9)	11 (1/9)	0 (0/9)	Synergy at: Ab80: 8/16 mg/L
<b>Marie MA, 2015 [43]</b>					
SUL/MEM	44 (24/54)	0 (0/54)	0 (0/54)	44 (24/54)	Exact FICIs or combination MICs not reported.
MEM/TZB	41 (22/54)	0 (0/54)	0 (0/54)	41 (22/54)	Exact FICIs or combination MICs not reported.
<b>Vourli S, 2015 [45]</b>					
CST/MEM	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at MEM concentrations 16-64mg/L and CST concentrations 0.0625-1.
CST/SAM	0 (0/2)	NA	NA	NA	No synergy
SAM/MEM	0 (0/5)	NA	NA	NA	No synergy
<b>Majewski P, 2014</b>					

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
<b>[47]</b>					
IMP/RIF	40 (4/10)	0 (0/10)	20 (2/10)	20 (2/10)	Synergy at: Isolate 12 (FICI=0.5): 16/1 mg/L, Isolate 34 (FICI=0.5): 16/1 mg/L, Isolate 53 (FICI=0.375): 8/0.5 or 4/1 mg/L, Isolate 91 : 8/0.5 or 4/1 mg/L,
<b>Percin D, 2014 [50]</b>					
CST/VAN	90 (9/10)	0 (0/10)	0 (0/10)	90 (9/10)	MICs for each isolate not available.
<b>Sun Y, 2014 [51]</b>					
CFS/MEM	0 (0/11)	NA	NA	NA	No synergy
MEM/AMK	0 (0/9)	NA	NA	NA	No synergy
MEM/CIP	9 (1/11)	0 (0/11)	9 (1/11)	0 (0/11)	Synergy at 16/32 mg/L
MEM/AZM	0 (0/12)	NA	NA	NA	No synergy
<b>Wang Y, 2014 [52]</b>					
IMP/RIF	67 (12/16)	61 (11/16)	6 (1/16)	0 (0/16)	Synergy at: 1/2, 2/2, 0.5/1, 2/1, 2/1, 4/4, 2/1, 2/1, 4/1, 8/4, 8/0.25, 1/1, 16/8, 8/1 and 16/2 mg/L
<b>Cetin ES, 2013 [53]</b>					
RIF/SAM	100 (7/7)	57 (4/7)	14 (1/7)	29 (2/7)	Synergy at: Isolate 5: 1/1 or 0.125/8 mg/L, Isolate 11: 0.5/4 mg/L, Isolate 12: 1/2 or 0.125/16 mg/L, Isolate 14: 4/4 or 0.5/32 mg/L, Isolate 15: 1/1 or 0.125/8 mg/L, Isolate 16: 1/2 or 0.125/16 mg/L, Isolate 20: 1/8 mg/L
RIF/CFS	29 (2/7)	14 (1/7)	0 (0/7)	14 (1/7)	Synergy at: Isolate 11: 1/16 mg/L, isolate 20: 64/0.5 or 32/1 mg/L
<b>O'Hara JA, 2013 [56]</b>					
CST/DOR	67 (2/3)	33 (1/3)	33 (1/3)	0 (0/3)	Synergy at: JA637 (FICI 0.31): 64/2 or 16/8 mg/L, JA566 (FICI 0.13): 0.25/2 mg/L
CST/VAN	100 (3/3)	0 (0/3)	67 (2/3)	33 (1/3)	Synergy at: JA637 (FICI 0.28): 64/8 or 8/64 mg/L,

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
					JA566 (FICI 0.14): 0.5/4 or 0.0625/32 mg/L, JA942 (FICI 0.25): 32/32 mg/L
<b>Principe L, 2013 [57]</b>					No synergy
DOR/VAN	0 (0/3)	NA	NA	NA	
DOR/TGC	100 (3/3)	33 (1/3)	0 (0/3)	67 (2/3)	Synergy at; ≤8/2, ≤16/2, ≤32/1.
DOR/AMK	25 (1/4)	0 (0/4)	0 (0/4)s	25 (1/4)	Synergy at ≤16/64 mg/L
DOR/CST	0 (0/1)	NA	NA	NA	
SAM/DOR	0 (0/1)	NA	NA	NA	
DOR/RIF	0 (0/1)	NA	NA	NA	
<b>Deveci A, 2012 [59]</b>					
SUL/CAZ	70 (7/10)	10 (1/10)	60 (6/10)	0 (0/10)	Synergy at: 16/32, 8/32, 32/2, 32/2, 64/4, 32/2 and 8/4 mg/L,
SUL/MEM	0 (0/9)	NA	NA	NA	
SUL/CRO	40 (4/10)	0 (0/10)	40 (4/10)	0 (0/10)	Synergy at: 16/512, 256/64, 16/64, 32/128 mg/L
SUL/CIP	80 (8/10)	20 (2/10)	60 (6/10)	0 (0/10)	Synergy at: 8/0.5, 16/2, 16/8, 128/1, 64/1, 128/0.5, 64/1, 8/1 mg/L
SUL/GEN	80 (8/10)	20 (2/10)	60 (6/10)	0 (0/10)	Synergy at: 8/16, 8/8, 8/64, 16/16, 32/8, 32/8, 32/8, 8/8 mg/L
SUL/FEP	44 (4/9)	0 (0/9)	44 (4/9)	0 (0/9)	Synergy at: 64/4, 64/4, 64/4, 32/4 mg/L
<b>Vidaillac C, 2012 [61]</b>					
CST/VAN	100 (1/1)	100 (1/1)	0 (0/1)	0 (0/1)	FICI 0.18 → Synergy at: 1/8 or 0.5/16 mg/L
CST/TMP	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	FICI 0.37 → Synergy at: 2/4 or 1/8 mg/L
CST/SXT	100 (1/1)	100 (1/1)	0 (0/1)	0 (0/1)	FICI 0.20 (?, <0.25) → Synergy at: <2/2/38 mg/L
<b>Santimaleeworagun</b>					

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
<b>W, 2011 [62]</b>					
SUL/IMP	0 (0/6)	NA	NA	NA	No synergy
SUL/FOF	67 (4/6)	33 (2/6)	17 (1/6)	17 (1/6)	Synergy at: AB164 (FICI 0.48<0.5): <8/32 mg/L, AB167 (FICI 0.37): 8/32 or 4/64 mg/L, AB198 (FICI 0.28): 8/4 or 1/32 mg/L, AB313 (FICI 0.47<0.5): <16/128 mg/L
<b>Tan TY, 2011 [64]</b>					
PMB/TGC	75 (3/4)	0 (0/4)	50 (2/4)	25 (1/4)	Based on reported FICIs and MICs synergy was present in CHBD at the following concentrations: For isolate 18351: 4/0.5 or 1/2 mg/dl. For isolate 9447: 4/1 mg/L. For isolate 11171: 4/1 mg/L. No synergy in TKA at 2/2 mg/L.
PMB/RIF	100 (3/3)	33 (1/3)	33 (1/3)	33 (1/3)	Based on reported FICIs and MICs synergy was present in CHBD at the following concentrations: For isolate 27640: 2/1 or 0.5/4 mg/L For isolate 9447: 1/1 or 0.5/2 mg/dl. For isolate 11171: 4/1 mg/L. For isolate 11171: 4/8 mg/L.
TGC/RIF	33 (1/3)	0 (0/3)	33 (1/3)	0 (0/3)	Based on reported FICIs and MICs synergy was present in CHBD at 4/4 or 2/8 mg/L.
<b>Principe L, 2009 [73]</b>					
TGC/LVX	22 (4/18)	0 (0/18)	22 (4/18)	0 (0/18)	Synergy present in checkerboard at: 0.25/4 (isolate 5, 11 and 75), 2/4 (isolate 16).
TGC/TZP	0 (0/18)	NA	NA	NA	No synergy
TGC/AMK	14 (2/14)	7 (1/14)	7 (1/14)	0 (1/14)	Synergy present in checkerboard at: 1/16 (isolate 11) and 1/64 mg/L (isolate 71)

Study-combinations	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Notes
TGC/IMP	8 (1/12)	0 (0/12)	8 (1/12)	0 (0/12)	Synergy present in checkerboard at 0.25/8 mg/L
TGC/RIF	0 (0/13)	NA	NA	NA	No synergy
SAM/TGC	0 (0/6)	NA	NA	NA	No synergy
<b>Sader HS, 2005 [77]</b>					
SAM/FEP	100 (2/2)	50 (1/2)	50 (1/2)	0 (0/2)	Combination MICs: 8/4/32 and 16/8/16 mg/L
<b>Sader HS, 2005 [78]</b>					
ATM/FEP	0 (0/3)	NA	NA	NA	No synergy at 8/8 mg/L
ATM/CAZ	0 (0/4)	NA	NA	NA	No synergy at 8/8 mg/L
ATM/MEM	0 (0/3)	NA	NA	NA	No synergy at 8/4 mg/L
SAM/ATM	0 (0/1)	NA	NA	NA	No synergy at 8/4/8 mg/L
<b>Fernández-Cuenca F, 2003 [83]</b>					
AZM/IMP	0 (0/2)	NA	NA	NA	No synergy
AZM/CAZ	33 (1/3)	0 (0/3)	33 (1/3)	0 (0/3)	Synergy at 64/128 mg/L
AZM/AMK	0 (0/2)	NA	NA	NA	No synergy
AZM/CIP	0 (0/3)	NA	NA	NA	No synergy

#### 4.5 Proportion of synergy and assessment of clinical relevance of observed synergy in time-kill assays (study level data)

Study-combinations	Synergy % (n/N)	Synergy at concenstrations $\leq$ breakpoints % (n/N)	Synergy at concentrations $>$ breakpoints % (n/N)	Synergy but unclear if at concentration $\leq$ breakpoints % (n/N)	Concentrations at which synergy was evaluated
<b>Nwabor OF 2021 [4]</b>					TKA conducted at the following concentrations: FOF 1xMIC, other at $\frac{1}{2}$ and $\frac{1}{4}$ x MIC
FOF/DOR		NA	NA	NA	No synergy
FOF/CIP		NA	NA	NA	No synergy
FOF/TGC					Synergy at 128/2 and 128/1 mg/L
<b>Li J, 2020 [6]</b>					TKA only conducted at 0.5x and 1x MIC
CST/MEM	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	Synergy at: 4/32 and 4/16 mg/L.
CST/LVX	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	Synergy at: 4/16 and 4/8 mg/L.
<b>Mohd Sazlly Lim S 2020 [8], 2021 [9], 2021 [10,85]</b>					
SUL/FOF	50 (2/4)	0 (0/4)	50 (2/4)	0 (0/4)	Synergy at 128/128 (n=2) mg/L. Based on semi-mechanistic PK/PD modelling, the SUL/FOF regimen at best demonstrated a probability of target attainment of 2-log <sub>10</sub> kill at 24 h of 72%.
SUL/MEM	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at 64/32 and 128/64 mg/L. Based on semi-mechanistic PK/PD modelling, the MEM/SUL regimen at best demonstrated a probability of target attainment of 2-log <sub>10</sub> kill at 24 h of 34%.

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
<b>Rodriguez CH, 2020 [11]</b>					
SUL/AVI	100 (1/1)	100 (1/1)	0 (0/1)	0 (0/1)	Bactericidal activity at SUL/AVI concentrations 8/4mg/L
<b>Gaudereto JJ, 2019 [12]</b>					
CZA/MEM	0 (0/11)	NA	NA	NA	TKA conducted at 1x and 0.5x MIC. No synergy.
<b>Mataraci Kara E, 2019 [14]</b>					
CST/CZA	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy assessed in TKA only 1x or 4x the MIC
CZA/LVX	75 (3/4)	0 (0/4)	75 (3/4)	0 (0/4)	
CZA/TGC	75 (3/4)	0 (0/4)	75 (3/4)	0 (0/4)	
CZA/TOB	50 (1/2)	0 (0/2)	50 (1/2)	0 (0/2)	
CZA/MEM	75 (3/4)	0 (0/4)	75 (3/4)	0 (0/4)	
<b>Oliva A, 2019 [17]</b>					
CST/MEM	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	Synergy at 4/64 mg/L
CST/RIF	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at 4/2 and 4/256 mg/L
CST/VAN	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at at 4/16 and 256/16 mg/L
<b>Phee LM, 2015 [19] and 2019 [20]</b>					
CST/FA	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	Synergy at 2/16 mg/L
<b>Poulakou G, 2019 [21]</b>					
CST/DAP	0 (0/1)	NA	NA	NA	No synergy

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
<b>Shinohara DR, 2019 [22]</b>					
PMB/VAN	67 (2/3)	0 (0/3)	67 (2/3)	0 (0/3)	TKA only conducted at 0.5 x MIC (8/128, 8/128 and 2/128 mg/L)
<b>Wang J, 2019 [23]</b>					
CST/MEM	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy only assessed at 4/16 and 8/16mg/L.
<b>Singham-In U, 2018 [25]</b>					
IMP/FOF	89 (8/9)	0 (0/9)	89 (8/9)	0 (0/9)	Concentrations used in TKA were above breakpoints
<b>Lenhard JR, 2017 [27,28]</b>					
PMB/MEM	0 (0/2)	NA	NA	NA	TKA conducted at: SAM 132/70 mg/L, MEM 55mg/L, PMB 1.5 mg/L
PMB/SAM	0 (0/2)	NA	NA	NA	
MEM/SAM	0 (0/2)	NA	NA	NA	
PMB/MEM/SAM	50 (1/2)	0 (0/2)	50 (1/2)	0 (0/2)	
<b>Wei W, 2017 [30]</b>					
CST/LVX	0 (0/1)	NA	NA	NA	No synergy
<b>Wei WJ, 2017 [31]</b>					
CST/CHL	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at 2/32mg/L
<b>Bowler SL, 2016 [33]</b>					
CST/FA	67 (2/3)	0 (0/3)	67 (2/3)	0 (0/3)	TKA conducted at; CST 2 mg/L, VAN 20 mg/L, DOR 8 mg/L, FA 8 mg/L
CST/VAN	33 (1/3)	33 (1/3)	0 (0/3)	0 (0/3)	

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
CST/DOR	33 (1/3)	33 (1/3)	0 (0/3)	0 (0/3)	
<b>Laishram S, 2016 [35]</b>					
SUL/MEM	58 (29/50)	0 (0/50)	8 (4/50)	50 (25/50)	Based on concentrations used (0.5x MIC) and reported MIC50 synergy was present at above breakpoints in TKA against at least 4 isolates.
<b>Park GC, 2016 [37]</b>					
CST/DOR	59 (10/17)	59 (10/17)	0 (0/17)	0 (0/17)	TKA assays were conducted at the following concentrations: CST 2mg/L, TGC 2mg/L, DOR 8mg/L
CST/TGC	58 (7/12)	58 (7/12)	0 (0/12)	0 (0/12)	
TGC/DOR	11 (5/46)	11 (5/46)	0 (0/46)	0 (0/46)	
<b>Yang H, 2016 [38]</b>					
CST/VAN	0 (0/1)	0 (0/1)	0 (0/1)	0 (0/1)	No synergy at 2/20 mg/L
<b>Yang YS, 2016 [39]</b>					
MEM/MIN	0 (0/3)	NA	NA	NA	No synergy at
CFS/MIN	50 (1/2)	0 (0/2)	50 (1/2)	0 (0/2)	Synergy at 16/16/16 mg/L
<b>García-Salguero C, 2015 [42]</b>					
PLZ/FOF	0 (0/2)	NA	NA	NA	No synergy at 4/64 mg/L. Regrowth at 24 hours, despite initial bactericidal killing
<b>Rodriguez CH, 2015 [44]</b>					
IMP/MIN	0 (0/1)	NA	NA	NA	TKA conducted at the following concentrations: IMP 8mg/L, MIN 4 mg/L, RIF 4 mg/L
IMP/RIF	0 (0/1)	NA	NA	NA	

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
<b>Galani I, 2014 [46]</b>					
CST/DAP	0 (0/4)	NA	NA	NA	TKA conducted at 0.25, 0.5 and 1x MIC
<b>Nastro M, 2014 [48]</b>					
CST/RIF	100 (4/4)	0 (0/4)	100 (4/4)	0 (0/4)	Synergy at RIF 4 mg/L, CST 2 mg/L
<b>Oleksium LM, 2014 [49]</b>					
CST/DOR	83 (5/6)	83 (5/6)	0 (0/6)	0 (0/6)	TKA conducted at the following concentrations: CST 2mg/L, DOR 8mg/L, SUL 4mg/L
CST/SUL	33 (2/6)	33 (2/6)	0 (0/6)	0 (0/6)	
CST/DOR/SUL	100 (6/6)	100 (6/6)	0 (0/6)	0 (0/6)	
SUL/DOR	24 (4/17)	24 (4/17)	0 (0/17)	0 (0/17)	
<b>Percin D, 2014 [50]</b>					
CST/VAN	100 (10/10)	100 (10/10)	0 (0/10)	0 (0/10)	TKA was conducted at VAN 20 mg/L and CST 2 mg/L.
<b>O'Hara JA, 2013 [56]</b>					
CST/DOR	100 (3/3)	100 (3/3)	0 (0/3)	0 (0/3)	TKA conducted at: CST 2mg/L, DOR 8mg/L, VAN 20 mg/L.
CST/VAN	67 (2/3)	67 (2/3)	0 (0/3)	0 (0/3)	
DOR/VAN	0 (0/3)	NA	NA	NA	
CST/VAN/DOR	100 (3/3)	100 (3/3)	0 (0/3)	0 (0/3)	
<b>Queenan AM, 2013 [58]</b>					
DOR/CIP	0 (0/1)	NA	NA	NA	TKA conducted at maximum clinically achievable concentrations (DOR 18.8 mg/L, CIP 4.56 mg/L, LVX 11.5 mg/L).
DOR/LVX	0 (0/1)	NA	NA	NA	
<b>Peck KR, 2012 [60]</b>					

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
CST/IMP	0 (0/2)	NA	NA	NA	TKA only conducted at 0.5x and 1xMIC. Graphs available only for CST/IMP. Discordant results comparing the table to the TKA curves (reported synergy in the table but no synergy examining the TKA curve).
CST/RIF	100 (1/1)	0 (0/1)	0 (0/1)	100 (1/1)	
SAM/IMP	100 (6/6)	0 (0/6)	0 (0/6)	100 (6/6)	
<b>Vidaillac C, 2012 [61]</b>					
CST/VAN	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	TKA conducted only at 0.25x (CST 2 mg/L, VAN 32 mg/L, TMP 8 mg/L and SXT 4/76.5 mg/L) and 0.5x (CST 8 mg/L, VAN 64 mg/L, TMP 16 mg/L and SXT 8/153 mg/L) the MIC
CST/TMP	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	
CST/SXT	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	
<b>Pachón-Ibáñez ME, 2011 [63]</b>					
RIF/IMP	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	TKA conducted only at 1x MIC and at Cmax (i.e. at concentrations > breakpoints)
RIF/SUL	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	
<b>Santimaleeworagun W, 2011 [62]</b>					
SUL/FOF	83 (5/6)	0 (0/6)	83 (5/6)	0 (0/6)	TKA was only conducted at SUL 1xMIC (i.e. above breakpoints of resistance).
<b>Tan TY, 2011 [64]</b>					
PMB/TGC	0 (0/4)	NA	NA	NA	2/2 mg/L
PMB/RIF	33 (1/3)	33 (1/3)	0 (0/3)	0 (0/3)	2/2 mg/L

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
TGC/RIF	0 (0/3)	NA	NA	NA	2/2 mg/L
<b>Pankuch GA, 2010 [67]</b>					
DOR/LVX	60 (3/5)	0 (0/5)	60 (3/5)	0 (0/5)	Synergy at 4/16, 8/16 and 16/18 mg/L
DOR/AMK	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at 32/64 and 8/512 mg/L
DOR/CST	100 (4/4)	0 (0/4)	100 (4/4)	0 (0/4)	Synergy at 4/2, 4/8, 8/4 and 8/2 mg/L
<b>Rodriguez CH, 2010 [68]</b>					
IMP/RIF	0 (0/4)	NA	NA	NA	8/4 mg/L.
IMP/GEN	0 (0/2)	NA	NA	NA	8/4 mg/L.
<b>Urban C, 2010 [69]</b>					
DOR/RIF	40 (2/5)	20 (1/5)	20 (1/5)	0 (0/5)	TKA conducted at 1/4 x MIC. Synergy at: 2/8 and 4/8 mg/L
<b>Yuan Z, 2010 [70] and Lim TP, 2008 [71]</b>					
AMK/LVX	0 (0/1)	NA	NA	NA	
AMK/FEP	100 (1/1)	0 (0/1)	100 (1/1)		Synergy was defined based on the interactive index method. Based on the available graphs it seems that >2 log CFU/ml reduction were only observed at concentrations > breakpoints
FEP/LVX	100 (1/1)	0 (0/1)	100 (1/1)		
<b>Lim TP, 2009 [72]</b>					
MEM/RIF	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	Synergy at 64/2 mg/L
TGC/MEM	0 (0/1)	NA	NA	NA	No synergy at 2/64 mg/L

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
TGC/RIF	100 (1/1)	100 (1/1)	0 (0/1)	0 (0/1)	Synergy at 2/2 mg/L
<b>Principe L, 2009 [73]</b>					
TGC/LVX	0 (0/2)	NA	NA	NA	Regrowth in TKA at 0.25/4 mg/L
TGC/AMK	100 (1/1)	100 (1/1)	0 (0/1)	0 (0/1)	Synergy in TKA at 1/64 mg/L
TGC/IMP	0 (0/1)	NA	NA	NA	Regrowth in TKA at 0.25/8 mg/L
<b>Lee CH, 2008 [75]</b>					
SUL/MEM	50 (1/2)	0 (0/2)	50 (1/2)	0 (0/2)	TKA conducted only at 1xMIC. Synergy at 16/64 mg/L
<b>Lee NY, 2007 [76]</b>					
SUL/IMP	0 (0/4)	NA	NA	NA	Although only partial synergy (FICIs 0.56-0.75) is reported in checkerboard the combination MIC in agar dilution were ≤ breakpoints; 8/0.5, 8/2, 8/2, 8/2 mg/L.
SUL/MEM	0 (0/4)	NA	NA	NA	Although only partial synergy (FICIs 0.56-0.75) is reported in checkerboard the combination MIC in agar dilution were ≤ breakpointss; 8/1, 8/4, 8/4, 8/4 mg/L.
<b>Choi JY, 2004 [79]</b>					
SUL/IMP	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	TKA conducted at 0.5x and 1x MIC. Synergy at 32/8 mg/L
<b>Jung R, 2004 [80]</b>					
FEP/MXF	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	TKA conducted at 0.5x and 1x MIC. Synergy at 32/8 and 32/4 mg/L.
<b>Montero A, 2004 [81]</b>					

Study-combinations	Synergy % (n/N)	Synergy at concenstrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
IMP/RIF	100 (2/2)	0 (0/2)	100 (2/2)	0 (0/2)	TKA conducted at 1/2 to 1/32 x MIC. Synergy at 2/4 mg/L (strain D) and 32/2mg/L (Strain E). Strain D: No differences compared to monotherapy in the mouse model. Strain E: Significantly reduced lung bacterial counts, no significant reduction of bacteraemia, similar survival (100% with the combination + 100% with RIF monotherapy).
IMP/SUL	0 (0/1)	NA	NA	NA	TKA conducted at 1/2 to 1/32 x MIC. No synergy in TKA. Not evaluated in the animal model.
<b>Yoon J, 2004 [82]</b>					
PMB/IMP	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	Synergy at 2/8 mg/L
<b>Roussel-Delvallez M, 1996 [84]</b>					
IMP/SUL/AMK	0 (0/8)	NA	NA	NA	TKA was conducted at following concentrations: TIM 112 mg/L, TZP 100 mg/L, IMP 25 mg/L, AMK 15 mg/L. Only mean killing is reported. Initial bactericidal killing was observed with some combinations-strains but "regrowth was observed for all strains at 24 hours".
IMP/TIM/AMK	0 (0/8)	NA	NA	NA	
TZP/SUL/AMK	0 (0/8)	NA	NA	NA	
TZP/TIM/AMK	0 (0/8)	NA	NA	NA	

#### 4.6 Proportion of synergy and assessment of clinical relevance of observed synergy in studies using dynamic in vitro PK/PD models (study level data)

Study-combinations	Method	Synergy % (n/N)	Comments
<b>Lenhard JR, 2017 [27,28]</b>			
PMB/MEM	HFIM	0 (0/1)	Doses simulating human regimens were used (PMB 3.33mg/kg then 1.43mg/kg every 12 hours, MEM 2gr every 8 hour as 3h-infusions, SAM 8/4g every 8 hours as 3h-infusions).
PMB/SAM		0 (0/1)	
MEM/SAM		0 (0/1)	
PMB/MEM/SAM		100 (1/1)	
<b>Yuan Z, 2010 [70] and Lim TP, 2008 [71]</b>			
AMK/LVX	HFIM	0 (0/1)	Regrowth despite initial killing at 4 hours.
AMK/FEP		0 (0/1)	Regrowth despite initial killing at 4 hours.
<b>Córdoba J, 2015 [41]</b>			
CST/IMP	Other dynamic in vitro PK/PD model	0 (0/1)	Simulation of human treatment regimens
CST/DAP		100 (1/1)	
IMP/ETP		0 (0/3)	
RIF/CFS		0 (0/7)	
<b>Housman ST, 2013 [54]</b>			Simulated regimens: SAM 9g q8h (3h inf), DOR 2gr q8h (4h inf), TGC 200mg q12h (0.5h inf).
TGC/DOR	Other dynamic in vitro PK/PD model	0 (0/2)	No synergy.
SAM/DOR		0 (0/3)	Increased killing with SAM/DOR vs monotherapies against all 3 strains but with regrowth by 24 hours.
SAM/TGC		0 (0/1)	No synergy.
<b>Lee HJ, 2013 [55]</b>			
CST/RIF	Other dynamic in vitro PK/PD model	100 (1/1)	Regimens mimicking human serum concentration after usual doses in critically-ill patients.

#### 4.7 Proportion of synergy and assessment of clinical relevance of observed synergy in studies using animal models (study level data)

Study-combinations	Method	Outcomes assessed	Synergy % (n/N)	Comments
<b>Cebrero-Cangueiro T, 2021 [1] and Nordmann P, 2020 [2]</b>				
MEM/IMP	Intraperitoneal infection mouse model	Survival, sterilization of cultures, bacterial loads	0 (0/2)	Decreased bacterial loads with combination vs monotherapy. But similar mortality and bacterial clearance comparing meropenem monotherapy to combination therapy.
<b>Poulakou G, 2019 [21]</b>				
CST/DAP	Intraperitoneal infection mouse model	Survival and bacterial loads	100 (1/1)	The combination significantly improved survival and reduced bacterial loads in tissues compared to monotherapies.
<b>Wei W, 2017 [30]</b>				
CST/LVX	<i>G. mellonella</i> model	Survival	0 (0/1)	Same survival comparing combination therapy to monotherapy
<b>Yang H, 2016 [38]</b>				
CST/VAN	<i>G. mellonella</i> model	Survival	100 (1/1)	Survival rate in <i>G. mellonella</i> model higher than monotherapies, but high survival even with monotherapies.
<b>O'Hara JA, 2013 [56]</b>				
CST/DOR	<i>G. mellonella</i> model (simulation of human doses)	Survival	0 (0/3)	No synergy
CST/VAN			0 (0/3)	
DOR/VAN			100 (3/3)	The clinical relevance of the <i>G. mellonella</i> model is unclear because of mechanisms of action likely not relevant to humans; high survival even with DOR and VAN monotherapies, and high survival with DOR/VAN despite lack of in vitro synergy
CST/VAN/DOR			100 (3/3)	
<b>Queenan AM, 2013 [58]</b>				

Study-combinations	Method	Outcomes assessed	Synergy % (n/N)	Comments
DOR/CIP	intraperitoneal infection mouse model	Survival	0 (0/1)	No synergy
DOR/LVX			100 (1/1)	Improved survival in the mouse model (the isolate had relatively low MICs: DOR 16 mg/L and LVX 8 mg/L).
<b>Pachón-Ibáñez ME, 2011 [63]</b>				
RIF/IMP	Pneumonia mouse model	Survival, sterilization of cultures, bacterial loads	0 (0/2)	In the animal model survival with RIF/IMP (80 and 33%) and RIF/SUL (60 and 53%) did not differ significantly compared to RIF monotherapy (73 and 40%). Lung clearance and blood culture sterilization was higher against one of the two strains with RIF/SUL.
RIF/SUL			50 (1/2)	
<b>Pachón-Ibáñez ME, 2010 [66]</b>				
SUL/IMP	Pneumonia and meningitis mouse models	Survival, sterilization of cultures, bacterial loads	100 (1/1)	Higher survival and bacterial clearance in animal model compared to monotherapies.
RIF/IMP			0 (0/1)	Survival not improved comparing RIF monotherapy (71%) to combination therapy (60%), despite improved bacterial clearance.
RIF/SUL			0 (0/1)	Survival not improved comparing RIF monotherapy (71%) to combination therapy (47%), despite improved bacterial clearance.
<b>Yuan Z, 2010 [70] and Lim TP, 2008 [71]</b>				
AMK/LVX	Pneumonia mouse model	Survival, bacterial loads	0 (0/1)	Similar survival with AMK monotherapy.
AMK/FEP			1 (1/1)	Improved survival and reduction of tissue bacterial burden in the mouse model.
FEP/LVX			0 (0/1)	Similar survival with FEP monotherapy.
<b>Song YC, 2009 [74]</b>				
IMP/RIF	Pneumonia mouse model	Survival, sterilization of cultures,	100 (3/3)	Synergistic ( $\geq 2\Delta$ log reduction in lung bacterial loads compared to RIF monotherapy) against all 3 strains, but

Study-combinations	Method	Outcomes assessed	Synergy % (n/N)	Comments
		bacterial loads		100% survival with both monotherapy and combination.
RIF/AMK			0 (0/1)	Not better than monotherapy
IMP/AMK			0 (0/1)	Not better than monotherapy
<b>Montero A, 2004 [81]</b>				
IMP/RIF	Mouse pneumonia model	Survival, sterilization of cultures, bacterial loads	50 (1/2)	Strain D: No differences compared to monotherapy in the mouse model. Strain E: Significantly reduced lung bacterial counts, no significant reduction of bacteraemia, similar survival (100% with the combination + 100% with RIF monotherapy).

#### 4.8 Proportion of synergy and assessment of clinical relevance of observed synergy in other methods (study level data)

Study-combinations	Method	Synergy % (n/N)	Synergy at concentrations $\leq$ breakpoints % (n/N)	Synergy at concentrations $>$ breakpoints % (n/N)	Synergy but unclear if at concentration $\leq$ breakpoints % (n/N)	Concentrations at which synergy was evaluated
<b>Limsrivanichakorn S, 2020 [7]</b>						
CFS/MXF	E-test fixed ratio method	2.5 (2/80)	0 (0/80)	0 (0/80)	2.5 (2/80)	Unclear at which concentration synergy was present
<b>Rodriguez CH, 2020 [11]</b>						
SUL/AVI	Agar dilution	92 (35/38)	92 (35/38)	0 (0/38)	0 (0/38)	Avibactam at a fixed concentration of 4mg/L reduced the MIC of SUL to $\leq$ 4mg/L in 35 of the 38 eligible isolates.
<b>Gaudereto JJ, 2019 [12]</b>						
CZA/MEM	DDST	1.8 (2/11)	0 (0/11)	0 (0/11)	1.8 (2/11)	
<b>Shinohara DR, 2019 [22]</b>						
PMB/VAN	Agar/disk	100 (3/3)	100 (3/3)	0 (0/3)	0 (0/3)	Agar containing CST at 0.5 x MIC (8, 8 and 4 mg/L)
PMB/VAN	Agar/gradient	100 (3/3)	100 (3/3)	0 (0/3)	0 (0/3)	
<b>Madadi-Goli N, 2017 [29]</b>						
TGC/LVX	Fixed-ratio E-test method	0 (0/7)	NA	NA	NA	No synergy
SAM/LVX		100 (7/7)	71 (5/7)	29 (2/7)	0 (0/7)	Combination MICs: 3/3, 4/4, 4/4, 4/4, 4/4, 6/6, 6/6 mg/L

Study-combinations	Method	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
SAM/TGC		0 (0/7)	NA	NA	NA	No synergy
<b>Bae S, 2016 [32]</b>						MCBT conducted at concentrations equal to the breakpoints of resistance; concentrations: CST at 2 mg/L, SAM at 16/8 mg/L, AMK at 16 mg/L, AZM at 4 mg/L, ATM at 16 mg/L, CAZ at 16 mg/L, MEM at 8 mg/L, RIF at 2 mg/L, TGC at 2 mg/L, SXT at 4/76 mg/L, VAN at 4 mg/L, and TEC at 16 mg/L.
SAM/RIF	MCBT	13 (1/8)	13 (1/8)	0 (0/8)	0 (0/8)	
SAM/SXT		14 (1/7)	14 (1/7)	0 (0/7)	0 (0/7)	
SAM/TEC		13 (1/8)	13 (1/8)	0 (0/8)	0 (0/8)	
AMK/CAZ		17 (1/6)	17 (1/6)	0 (0/6)	0 (0/6)	
AMK/SXT		17 (1/6)	17 (1/6)	0 (0/6)	0 (0/6)	
AZM/CAZ		13 (1/8)	13 (1/8)	0 (0/8)	0 (0/8)	
AZM/SXT		17 (1/6)	17 (1/6)	0 (0/6)	0 (0/6)	
AZM/TEC		13 (1/8)	13 (1/8)	0 (0/8)	0 (0/8)	
ATM/CAZ		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
ATM/SXT		14 (1/7)	14 (1/7)	0 (0/7)	0 (0/7)	
ATM/TEC		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
CAZ/MEM		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
CAZ/RIF		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
CAZ/TGC		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
CAZ/SXT		14 (1/7)	14 (1/7)	0 (0/7)	0 (0/7)	
CAZ/VAN		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
MEM/RIF		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
MEM/SXT		14 (1/7)	14 (1/7)	0 (0/7)	0 (0/7)	
MEM/TEC		11 (1/9)	11 (1/9)	0 (0/9)	0 (0/9)	
RIF/SXT		14 (1/7)	14 (1/7)	0 (0/7)	0 (0/7)	
SXT/VAN		14 (1/7)	14 (1/7)	0 (0/7)	0 (0/7)	
AMK/RIF		33 (2/6)	33 (2/6)	0 (0/6)	0 (0/6)	

Study-combinations	Method	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
CAZ/TEC		22 (2/9)	22 (2/9)	0 (0/9)	0 (0/9)	
CST/RIF		100 (9/9)	100 (9/9)	0 (0/9)	0 (0/9)	
CST/TEC		100 (9/9)	100 (9/9)	0 (0/9)	0 (0/9)	
CST/VAN		89 (9/9)	89 (9/9)	0 (0/9)	0 (0/9)	
CST/MEM		89 (9/9)	89 (9/9)	0 (0/9)	0 (0/9)	
CST/ATM		89 (9/9)	89 (9/9)	0 (0/9)	0 (0/9)	
CST/CAZ		67 (6/9)	67 (6/9)	0 (0/9)	0 (0/9)	
CST/SAM		63 (5/8)	63 (5/8)	0 (0/8)	0 (0/8)	
CST/SXT		38 (3/8)	38 (3/8)	0 (0/8)	0 (0/8)	
CST/AMK		67 (4/7)	67 (4/7)	0 (0/7)	0 (0/7)	
CST/AZM		50 (4/8)	50 (4/8)	0 (0/8)	0 (0/8)	
CST/TGC		0 (0/9)	NA	NA	NA	
<b>Hong DJ, 2016 [34]</b>						
CST/MEM	Fixed-ratio E-test method	85 (35/41)	5 (2/41)	0 (0/41)	81 (33/41)	Based on reported MICs and FICIs ≤ 0.5 it was possible to confirm synergy at concentrations ≤ breakpoints in only 2 cases (with the CST/MEM combination)
CST/IMP		46 (19/41)	0 (0/41)	0 (0/41)	46 (19/41)	
CST/RIF		81 (33/41)	0 (0/41)	0 (0/41)	81 (33/41)	
<b>Yavaş S, 2016 [40]</b>						
SUL/MEM	Fixed-ratio E-test method	14 (1/7)	0 (0/7)	0 (0/7)	14 (1/7)	FICI=0.5 but MICs not reported for the specific isolate
<b>Marie MA, 2015 [43]</b>						

Study-combinations	Method	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
SUL/MEM	E-test/agar method	41 (22/54)	0 (0/54)	0 (0/54)	41 (22/54)	Exact FICIs or combination MICs not reported. Agar contained SUL or TZB at ½ x MIC.
MEM/TZB		35 (19/54)	0 (0/54)	0 (0/54)	35 (19/54)	
<b>Phee LM, 2015 [19]</b>						
CST/FA	Disk/agar method	100 (3/3)	0 (0/3)	100 (3/3)	0 (0/3)	Agar containing CST at 0.5 xMIC i.e. 256 (FA zone diameter 21.5mm), 2 (FA zone diameter 16mm) and 256 mg/L (FA zone diameter 21.5mm).
<b>Galani I, 2014 [46]</b>						
CST/DAP	E-test/agar method	0 (0/4)	NA	NA	NA	Daptomycin MIC determined by E-test in agar containing CST at 0.25 and 0.5 x MIC.
<b>Nastro M, 2014 [48]</b>						
CST/RIF	E-test/agar method	100 (4/4)	0 (0/4)	100 (4/4)	0 (0/4)	CST MIC determined by E-test in agar containing RIF at 4 mg/L.
<b>Wang Y, 2014 [52]</b>						
IMP/RIF	double-disk synergy	100 (1/1)	0 (0/1)	100 (1/1)	0 (0/1)	The sizes of the inhibition zones increased to 13.6 mm when 4 ml/L imipenem (6.2 mm) was combined with 4 mg/L of rifampicin (9.0 mm)
<b>Cetin ES, 2013 [53]</b>						
RIF/SAM	Perpendicular	0 (0/7)	NA	NA	NA	No synergy
RIF/CFS	E-test method	0 (0/7)	NA	NA	NA	

Study-combinations	Method	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
<b>Tan TY, 2011 [64]</b>						
PMB/TGC	Perpendicular E-test method	0 (0/4)	NA	NA	NA	No synergy
PMB/RIF		33 (1/3)	0 (0/3)	0 (0/3)	33 (1/3)	Clinical relevance with the perpendicular E-test method difficult to judge (not possible to estimate exact combination MICs)
TGC/RIF		33 (1/3)	0 (0/3)	0 (0/3)	33 (1/3)	
<b>Kiratisin P, 2010 [65]</b>						
CFS/DOR	Perpendicular E-test method	21 (4/19)	0 (0/19)	0 (0/19)	21 (4/19)	Clinical relevance with the perpendicular E-test method difficult to judge (not possible to estimate exact combination MICs)
DOR/DOX		0 (0/21)	NA	NA	NA	
DOR/RIF		0 (0/17)	NA	NA	NA	
DOR/NET		0 (0/21)	NA	NA	NA	
DOR/MXF		0 (0/21)	NA	NA	NA	
CFS/IMP		47 (9/19)	0 (0/19)	0 (0/19)	47 (9/19)	
IMP/DOX		0 (0/21)	NA	NA	NA	
IMP/RIF		0 (0/17)	NA	NA	NA	
IMP/NET		0 (0/21)	NA	NA	NA	
IMP/MXF		5 (1/21)	0 (0/21)	0 (0/21)	5 (1/21)	
CFS/MEM		53 (10/19)	0 (0/19)	0 (0/19)	53 (10/19)	
MEM/DOX		0 (0/21)	NA	NA	NA	
MEM/RIF		0 (0/17)	NA	NA	NA	
MEM/NET		0 (0/21)	NA	NA	NA	
MEM/MXF		0 (0/21)	NA	NA	NA	

Study-combinations	Method	Synergy % (n/N)	Synergy at concentrations ≤ breakpoints % (n/N)	Synergy at concentrations > breakpoints % (n/N)	Synergy but unclear if at concentration ≤ breakpoints % (n/N)	Concentrations at which synergy was evaluated
Lee NY, 2007 [76]						
SUL/IMP	Agar dilution	100 (4/4)	100 (4/4)	0 (0/4)	0 (0/4)	Combined MIC: 8/0.5, 8/2, 8/2, 8/2 mg/L
SUL/MEM		100 (4/4)	100 (4/4)	0 (0/4)	0 (0/4)	Combined MIC: 8/1, 8/4, 8/4, 8/4 mg/L

## 5 Explanations for articles excluded as irrelevant

Following a reviewer's suggestion, reasons for retrieval of irrelevant articles by the search strategy used are discussed here.

Specifically, the search terms (synerg\* [ti] OR combin\* [ti] OR "Drug Combinations"[Mesh] OR "Drug Synergism"[Mesh] OR "Drug Therapy, Combination"[Mesh]), resulted in retrieval of the following types of non-relevant articles:

- 1) Irrelevant articles containing the term "synerg\*" in the title, e.g.
  - a. Articles evaluating synergistic interactions between different bacterial species (e.g. PMID: 25467269)
  - b. "Synergistic effect of thermophilic temperature and biosurfactant produced by *Acinetobacter calcoaceticus* BU03 on the biodegradation of phenanthrene in bioslurry system." (PMID: 21530078)
  - c. "Distinct effector-binding sites enable synergistic transcriptional activation by BenM, a LysR-type regulator." (PMID: 17291527)
- 2) Irrelevant articles containing the term "combin\*" in the title, e.g.
  - a. "Combined microbial degradation of crude oil under alkaline conditions by *Acinetobacter baumannii* and *Talaromyces* sp." (PMID: 33485133)
  - b. "Combined Effects Of Low Incubation Temperature, Minimal Growth Medium, And Low Hydrodynamics Optimize *Acinetobacter baumannii* Biofilm Formation" (PMID: 31814741)
- 3) Articles evaluating beta-lactam/ beta-lactamase combinations (e.g. PMID: 27312582)
- 4) Articles evaluating the combination trimethoprim/sulfamethoxazole (e.g. PMID: 31427295)
- 5) Articles evaluating the effect of combination therapy on metabolomics (e.g. PMID: 33387481)
- 6) Articles evaluating the effect of combination therapy on persistence (e.g. PMID: 31818819)

## 6 List of potentially relevant non-English articles excluded

### Chinese:

- 1) Mao HB, He M, He SN. [Significance of Lipopolysaccharide Lipid A Gene Mutation of Extensively Drug-resistant *Acinetobacter baumannii* on Polymyxin Resistance and Its Influence on Treatment]. **Sichuan Da Xue Xue Bao Yi Xue Ban**. 2021 Jan;52(1):124-128. doi: 10.12182/20210160208.
- 2) Lu Y, Zhang Y, Zhou H, Yu F, Sun S, Rui Y. [Combined drug sensitivity test of 50 strains of extensively drug-resistant *Acinetobacter baumannii*]. **Nan Fang Yi Ke Da Xue Xue Bao**. 2014 Nov;34(11):1697-701.
- 3) Zhao C, Xie W, Zhang W, Ye Z, Wu H. [Mechanism of drug resistance of carbapenems-resistant *Acinetobacter baumannii* and the application of a combination of drugs in vitro]. **Zhonghua Shao Shang Za Zhi**. 2014 Apr;30(2):166-70.
- 4) Ai Y, Dou SS, Lu SJ. Study on in vitro drug sensitivity of minocycline combined with 11 antibiotics against Multidrug resistant *Acinetobacter baumannii*. **Chinese Journal of New Drugs**. 2018 - Volume 27, Issue 6, pp. 702-707
- 5) Ke Q, Lü Y, Wang F. In vitro activity of meropenem in combination with sulbactam or cefoperazone-sulbactam against multidrug resistant *acinetobacter baumannii*. **Chinese Journal of Infection and Chemotherapy**. 2015 - Volume 15, Issue 6, pp. 548-551
- 6) Bai Y, Sun Y, Wang J, Liu X, Wen K, Niu H, Cao J, Tang MJ, Wang R. In vitro antibacterial activity of colistin in combination with other antibacterials against the 73 strains of multidrug-resistant *acinetobacter baumannii*. **Chinese Pharmaceutical Journal**. 2015 - Volume 50, Issue 5, pp. 427-430
- 7) Wang TS, Su JR. Combined antimicrobial susceptibility test against pan-drug-resistant *Acinetobacter baumannii* with E-test and microdilution checkerboard assay. **Chinese Journal of Microbiology and Immunology (China)**, 2013 - Volume 33, Issue 2, pp. 144-147
- 8) Wang TS, Su JR. Different activities of antimicrobial combinations against multidrug resistant *Acinetobacter baumannii* in vitro. **Chinese Journal of Microbiology and Immunology (China)**. 2011 - Volume 31, Issue 10, pp. 898-902
- 9) Xie F, Ding YJ, Zhou SD. Effect of two antibiotics combination on multi-drug resistant *acinetobacter calcoaceticus-baumannii*. **Chinese Pharmaceutical Journal**. 2010 - Volume 45, Issue 6, pp. 476-478

### Turkish:

- 1) Akyüz S, Parlak M, Güdücüoğlu H. [In-vitro Activity of Ceftolozane-Tazobactam in Combination with Various Antibiotics Against Multidrug-resistant *Acinetobacter baumannii* Isolated from Intensive Care Patients]. **Mikrobiyol Bul**. 2020 Jan;54(1):154-162. doi: 10.5578/mb.68981.
- 2) Zarakolu P, Ayaz ÇM, Metan G. [Various antibiotic combinations against carbapenem resistant *Acinetobacter baumannii* infections and in vitro synergy test results (2002-2016)]. **Mikrobiyol Bul**. 2018 Apr;52(2):190-197. doi: 10.5578/mb.61903.

- 3) Çetinkol Y, Telli M, Altunçekiç Yıldırım A, Çalgın MK. [Evaluation of the efficacy of colistin/sulbactam combination on carbapenem-resistant *Acinetobacter baumannii* strains]. **Mikrobiyol Bul.** 2016 Jul;50(3):460-5. doi: 10.5578/mb.26289.
- 4) Turk Dagi H, Kus H, Arslan U, Tuncer I. [In vitro synergistic activity of sulbactam in combination with imipenem, meropenem and cefoperazone against carbapenem-resistant *Acinetobacter baumannii* isolates]. **Mikrobiyol Bul.** 2014 Apr;48(2):311-5. doi: 10.5578/mb.7104.
- 5) Cıkman A, Ceylan MR, Parlak M, Karahocagil MK, Berktaş M. [Evaluation of Colistin-Ampicillin/Sulbactam Combination Efficacy in Imipenem-Resistant *Acinetobacter baumannii* Strains]. **Mikrobiyol Bul.** 2013 Jan;47(1):147-51. doi: 10.5578/mb.4523.
- 6) Ozseven AG, Sesli Çetin E, Ozseven L. [Do different interpretative methods used for evaluation of checkerboard synergy test affect the results?]. **Mikrobiyol Bul.** 2012 Jul;46(3):410-20.

#### **French:**

- 1) Elkhaili H, Pompei D, Linger L, Kamili N, Monteil H, Jehl F. [Kinetics of bactericidal activity of cefepime and ceftiofime alone or combined with gentamicin, amikacin or ciprofloxacin against *Acinetobacter baumannii*, *Stenotrophomonas maltophilia* and *Enterobacter cloacae* hyperproductive in cephalosporinase]. **Pathol Biol (Paris).** 1996 May;44(5):367-73.
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- 3) Le Noc P, Croize J, Bryskier A, Le Noc D. [In vitro antibacterial activity of ceftiofime in combination with 4 aminoglycosides and 2 fluoroquinolones]. **Pathol Biol (Paris).** 1988 Jun;36(5 Pt 2):762-7.
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#### **Korean:**

- 1) Sung H, Choi SJ, Yoo S, Kim MN. [In vitro antimicrobial synergy against imipenem-resistant *Acinetobacter baumannii*]. **Korean J Lab Med.** 2007 Apr;27(2):111-7. doi: 10.3343/kjlm.2007.27.2.111.
- 2) Hang JJ, Kim MN, Lee K, Hong SB, Lim CM, Koh Y. The comparative efficacy of colistin monotherapy and combination therapy based on in vitro antimicrobial synergy in ventilator-associated pneumonia caused by multi-drug resistant *Acinetobacter baumannii*. **Tuberculosis and Respiratory Diseases.** 2009 - Volume 67, Issue 3, pp. 212-220

## Japanese:

- 1) Deguchi K. [Investigation in vitro synergism on ampicillin with cloxacillin and dibekacin against glucose non-fermenting gram-negative bacilli and Serratia (author's transl)]. **Jpn J Antibiot.** 1978 Oct;31(10):610-3.

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