AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Gram-negative Surveillance Outcome Program (GnSOP)

Blood stream infection report

2022

(Final report)

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Contents

Key findings

- From 1 January 2022 to 31 December 2022, a total of 9,739 episodes of gram-negative bacteraemia were reported, mostly *Enterobacterales* (90.1%), with some *Pseudomonas aeruginosa* (8.6%) and *Acinetobacte*r (1.3%). Of the *Enterobacterales*, three genera – *Escherichia* (60.1%), *Klebsiella* (20.9%) and *Enterobacter* (5.7%) – contributed 86.7% of all *Enterobacterales* bacteraemias.
- The all-cause 30-day mortality rate for gram-negative bacteraemia was 13.0% (12.5% for *Enterobacterales*, 18.4% for *P. aeruginosa*, and 13.0% for *Acinetobacter* species).
- Urinary tract infection was the most frequent source of sepsis or clinical manifestation (*Enterobacterales* 45.1%; *P. aeruginosa* 29.8%). For *Enterobacterales*, device related urinary tract infections were more common with hospital-onset (HO) than community-onset (CO) episodes (23.6% versus 9.4%, $P < 0.01$).
- Of *E. coli* isolates causing CO bacteraemia, which accounted for 82.5% of all *E. coli* bacteraemia cases, 12.1% were ceftriaxone resistant.
- In 2022, 14.4% of *E. coli* (CO 13.8%, HO 17.2%) and 7.5% of *Klebsiella pneumoniae* complex isolates (CO 5.3%, HO 12.7%) resistant to extended-spectrum β-lactams (ESBL phenotype).
- Fluoroquinolone resistance in *E. coli* increased to 13.7% in 2022 (2021 12.3%, up 11.1%), most notably in New South Wales (16.4%, up from 12.1% in 2021) and South Australia (14.6%, up from 8.5% in 2021).
- Fluoroquinolone resistance is commonly linked to cephalosporin resistance caused by ESBLs of the CTX-M type. A little over two-thirds (255/358, 71.2%) of *E. coli* that were ciprofloxacin resistant and had confirmed β-lactamase gene(s) belonged to ST131 (198, 55.3%) or ST1193 (n = 57, 15.9%).
- Rates of carbapenemase-producing *Enterobacterales* (CPE) in bacteraemic isolates remain low (0.3% overall, mostly carrying $bla_{\text{IMP-4}}$). For *Enterobacter cloacae* complex the figure is higher at 2.1% overall (CO 0.8%, HO 3.5%).
- *mcr-9* or *mcr-10* were the only *mcr* genes detected. Half (8/18, 50.0%) were not linked to other resistance mechanisms.
- The impact of COVID-19 on the reduction in antimicrobial resistance in 2021 remains unclear, as a number of contributing factors may be involved.

1. Background and objectives

This seventh report on the Gram-negative Surveillance Outcome Programs operated by the Australian Group on Antimicrobial Resistance (AGAR) presents analyses of antimicrobial resistance (AMR) associated with episodes of bacteraemia (blood stream infection) reported by 55 participating Australian public and private laboratories across Australia in 2022.

AGAR currently focuses on bloodstream infections and has three major programs: the Gram-negative Surveillance Outcome Program (GnSOP), the Australian Enterococcal Surveillance Outcome Program (AESOP) and the Australian Staphylococcal Surveillance Outcome Program (ASSOP). AGAR's focus on bacteraemia allows examination of laboratory-confirmed, invasive infections and comparison of rates over time for hospitals, states and territories. AGAR compares Australian data with the European Antimicrobial Resistance Surveillance Network, enabling benchmarking and trend projections. AGAR has collected ongoing data on the prevalence of antimicrobial resistance in Australia over a long period using standardised methods.

The 55 hospitals across Australia that currently contribute to AGAR, including six private institutions, are listed in Table 1. In 2022, one hospital from Queensland was only able to participate for Quarter one, and three additional hospitals from New South Wales (*n* = 2) and Queensland (*n* = 1) contributed data.

AGAR publishes detailed annual reports on each program on its website (www.agargroup.org.au), and also in the Communicable Diseases Intelligence (CDI) journal.

Table 1: Hospitals that contributed to AGAR, by state and territory, AGAR, 2022

State or territory	Hospital
New South Wales	Children's Hospital Westmead
	Concord Repatriation General Hospital
	Gosford Hospital
	John Hunter Hospital
	Liverpool Hospital
	Nepean Hospital
	Prince of Wales Hospital
	Royal North Shore Hospital
	Royal Prince Alfred Hospital
	St Vincent's Hospital, Sydney*
	Sydney Children's Hospital
	Westmead Hospital
	Wollongong Hospital
Victoria	Alfred Hospital
	Austin Hospital (Austin Health)
	Monash Children's Hospital†
	Monash Medical Centre (Dandenong Hospital)†
	Monash Medical Centre (Monash Health)
	Royal Melbourne Hospital
	Royal Women's and Children's Hospital
	St Vincent's Hospital*
Queensland	Gold Coast Hospital
	Mater Private Hospital Townsville§, #
	Prince Charles Hospital**
	Princess Alexandra Hospital**
	Queensland Children's Hospital**
	Royal Brisbane and Women's Hospital
	Greenslopes Private Hospital§, #
South Australia	Flinders Medical Centre
	Royal Adelaide Hospital
	Women's and Children's Hospital††
Western Australia	Fiona Stanley Hospital
	Joondalup Hospital*
	North-west regional Western Australia (Broome, Derby, Fitzroy Crossing, Halls Creek, Karratha, Kununurra, Newman, Onslow, Paraburdoo, Port Hedland, Roebourne, Tom Price, Wyndham) §§
	Perth Children's Hospital§§
	Royal Perth Hospital##
	Sir Charles Gairdner Hospital
	St John of God Hospital, Murdoch#
Tasmania	Launceston General Hospital
	Royal Hobart Hospital
Northern Territory	Alice Springs Hospital
	Royal Darwin Hospital
Australian Capital Territory	Canberra Hospital

* Public/Private hospital
† Microbiology services provided by Monash Medical Centre (Monash Health)
§ Microbiology services provided by Sullivan Nicolaides Pathology
# Private hospital

** Microbiology services provided by Pathology Queensland Central Laboratory
†† Microbiology services provided by SA Pathology, Royal Adelaide Hospital
§§ Microbiology services provided by PathWest Laboratory Medicine WA, Queen Elizabeth II Medical Centre
Microbiology services provided by PathWest Laboratory Medicine WA, Fiona Stanley Hospital

Note: In 2022, the Prince Alfred Hospital (NSW) and Queensland Childrens Hospital recommenced the survey. Gosford Hospital (NSW), Prince of Wales Hospital (NSW), and the Mater Private Hospital Townsville (Qld) participated for the first time.

1.1. Gram-negative Surveillance Outcome Program

AGAR began surveillance of the key gram-negative pathogens *E. coli* and *Klebsiella* species in 1992. Surveys were conducted every two years until 2008, when annual surveys commenced, alternating between community-onset (CO) and hospital-onset (HO) infections.

E. coli is the most common cause of CO urinary tract infections, whereas *Klebsiella* species are less common but are known to harbour important resistance mechanisms. In 2004, another genus of gram-negative pathogens in which resistance can be of clinical importance – *Enterobacter* – was added. *Enterobacter* species are less common in the community, but of high importance because of their intrinsic resistance to first-line antimicrobials used in this setting. Taken together, the three groups of species surveyed are valuable sentinels for multidrug resistance and emerging resistance in enteric gram-negative bacilli. In 2013, AGAR initiated the yearly *Enterobacterales* Sepsis Outcome Program (EnSOP), which focused on the prospective collection of resistance and demographic data on all isolates from patients with documented bacteraemia. In 2015, *Pseudomonas aeruginosa* and *Acinetobacter* species were added, and the program evolved into the Gram-negative Sepsis Outcome Program (GnSOP), since renamed the Gram-negative Surveillance Outcome Program. The term “Sepsis” in the program was changed in 2021 to “Surveillance” to better reflect AGAR’s surveillance of episodes of bacteraemia rather than sepsis.

Resistance to β-lactams due to β-lactamases is of particular interest, especially extended-spectrum β-lactamases (ESBLs), which inactivate the third-generation cephalosporins. Other resistances of interest are to agents that are important for treatment of these serious infections, such as gentamicin and ciprofloxacin, and to reserve agents such as meropenem.

The objectives of the 2022 surveillance program were to:

- Monitor resistance in *Enterobacterales*, *P. aeruginosa* and *Acinetobacter* species isolated from blood cultures taken from patients presenting to the hospital or already in hospital.
- Study the extent of co-resistance and multidrug resistance in the major species.
- Detect emerging resistance to reserve agents such as carbapenems and colistin.
- Examine the molecular basis of resistance to third-generation cephalosporins, quinolones and carbapenems.

2. Summary of methods

Fifty-five hospitals, covering state and territory of Australia, were enrolled in the 2022 AGAR programs. The 33 laboratories servicing the hospitals participating in AGAR collected all isolates from unique patient episodes of bacteraemia for ASSOP and AESOP, and either all or up to 200 isolates for GnSOP, from 1 January 2022 to 31 December 2022. Approval to conduct the prospective data collection, including de-identified demographic data, was given by the research ethics committees associated with each participating hospital.

In patients with more than one isolate, a new episode was defined as a new positive blood culture more than two weeks after the initial positive culture. An episode was defined as community onset (CO) if the first positive blood culture was collected 48 h or less after admission, and as hospital onset (HO) if collected more than 48 h after admission.

AGAR meets the data security requirements of the Antimicrobial Use and Resistance in Australia (AURA) Surveillance System. These arrangements ensure that data conform to appropriate standards of data management and quality, and that data are used in accordance with appropriate approvals. The Australian Society for Antimicrobials (ASA), as data custodian for AGAR data, is responsible for:

- Approving access to, and use of, AGAR data.
- Ensuring that AGAR data are protected from unauthorised access, alteration or loss.
- Ensuring compliance with relevant legislation and policies regarding administration, quality assurance, and data access and release.

2.1. Data fields

Laboratory data collected for each episode included an accession number, the date of collection, the organism isolated (genus and species), and the antimicrobial susceptibility test results (minimum inhibitory concentrations) for each species. The patient's date of birth, sex and postcode of residence were also provided. If the patient was admitted to hospital, the dates of admission and discharge were recorded. Depending on the level of participation in AGAR, limited clinical and outcome data were also provided. These included the principal clinical manifestation, device related infection (yes or no), and the outcome (died, all-cause or survived) at seven and 30 days (see Appendix A).

2.2. Species identification

Isolates were identified to species level, if possible, by the routine method used at each institution, either the Vitek® or BD Phoenix™ automated Microbiology systems, and if available, matrix assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry (Bruker MALDI biotyper® or Vitek® MS).

For this report, the following speciescomplexes are defined:

- *Acinetobacter baumannii* complex comprises *A. calcoaceticus*, *A. baumannii*, *A. dijkshoorniae*, *A. nosocomialis*, *A. pittii*, and *A. seifertii*
- *Enterobacter cloacae* complex comprises *E. cloacae, E. asburiae, E. bugandensis, E. kobei, E. ludwigii, E. hormaechei* and *E. nimipressuralis*
- *Klebsiella pneumoniae* complex comprises *K. pneumoniae*, *K. quasipneumoniae* and *K. variicola*
- *Citrobacter freundii* complex comprises *C. freundii, C. braakii, C. gillenii, C. murliniae, C. rodenticum, C. sedlakii, C. werkmanii* and *C. youngae*.

Klebsiella aerogenes was previously known as *Enterobacter aerogenes*.

2.3. Susceptibility testing

Susceptibility testing of isolates is described in Appendix B. The analysis used breakpoints from the Clinical and Laboratory Standards Institute (CLSI) M100–Ed33[1] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v13.0.[2]

2.4. Whole genome sequencing

All isolates fitting the following criteria were referred to a central laboratory (Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research). *E. coli*, *Klebsiella* spp., *Proteus* spp. and *Salmonella* spp. with a ceftazidime or ceftriaxone minimum inhibitory concentration (MIC) >1 mg/L, or cefoxitin MIC >8 mg/L; any other *Enterobacterales* with cefepime MIC >1 mg/L; *Salmonella* spp. with ciprofloxacin MIC > 0.25 mg/L; all *Enterobacterales* with meropenem MIC >0.25 mg/L; all *Acinetobacter* species or *P. aeruginosa* with meropenem MIC ≥ 8 mg/L; all isolates with amikacin MIC >32 mg/L, and all isolates with colistin MIC > 4 mg/L Whole genome sequencing (WGS) was performed on all referred isolates using the Illumina NextSeq™ 500 platform (Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, Centre for Infectious Diseases and Microbiology and Microbiology Laboratory Services [CIDMLS], Institute of Clinical Pathology and Medical Research [ICPMR], Westmead Hospital) Data were analysed using a modified version of the Nullarbor bioinformatic pipeline.[3]

2.5. Statistical analysis

Confidence intervals of proportions, Fisher's exact test for categorical variables, and chi-square test for trend were calculated, if appropriate, using GraphPad Prism version 10.0.0 for Windows (GraphPad Software, La Jolla, California).

3. Results

3.1. Isolates recovered

During 2022, a total of 9,739 gram-negative bloodstream isolates (23 genera, 60 species/complexes) were reported from 55 participating hospitals.

Enterobacterales accounted for 90.1%, followed by *P. aeruginosa* (8.6%) and *Acinetobacter* (1.3%). Of the *Enterobacterales*, three genera – *Escherichia* (60.1%), *Klebsiella* (20.9%) and *Enterobacter* (5.7%) – contributed 86.7% of all isolates. Overall, the top 10 ranked species were *E. coli* (54.1%), *K. pneumoniae* complex (14.3%), *P. aeruginosa* (8.6%), *E. cloacae* complex (4.9%), *Proteus mirabilis* (3.3%), *K. oxytoca* (3.0%), *Serratia marcescens* (2.6%), *K. aerogenes* (1.3%), *Morganella morganii* (1.1%), *Salmonella* species (non-typhoidal) and *Citrobacter freundii* complex (1.0%, equal rank). These 11 species contributed 95.5% of all isolates (Table 2).

The proportion of isolates from paediatric patients (<18 years of age) was 4.3% (*n* = 423; *Enterobacterales n* = 375, *P. aeruginosa n* = 38 and *Acinetobacter* spp. *n* = 10). *Enterobacter cloacae* complex and *Salmonella* spp. episodes were more common among paediatric patients than adults (8.4% versus 4.8% and 11.9% versus 0.9%, respectively) (data not shown).

Table 2: Number of each species recovered, by state and territory, AGAR, 2022

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Gram-negative species*	3,210	1,960	1,398	785	1,325	426	296	339	9,739
Acinetobacter	23	25	26	12	15	9	12	4	126
Acinetobacter baumannii complex	10	18	22	3	4	3	9	1	70
Acinetobacter lwoffii	4	0	0	4	3	2	2	1	16
Acinetobacter species†	2	6	0	1	5	1	1	0	16
Acinetobacter ursingii	5	0	2	3	1	0	0	1	12
Acinetobacter radioresistens	1	0	0	1	0	2	0	1	5
Acinetobacter johnsonii	0	0	1	0	0	1	0	0	2
Acinetobacter guillouiae	0	0	0	0	1	0	0	0	1
Acinetobacter gyllenbergii	0	0	1	0	0	0	0	0	1
Acinetobacter haemolyticus	0	0	0	0	1	0	0	0	1
Acinetobacter junii	1	0	0	0	0	0	0	0	1
Acinetobacter soli	0	1	0	0	0	0	0	0	1
Enterobacterales	2,915	1,789	1,218	697	1,197	381	271	305	8,773
Escherichia coli	1,773	1,056	712	441	696	231	174	190	5,273
Klebsiella pneumoniae complex	446	283	227	83	212	50	52	42	1,395
Enterobacter cloacae complex	170	98	88	23	52	19	9	18	477
Proteus mirabilis	113	69	44	31	48	9	4	6	324
Klebsiella oxytoca	87	78	30	28	43	16	5	10	297
Serratia marcescens	105	52	36	7	35	8	4	10	257
Klebsiella aerogenes	39	30	15	13	18	7	3	5	130
Morganella morganii	49	19	12	11	9	7	2	1	110
Citrobacter freundii complex	33	20	7	7	20	5	0	5	97
Salmonella species (non-typhoidal)	21	16	17	0	18	12	10	3	97
Citrobacter koseri	26	12	9	8	14	4	4	3	80
Salmonella species (typhoidal)	9	16	2	1	5	1	1	3	38
Raoultella ornithinolytica	9	3	2	1	7	3	0	3	28
Enterobacter species†	0	0	0	23	0	0	0	0	23
Providencia rettgeri	4	7	3	3	1	0	0	1	19

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Providencia stuartii	5	3	1	0	3	0	1	0	13
Pantoea agglomerans	1	4	1	1	3	2	0	0	12
Proteus hauseri	6	2	0	1	1	0	1	0	11
Hafnia alvei	1	2	2	1	4	0	0	0	10
Klebsiella species†	2	1	1	3	0	1	0	0	8
Pantoea septica	2	3	0	0	0	1	0	2	8
Pantoea species†	1	3	1	0	2	1	0	0	8
Raoultella planticola	2	2	1	0	0	2	0	0	7
Proteus vulgaris	2	1	0	0	2	0	0	1	6
Serratia liquefaciens complex	2	2	0	1	0	1	0	0	6
Raoultella species†	0	3	0	1	0	0	0	0	4
Serratia species†	0	0	0	4	0	0	0	0	4
Citrobacter amalonaticus	1	1	0	0	1	0	0	0	3
Cronobacter sakazakii	0	0	2	0	1	0	0	0	3
Citrobacter species†	0	0	0	2	0	0	0	0	2
Escherichia hermannii	2	0	0	0	0	0	0	0	2
Kluyvera ascorbata	1	0	1	0	0	0	0	0	2
Pluralibacter gergoviae	1	0	1	0	0	0	0	0	2
Proteus penneri	0	1	1	0	0	0	0	0	2
Serratia rubidaea	0	0	0	0	1	0	0	1	2
Citrobacter farmeri	0	0	0	0	0	0	0	1	1
Enterobacter cancerogenus	1	0	0	0	0	0	0	0	1
Escherichia vulneris	1	0	0	0	0	0	0	0	1
Leclercia adecarboxylata	0	0	1	0	0	0	0	0	1
Lelliottia amnigena	0	1	0	0	0	0	0	0	1
Pantoea dispersa	0	0	0	1	0	0	0	0	1
Plesiomonas shigelloides	0	1	0	0	0	0	0	0	1
Proteus species†	0	0	0	1	0	0	0	0	1
Serratia ficaria	0	0	1	0	0	0	0	0	1
Shigella flexneri	0	0	0	0	0	0	1	0	1
Yersinia enterocolitica	0	0	0	0	1	0	0	0	1
Yersinia pseudotuberculosis	0	0	0	0	0	1	0	0	1
Yokenella regensburgei	0	0	0	1	0	0	0	0	1
Pseudomonas aeruginosa	272	146	154	76	113	36	13	30	840

* *Acinetobacter*, *Enterobacterales* and *Pseudomonas aeruginosa*
† Species not determined

Note: *Acinetobacter baumannii* complex includes *A. nosocomalis* (*n* = 6) and *A. pittii* (*n* = 5); *Citrobacter freundi* complex includes *C. braakii* (*n* = 7) and *C. youngae* (*n* = 2); *Enterobacter cloacae* complex includes *E. asburiae* (*n* = 5), *E. bugandensis* (*n* = 5), *E. hormaechei* (*n* = 5), *E. ludwigii* (*n* = 1); *Klebsiella pneumoniae* complex *K. variicola* (*n* = 121) and *K. quasipneumoniae* (*n* = 3).

3.2. Place of onset of bacteraemia

Almost all patients with gram-negative bacteraemia were admitted to hospital (9,562, 98.2%).

Information on place of onset of bacteraemia was available for all gram-negative episodes (Table 3).

For gram-negative species, 74.6% of all episodes were CO, with differences between *Enterobacterales* (76.5%), *Acinetobacter* species (66.7%) and *P. aeruginosa* (56.4%). The proportion of *Enterobacterales* that were CO was significantly lower in paediatric patients (67.5%, 253/375) than adults (76.9%, 6,455/8,398) ($P < 0.01$), most notable for *E. coli* (paediatrics 74.0%, adults 82.8%) and *K. pneumoniae* complex isolates (paediatrics 40.0%, adults 70.4%) (data not shown).

Table 3: Species recovered from patients with bacteraemia, by place of onset, AGAR, 2022

Organism	Community onset % (*n*)	Hospital onset % (*n*)	Total, 100%
Gram-negative species*	74.6 (7,266)	25.4 (2,473)	9,739
Acinetobacter	66.7 (84)	33.3 (42)	126
Acinetobacter baumannii complex	58.6 (41)	41.4 (29)	70
Acinetobacter lwoffii	81.3 (13)	18.8 (3)	16
Acinetobacter species†	75.0 (12)	25.0 (4)	16
Acinetobacter ursingii	66.7 (8)	33.3 (4)	12
Other *Acinetobacter* species (*n* = 7)	83.3 (10)	16.7 (2)	12
Enterobacterales	76.5 (6,708)	23.5 (2,065)	8,773
Escherichia coli	82.5 (4,349)	17.5 (924)	5,273
Klebsiella pneumoniae complex	69.4 (968)	30.6 (427)	1,395
Enterobacter cloacae complex	52.4 (250)	47.6 (227)	477
Proteus mirabilis	82.4 (267)	17.6 (57)	324
Klebsiella oxytoca	66.0 (196)	34.0 (101)	297
Serratia marcescens	44.4 (114)	55.6 (143)	257
Klebsiella aerogenes	60.8 (79)	39.2 (51)	130
Morganella morganii	70.9 (78)	29.1 (32)	110
Citrobacter freundii complex	74.2 (72)	25.8 (25)	97
Salmonella species (non-typhoidal)	91.8 (89)	8.2 (8)	97
Citrobacter koseri	82.5 (66)	17.5 (14)	80
Salmonella species (typhoidal)	94.7 (36)	5.3 (2)	38
Raoultella ornithinolytica	78.6 (22)	21.4 (6)	28
Enterobacter species†	82.6 (19)	17.4 (4)	23
Providencia rettgeri	84.2 (16)	15.8 (3)	19
Providencia stuartii	92.3 (12)	7.7 (1)	13
Pantoea agglomerans	66.7 (8)	33.3 (4)	12
Proteus hauseri	90.9 (10)	9.1 (1)	11
Hafnia alvei	70.0 (7)	30.0 (3)	10
Other *Enterobacterales* species (*n* = 29)	61.0 (50)	39.0 (32)	82
Pseudomonas aeruginosa	56.4 (474)	43.6 (366)	840

* *Acinetobacter*, *Enterobacterales* and *Pseudomonas aeruginosa*
† Species not determined

Note: *Acinetobacter baumannii* complex includes *A. nosocomalis* (*n* = 6) and *A. pittii* (*n* = 5); *Citrobacter freundi* complex includes *C. braakii* (*n* = 7) and *C. youngae* (*n* = 2); *Enterobacter cloacae* complex includes *E. asburiae* (*n* = 5), *E. bugandensis* (*n* = 5), *E. hormaechei* (*n* = 5), *E. ludwigii* (*n* = 1); *Klebsiella pneumoniae* complex *K. variicola* (*n* = 121) and *K. quasipneumoniae* (*n* = 3).

3.3. Onset versus 30-day all-cause mortality

Information on 30-day all-cause mortality, when place of onset was known (CO vs HO), was available for 7,052 (72.4%) episodes involving gram-negative species.

The 30-day all-cause mortality rate was 12.5% (789/6,318) for *Enterobacterales*, 18.4% (115/626) for *P. aeruginosa* and 13.0% (14/108) for *Acinetobacter*. There was no significant difference in 30-day all-cause mortality between CO and HO episodes (Table 4). There was a significant difference in 30-day all-cause mortality between paediatric patients (3.7%, 11/295) and adults (12.9%, 778/6,023) for *Enterobacterales* ($P < 0.01$). The 30-day all-cause mortality among persons aged 90 days or less with episodes of *Enterobacterales* was 7.6% (8/105).

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), AGAR, 2022

Organism	Community onset		Hospital onset		Total	
	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Gram-negative species*	5,178	12.4 (642)	1,874	14.7 (276)	7,052	13.0 (918)
Acinetobacter	71	15.5 (11)	37	8.1 (3)	108	13.0 (14)
Acinetobacter baumannii complex	32	12.5 (4)	24	12.5 (3)	56	12.5 (7)
Acinetobacter species†	12	16.7 (2)	4	0.0 (0)	16	12.5 (2)
Acinetobacter lwoffii	10	30.0 (3)	3	0.0 (0)	13	23.1 (3)
Acinetobacter ursingii	7	0.0 (0)	4	0.0 (0)	11	0.0 (0)
Other *Acinetobacter* species (*n* = 7)	10	20.0 (2)	2	0.0 (0)	12	16.7 (2)
Enterobacterales	4,758	11.9 (565)	1,560	14.4 (224)	6,318	12.5 (789)
Escherichia coli	2,998	11.1 (334)	690	13.3 (92)	3,688	11.6 (426)
Klebsiella pneumoniae complex	707	12.2 (86)	319	13.8 (44)	1,026	12.7 (130)
Enterobacter cloacae complex	188	10.1 (19)	180	16.1 (29)	368	13.0 (48)
Proteus mirabilis	203	20.7 (42)	44	18.2 (8)	247	20.2 (50)
Klebsiella oxytoca	143	11.9 (17)	74	14.9 (11)	217	12.9 (28)
Serratia marcescens	83	16.9 (14)	106	12.3 (13)	189	14.3 (27)
Klebsiella aerogenes	66	16.7 (11)	36	13.9 (5)	102	15.7 (16)
Morganella morganii	58	20.7 (12)	25	24.0 (6)	83	21.7 (18)
Citrobacter freundii complex	57	15.8 (9)	22	13.6 (3)	79	15.2 (12)
Salmonella species (non-typhoidal)	58	0.0 (0)	7	0.0 (0)	65	0.0 (0)
Citrobacter koseri	48	10.4 (5)	12	25.0 (3)	60	13.3 (8)
Raoultella ornithinolytica	19	10.5 (2)	5	0.0 (0)	24	8.3 (2)
Enterobacter species†	19	5.3 (1)	4	75.0 (3)	23	17.4 (4)
Salmonella species (typhoidal)	22	0.0 (0)	0	n/a	22	0.0 (0)
Providencia rettgeri	14	21.4 (3)	2	100.0 (2)	16	31.3 (5)
Pantoea agglomerans	7	0.0 (0)	4	0.0 (0)	11	0.0 (0)
Providencia stuartii	10	20.0 (2)	0	n/a	10	20.0 (2)
Other *Enterobacterales* species (*n* = 30)	58	13.8 (8)	30	16.7 (5)	88	14.8 (13)
Pseudomonas aeruginosa	349	18.9 (66)	277	17.7 (49)	626	18.4 (115)

n/a = not applicable

* *Acinetobacter*, *Enterobacterales* and *Pseudomonas aeruginosa*
† Species not determined

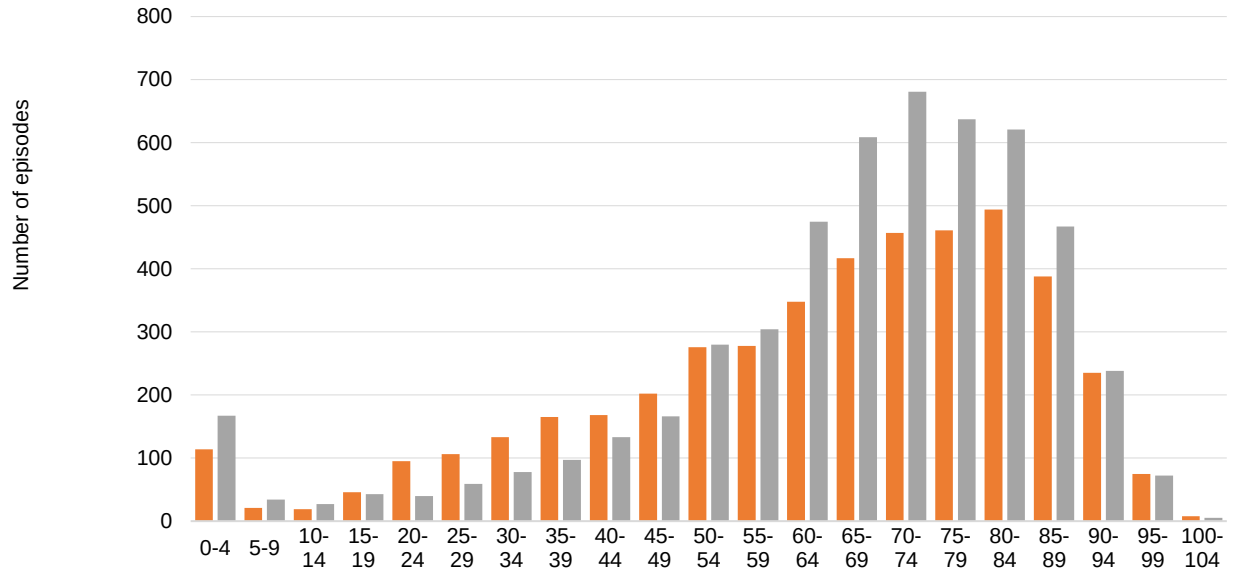
Note: *Acinetobacter baumannii* complex includes *A. nosocomalis* (*n* = 6) and *A. pittii* (*n* = 5); *Citrobacter freundi* complex includes *C. braakii* (*n* = 7) and *C. youngae* (*n* = 2); *Enterobacter cloacae* complex includes *E. asburiae* (*n* = 5), *E. bugandensis* (*n* = 5), *E. hormaechei* (*n* = 5), *E. ludwigii* (*n* = 1); *Klebsiella pneumoniae* complex *K. variicola* (*n* = 121) and *K. quasipneumoniae* (*n* = 3).

3.4. Patient age and sex

Information on age and sex was available for all patients with gram-negative bacteraemia. The proportion of males was 53.7% and females 46.3%.

Increasing age was a risk factor for bacteraemia (Figure 1); only 12.8% (1,244/9,739) of gram-negative species episodes were in patients aged less than 40 years. The proportion of patients aged 0–19 years was 4.8% (*n* = 471). Almost half (141/285, 49.5%) of the episodes in patients aged 0–4 years were from those aged 90 days or less.

Figure 1: Number of episodes of bacteraemia due to gram-negative species, by patient age group and sex, AGAR, 2022



	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	80-84	85-89	90-94	95-99	100-104
Female (n = 4,506)	114	21	19	46	95	106	133	165	168	202	276	278	348	417	457	461	494	388	235	75	8
Male (n = 5,233)	167	34	27	43	40	59	78	97	133	166	280	304	475	609	681	637	621	467	238	72	5

Note: x-axis = age range in years.

3.5. Principal clinical manifestations

The principal clinical manifestations, which represent the most likely primary site or source for the origin of the blood stream infection, are described below for patients with gram-negative bacteraemia.

The principal clinical manifestation was documented for 8,545 (87.7%) patient episodes of gram-negative bacteraemia. The most frequent clinical manifestations for episodes caused by *Enterobacterales* were urinary tract infection (45.1%) or biliary tract infection (15.0%); for *P. aeruginosa*, urinary tract infections (29.8%) or febrile neutropenia (18.4%) were the most common. For *Acinetobacter*, device-related infection without metastatic focus (23.3%) was the most common while 20.7% had no identifiable focus (Table 5).

Table 5: Principal clinical manifestation for gram-negative bacteraemia, by patient sex, AGAR, 2022

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Gram-negative species*	3,949	4,596	8,545
Acinetobacter	48	68	116
Device-related infection without metastatic focus	29.2 (14)	19.1 (13)	23.3 (27)
No identifiable focus	20.8 (10)	20.6 (14)	20.7 (24)
Skin and skin structure infection	10.4 (5)	22.1 (15)	17.2 (20)
Other clinical syndrome	14.6 (7)	19.1 (13)	17.2 (20)
Febrile neutropenia	10.4 (5)	5.9 (4)	7.8 (9)
Intra-abdominal infection other than biliary tract	4.2 (2)	4.4 (3)	4.3 (5)
Urinary tract infection	2.1 (1)	4.4 (3)	3.4 (4)
Biliary tract infection (including cholangitis)	4.2 (2)	2.9 (2)	3.4 (4)
Enterobacterales	3,629	4,046	7,675
Urinary tract infection	52.3 (1,897)	38.7 (1,565)	45.1 (3,462)
Biliary tract infection (including cholangitis)	12.9 (468)	16.9 (683)	15.0 (1,151)
Intra-abdominal infection other than biliary tract	8.7 (317)	11.5 (465)	10.2 (782)
Febrile neutropenia	8.0 (291)	10.5 (423)	9.3 (714)
No identifiable focus	7.1 (257)	7.7 (310)	7.4 (567)
Other clinical syndrome	5.0 (180)	6.9 (280)	6.0 (460)
Device-related infection without metastatic focus	3.1 (113)	3.3 (132)	3.2 (245)
Skin and skin structure infection	2.1 (76)	3.2 (128)	2.7 (204)
Osteomyelitis/septic arthritis	0.7 (24)	1.1 (43)	0.9 (67)
Device-related infection with metastatic focus	0.2 (6)	0.4 (17)	0.3 (23)
Pseudomonas aeruginosa	272	482	754
Urinary tract infection	21.7 (59)	34.4 (166)	29.8 (225)
Febrile neutropenia	19.9 (54)	17.6 (85)	18.4 (139)
Other clinical syndrome	12.1 (33)	11.6 (56)	11.8 (89)
Device-related infection without metastatic focus	9.2 (25)	10.0 (48)	9.7 (73)
No identifiable focus	10.3 (28)	8.7 (42)	9.3 (70)
Skin and skin structure infection	11.4 (31)	5.8 (28)	7.8 (59)
Intra-abdominal infection other than biliary tract	8.8 (24)	6.6 (32)	7.4 (56)
Biliary tract infection (including cholangitis)	5.9 (16)	4.1 (20)	4.8 (36)
Osteomyelitis/septic arthritis	0.4 (1)	0.8 (4)	0.7 (5)
Device-related infection with metastatic focus	0.4 (1)	0.2 (1)	0.3 (2)

* *Acinetobacter*, *Enterobacterales* and *Pseudomonas aeruginosa*

Urinary tract infection was the most frequent principal manifestation for CO episodes caused by *Enterobacterales* (51.2%) and *P. aeruginosa* (34.7%). For HO episodes, urinary tract infection (*Enterobacterales* 24.7%, *P. aeruginosa* 23.2%) and febrile neutropenia (*Enterobacterales* 22.5%, *P. aeruginosa* 24.1%) were the most common.

For *Enterobacterales* with urinary tract infection as the principal clinical manifestation, only a small proportion (388/3460, 11.2%) were regarded as a device related infection. This was higher for HO than CO episodes (CO: 285/3023, 9.4%; HO: 103/447, 23.6%, $P < 0.01$).

3.6. Length of hospital stay following bacteraemic episode

Information on length of hospital stay following bacteraemia was available for 8,894 (91.3%) episodes involving gram-negative species.

Over half (3,362/6,581, 51.1%) of patients with a CO gram-negative bacteraemia had a length of hospital stay of less than seven days. Just over one-third of patients with HO bacteraemia caused by *Acinetobacter* (14/41, 34.1%) remained in hospital for more than 30 days (Table 6).

Table 6: Length of hospital stay following gram-negative bacteraemia, by species and place of onset, AGAR, 2022

	Length of stay (days)				
Species	**<7, % (*n*)**	**7–14, % (*n*)**	**15–30, % (*n*)**	**>30, % (*n*)**	**Total**
Gram-negative species*	43.3 (3,852)	30.4 (2,708)	15.5 (1,381)	10.7 (953)	8,894
Community onset	51.1 (3,362)	30.6 (2,012)	12.2 (802)	6.2 (405)	6,581
Hospital onset	21.2 (490)	30.1 (696)	25.0 (579)	23.7 (548)	2,313
Acinetobacter	39.0 (46)	27.1 (32)	14.4 (17)	19.5 (23)	118
Community onset	50.6 (39)	32.5 (25)	5.2 (4)	11.7 (9)	77
Hospital onset	17.1 (7)	17.1 (7)	31.7 (13)	34.1 (14)	41
Enterobacterales	44.7 (3,574)	30.3 (2,427)	14.9 (1,193)	10.0 (803)	7,997
Community onset	52.1 (3,158)	30.2 (1,833)	11.7 (710)	6.0 (366)	6,067
Hospital onset	21.6 (416)	30.8 (594)	25.0 (483)	22.6 (437)	1,930
Escherichia coli	49.2 (2,357)	29.1 (1,392)	13.4 (641)	8.4 (400)	4,790
Community onset	55.1 (2,165)	28.8 (1,132)	10.7 (419)	5.3 (210)	3,926
Hospital onset	22.2 (192)	30.1 (260)	25.7 (222)	22.0 (190)	864
Klebsiella pneumoniae complex	35.7 (452)	33.6 (426)	18.2 (231)	12.4 (157)	1,266
Community onset	43.2 (376)	34.0 (296)	15.1 (131)	7.7 (67)	870
Hospital onset	19.2 (76)	32.8 (130)	25.3 (100)	22.7 (90)	396
Enterobacter cloacae complex	32.7 (147)	34.1 (153)	19.2 (86)	14.0 (63)	449
Community onset	42.9 (99)	38.5 (89)	12.6 (29)	6.1 (14)	231
Hospital onset	22.0 (48)	29.4 (64)	26.1 (57)	22.5 (49)	218
Other *Enterobacterales* (*n* = 44)	41.4 (618)	30.6 (456)	15.8 (235)	12.3 (183)	1,492
Pseudomonas aeruginosa	29.8 (232)	32.0 (249)	22.0 (171)	16.3 (127)	779
Community onset	37.8 (165)	35.2 (154)	20.1 (88)	6.9 (30)	437
Hospital onset	19.6 (67)	27.8 (95)	24.3 (83)	28.4 (97)	342

* *Acinetobacter*, *Enterobacterales* and *Pseudomonas aeruginosa*

3.7. Susceptibility testing results

The following sections present the results of susceptibility testing in priority indicator species, and antimicrobial resistance by place of onset and multi-drug resistance. Susceptibility testing methods are described in Appendix B.

Percentages of non-susceptibility in national priority indicator species

Overall percentages of resistance or non-susceptibility in the indicator species of national priority[4] using both CLSI breakpoints and EUCAST breakpoints, are shown in Table 7. Resistance (as defined by EUCAST) to key antimicrobial groups (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) for *E. coli* and *K. pneumoniae* complex are shown by state and territory in Figures 2 and 3; respectively. Resistance of *P. aeruginosa* to key antipseudomonal agents is shown in Figure 4. Detailed resistance by state and territory can be found in Appendix C.

Table 7: Activity of antimicrobial agents tested against isolates recovered from patients with Gram-negative blood stream infections, AGAR, 2022

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Acinetobacter baumannii complex					
Piperacillin-tazobactam	59	6.8 (4)	10.2 (6)	–*	–*
Ceftriaxone	63	71.4 (45)	4.8 (3)	–*	–*
Ceftazidime	59	11.9 (7)	3.4 (2)	–*	–*
Cefepime	40	5.0 (2)	7.5 (3)	–*	–*
Gentamicin	67	0.0 (0)	3.0 (2)	–†	3.0 (2)
Tobramycin	66	0.0 (0)	3.0 (2)	–†	3.0 (2)
Amikacin	52	0.0 (0)	1.9 (1)	–†	3.8 (2)
Ciprofloxacin	65	0.0 (0)	4.6 (3)	95.4 (62)	4.6 (3)
Meropenem	67	0.0 (0)	3.0 (2)	0.0 (0)	3.0 (2)
Enterobacter cloacae complex					
Piperacillin-tazobactam	470	5.7 (27)	18.3 (86)	–†	27.2 (128)
Ceftriaxone	475	0.4 (2)	28.4 (135)	0.4 (2)	28.4 (135)
Ceftazidime	475	1.1 (5)	23.6 (112)	3.6 (17)	24.6 (117)
Cefepime	475	3.6 (17)§	1.9 (9)	8.6 (41)	3.4 (16)
Gentamicin	473	0.0 (0)	5.5 (26)	–†	6.1 (29)
Tobramycin	465	2.4 (11)	3.7 (17)	–†	6.7 (31)
Amikacin	474	0.4 (2)	0.0 (0)	–†	0.6 (3)
Ciprofloxacin	475	1.1 (5)	5.3 (25)	1.1 (5)	5.3 (25)
Meropenem	475	0.2 (1)	2.5 (12)	0.4 (2)	2.1 (10)
Escherichia coli					
Ampicillin	5,257	1.5 (78)	50.0 (2,628)	–†	51.5 (2,706)
Amoxicillin–clavulanic acid (2:1 ratio)	4,567	9.9 (452)	7.4 (337)	–*	–*
Piperacillin–tazobactam	5,243	2.3 (121)	2.8 (147)	–†	5.9 (309)
Cefazolin	4,594	–**	22.2 (1,022)	77.8 (3,572)	22.2 (1,022)
Cefuroxime	611	1.6 (10)	16.4 (100)	82.0 (501)	18.0 (110)
Ceftriaxone	5,261	0.1 (6)	12.7 (667)	0.1 (6)	12.7 (667)
Ceftazidime	5,261	0.9 (46)	5.0 (263)	7.3 (384)	5.9 (309)
Cefepime	5,261	2.1 (109)§	2.1 (112)	6.6 (345)	3.1 (162)

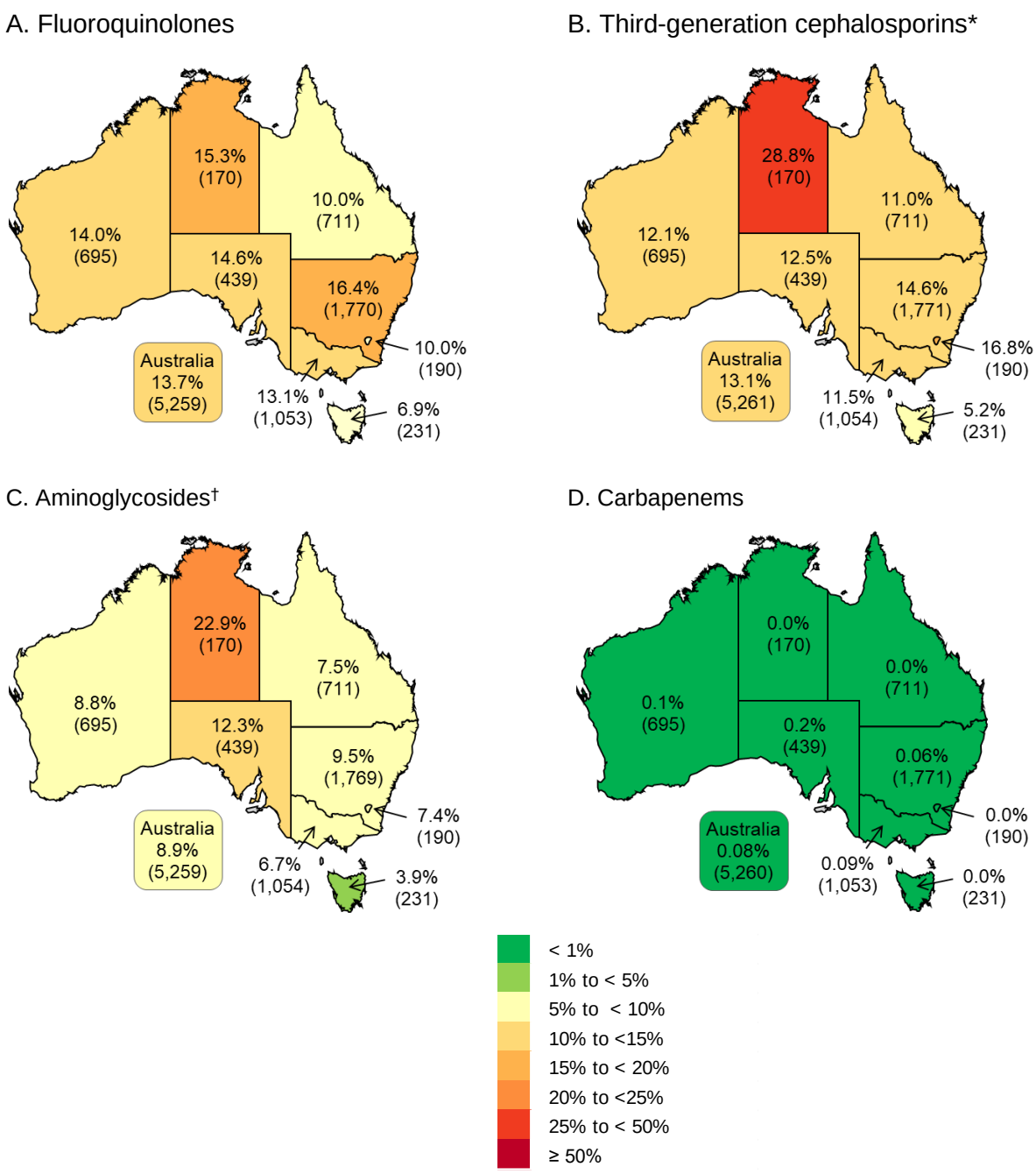
Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Gentamicin	5,259	0.1 (4)	7.9 (415)	–†	8.3 (437)
Tobramycin	5,233	5.8 (301)	2.4 (127)	–†	8.6 (450)
Amikacin	5,260	0.1 (3)	0.0 (2)	–†	0.9 (48)
Ciprofloxacin	5,259	3.7 (196)	13.7 (721)	3.7 (196)	13.7 (721)
Meropenem	5,260	0.0 (1)	0.1 (7)	0.1 (3)	0.1 (4)
Klebsiella aerogenes					
Piperacillin–tazobactam	129	10.1 (13)	20.9 (27)	–†	37.2 (48)
Ceftriaxone	129	0.8 (1)	33.3 (43)	0.8 (1)	33.3 (43)
Ceftazidime	129	3.1 (4)	30.2 (39)	3.9 (5)	33.3 (43)
Cefepime	129	2.3 (3)§	0.0 (0)	3.1 (4)	1.6 (2)
Gentamicin	129	0.0 (0)	2.3 (3)	–†	2.3 (3)
Tobramycin	129	2.3 (3)	0.0 (0)	–†	2.3 (3)
Amikacin	129	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	129	0.8 (1)	3.1 (4)	0.8 (1)	3.1 (4)
Meropenem	129	0.0 (0)	2.3 (3)	1.6 (2)	0.8 (1)
Klebsiella oxytoca					
Amoxicillin–clavulanic acid (2:1 ratio)	258	4.3 (11)	7.4 (19)	–*	–*
Piperacillin–tazobactam	295	1.7 (5)	8.1 (24)	–†	11.5 (34)
Cefuroxime	35	2.9 (1)	2.9 (1)	94.3 (33)	5.7 (2)
Ceftriaxone	296	0.3 (1)	5.7 (17)	0.3 (1)	5.7 (17)
Ceftazidime	296	0.3 (1)	0.3 (1)	0.3 (1)	0.7 (2)
Cefepime	296	0.0 (0)§	0.3 (1)	0.7 (2)	0.3 (1)
Gentamicin	297	0.0 (0)	1.0 (3)	–†	1.0 (3)
Tobramycin	296	1.0 (3)	0.0 (0)	–†	1.0 (3)
Amikacin	296	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	297	0.3 (1)	0.7 (2)	0.3 (1)	0.7 (2)
Meropenem	295	0.0 (0)	0.7 (2)	0.7 (2)	0.0 (0)
Klebsiella pneumoniae complex					
Amoxicillin–clavulanic acid (2:1 ratio)	1,230	4.6 (57)	3.2 (39)	–*	–*
Piperacillin–tazobactam	1,386	1.3 (18)	2.9 (40)	–†	8.7 (121)
Cefazolin	1,235	–**	10.1 (125)	89.9 (1,110)	10.1 (125)
Cefuroxime	138	4.3 (6)	5.8 (8)	89.9 (124)	10.1 (14)
Ceftriaxone	1,392	0.1 (1)	6.6 (92)	0.1 (1)	6.6 (92)
Ceftazidime	1,392	0.9 (13)	4.4 (61)	1.9 (26)	5.3 (74)
Cefepime	1,392	0.9 (13)§	1.7 (24)	3.3 (46)	2.2 (31)
Gentamicin	1,392	0.4 (5)	3.0 (42)	–†	3.4 (47)
Tobramycin	1,383	2.6 (36)	1.4 (20)	–†	4.1 (57)
Amikacin	1,392	0.0 (0)	0.1 (1)	–†	0.2 (3)
Ciprofloxacin	1,391	2.1 (29)	7.8 (109)	2.1 (29)	7.8 (109)
Meropenem	1,392	0.2 (3)	0.6 (8)	0.1 (1)	0.5 (7)
Proteus mirabilis					
Ampicillin	323	0.6 (2)	15.8 (51)	–†	16.4 (53)
Amoxicillin–clavulanic acid (2:1 ratio)	278	5.8 (16)	3.2 (9)	–*	–*
Piperacillin–tazobactam	322	0.0 (0)	0.0 (0)	–†	0.0 (0)
Cefuroxime	44	0.0 (0)	6.8 (3)	93.2 (41)	6.8 (3)

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Ceftriaxone	323	0.6 (2)	1.2 (4)	0.6 (2)	1.2 (4)
Ceftazidime	323	0.3 (1)	0.6 (2)	0.6 (2)	0.9 (3)
Cefepime	323	0.6 (2)§	0.6 (2)	0.9 (3)	0.6 (2)
Gentamicin	323	1.2 (4)	1.9 (6)	–†	5.0 (16)
Tobramycin	323	1.2 (4)	1.9 (6)	–†	3.7 (12)
Amikacin	323	0.0 (0)	0.3 (1)	–†	1.5 (5)
Ciprofloxacin	323	0.6 (2)	4.0 (13)	0.6 (2)	4.0 (13)
Meropenem	323	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Pseudomonas aeruginosa					
Piperacillin–tazobactam	832	8.5 (71)	6.1 (51)	85.3 (710)	14.7 (122)
Ceftazidime	837	5.5 (46)	5.1 (43)	89.4 (748)	10.6 (89)
Cefepime	838	3.3 (28)	2.9 (24)	93.8 (786)	6.2 (52)
Tobramycin	827	0.2 (2)	0.4 (3)	–†	0.7 (6)
Amikacin	836	0.2 (2)	0.2 (2)	–†	0.5 (4)
Ciprofloxacin	836	5.7 (48)	4.3 (36)	90.0 (752)	10.0 (84)
Meropenem	836	4.5 (38)	5.9 (49)	6.1 (51)	4.3 (36)
Salmonella species (non-typhoidal)					
Ampicillin	96	0.0 (0)	5.2 (5)	–†	5.2 (5)
Amoxicillin–clavulanic acid (2:1 ratio)	87	1.1 (1)	0.0 (0)	–*	–*
Piperacillin–tazobactam	96	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ceftriaxone	96	0.0 (0)	3.1 (3)	0.0 (0)	3.1 (3)
Ceftazidime	96	0.0 (0)	3.1 (3)	0.0 (0)	3.1 (3)
Cefepime	96	1.0 (1)§	1.0 (1)	2.1 (2)	1.0 (1)
Ciprofloxacin**	97	3.1 (3)	10.3 (10)	–†	13.4 (13)
Meropenem	96	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)
Serratia marcescens					
Piperacillin–tazobactam	212	0.9 (2)	0.0 (0)	–†	0.9 (2)
Ceftriaxone	257	0.4 (1)	3.1 (8)	0.4 (1)	3.1 (8)
Ceftazidime	257	0.4 (1)	1.6 (4)	0.4 (1)	1.9 (5)
Cefepime	257	0.4 (1)§	0.8 (2)	0.4 (1)	1.2 (3)
Gentamicin	257	0.0 (0)	1.9 (5)	–†	2.3 (6)
Tobramycin	255	16.1 (41)	1.2 (3)	–†	31.4 (80)
Amikacin	257	0.0 (0)	0.0 (0)	–†	0.0 (0)
Ciprofloxacin	257	1.6 (4)	2.3 (6)	1.6 (4)	2.3 (6)
Meropenem	257	0.0 (0)	1.6 (4)	0.8 (2)	0.8 (2)

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing

* No guidelines for indicated species
† No category defined
§ Includes sensitive dose, dependent category for CLSI
# The cefazolin concentration range available on the Vitek card used restricts the ability to accurately identify susceptible and intermediate (CLSI) categories
** The ciprofloxacin concentration range available on the Vitek® card used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. Results of gradient diffusion test strips or perfloxacin 5 µg disc when available, were provided

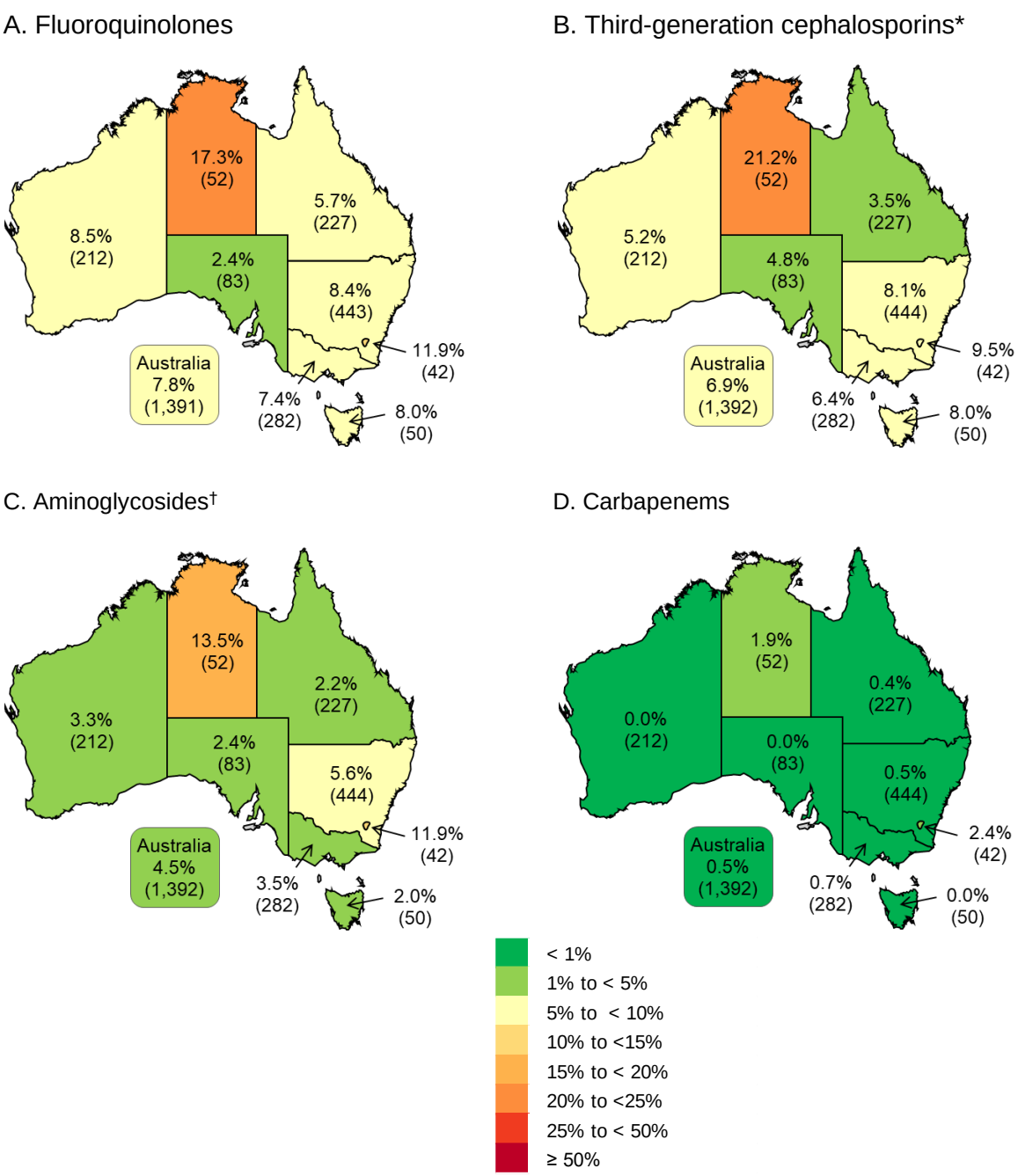
Figure 2. Percentage of *Escherichia coli* from patients with bacteraemia with resistance, as defined by EUCAST, to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) or carbapenems (D), Australia, AGAR, 2022



EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Third-generation cephalosporins refers to ceftriaxone and/or ceftazidime
† Aminoglycosides refers to gentamicin or tobramycin

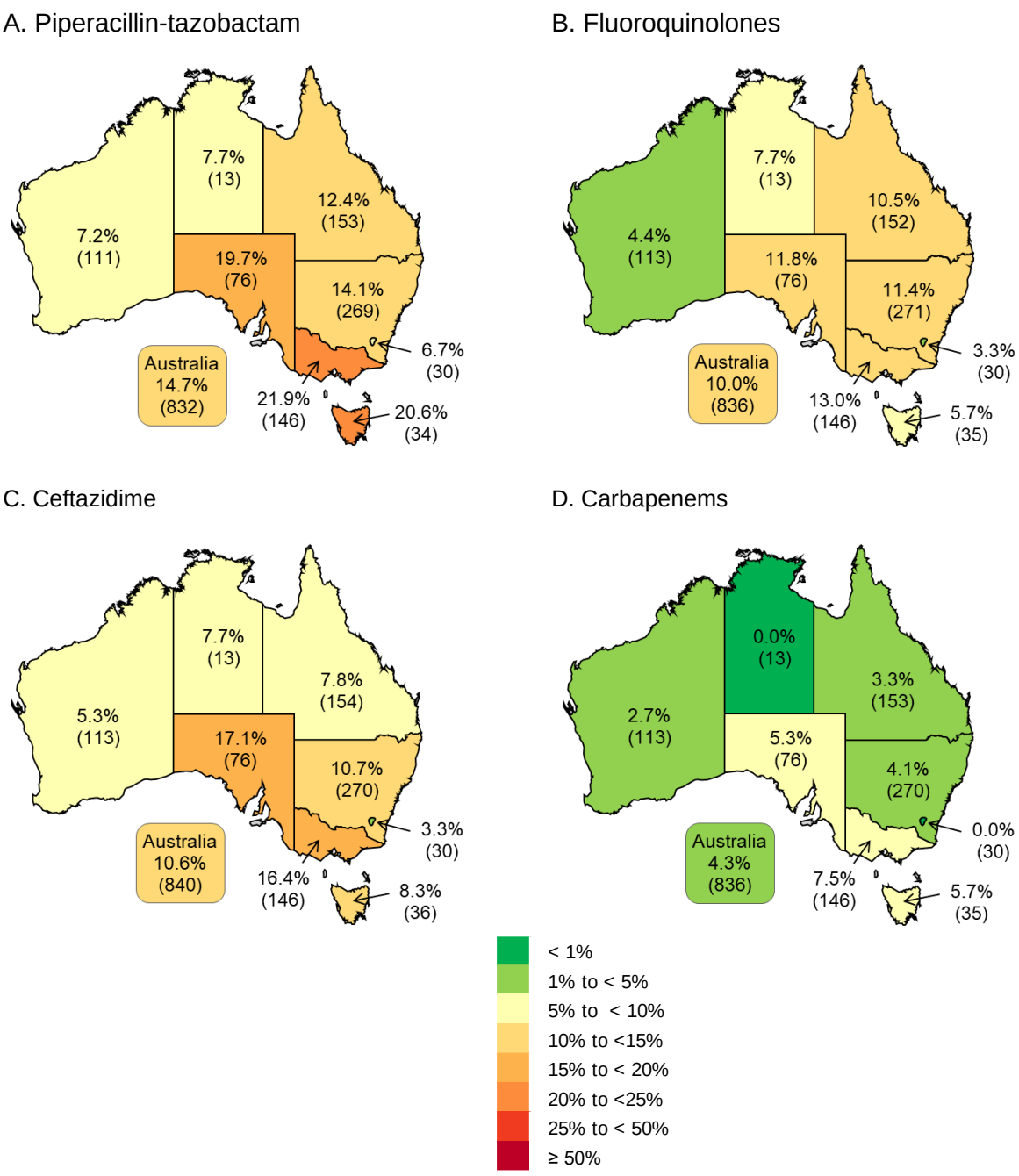
Figure 3. Percentage of *Klebsiella pneumoniae* complex from patients with bacteraemia with resistance, as defined by EUCAST, to fluoroquinolones (A), third-generation cephalosporins (B), aminoglycosides (C) and carbapenems (D), Australia, AGAR, 2022



EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Third-generation cephalosporins refers to ceftriaxone and/or ceftazidime
† Aminoglycosides refers to gentamicin or tobramycin

Figure 4. Percentage of *Pseudomonas aeruginosa* from patients with bacteraemia with resistance, as defined by EUCAST, to piperacillin–tazobactam (A), fluoroquinolones (B), ceftazidime (C) and carbapenems (D), Australia, AGAR, 2022



EUCAST = European Committee on Antimicrobial Susceptibility Testing

Antimicrobial resistance by place of onset

Antimicrobial resistances (CLSI and EUCAST) in indicator species by place of onset, if known, are shown in Table 8.

Table 8: Activity of antimicrobial agents tested against species recovered from patients with Gram-negative bloodstream infections, by place of onset, AGAR, 2022

	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
Species and antimicrobial	No.	I	R	S-IE	R	No.	I	R	S-IE	R
Acinetobacter baumannii complex										
Piperacillin–tazobactam	30	6.7	10.0	–*	–*	29	6.9	10.3	–*	–*
Ceftriaxone	36	77.8	5.6	–*	–*	27	63.0	3.7	–*	–*
Ceftazidime	31	19.4	3.2	–*	–*	28	3.6	3.6	–*	–*
Cefepime	21	9.5	4.8	–*	–*	19	0.0	10.5	–*	–*
Gentamicin	38	0.0	2.6	–†	2.6	29	0.0	3.4	–†	3.4
Tobramycin	38	0.0	2.6	–†	2.6	28	0.0	3.6	–†	3.6
Amikacin	34	0.0	0.0	–†	0.0	18	0.0	5.6	–†	11.1
Ciprofloxacin	38	0.0	5.3	94.7	5.3	27	0.0	3.7	96.3	3.7
Meropenem	38	0.0	2.6	0.0	2.6	29	0.0	3.4	0.0	3.4
Enterobacter cloacae complex										
Piperacillin–tazobactam	246	5.3	11.8	–†	20.7	224	6.3	25.4	–†	34.4
Ceftriaxone	249	0.4	23.7	0.4	23.7	226	0.4	33.6	0.4	33.6
Ceftazidime	249	1.2	17.3	5.2	18.5	226	0.9	30.5	1.8	31.4
Cefepime	249	2.4§	1.2	7.2	1.6	226	4.9§	2.7	10.2	5.3
Gentamicin	249	0.0	4.0	–†	4.8	224	0.0	7.1	–†	7.6
Tobramycin	242	2.5	2.5	–†	5.4	223	2.2	4.9	–†	8.1
Amikacin	249	0.8	0.0	–†	0.8	225	0.0	0.0	–†	0.4
Ciprofloxacin	249	1.2	3.2	1.2	3.2	226	0.9	7.5	0.9	7.5
Meropenem	249	0.0	0.8	0.0	0.8	226	0.4	4.4	0.9	3.5
Escherichia coli										
Ampicillin	4,338	1.5	48.1	–†	49.6	919	1.4	58.8	–†	60.2
Amoxicillin-clavulanic acid (2:1 ratio)	3,782	9.5	7.0	–*	–*	785	11.6	9.2	–*	–*
Piperacillin–tazobactam	4,323	2.2	1.8	–†	4.9	920	2.9	7.4	–†	10.7
Cefazolin	3,803	–*	21.1	78.9	21.1	791	–*	27.6	72.4	27.6
Cefuroxime	489	2.0	14.9	83.0	17.0	122	0.0	22.1	77.9	22.1
Ceftriaxone	4,340	0.1	12.1	0.1	12.1	921	0.1	15.2	0.1	15.2
Ceftazidime	4,340	0.9	4.6	7.1	5.6	921	0.7	6.7	8.3	7.4
Cefepime	4,340	2.0§	1.9	6.3	2.8	921	2.3§	3.3	7.6	4.5
Gentamicin	4,338	0.0	7.5	–†	7.9	921	0.2	9.6	–†	10.3
Tobramycin	4,316	5.5	2.3	–†	8.2	917	6.9	2.9	–†	10.6
Amikacin	4,339	0.1	0.0	–†	0.9	921	0.0	0.0	–†	1.1
Ciprofloxacin	4,338	3.6	12.8	3.6	12.8	921	4.6	17.8	4.6	17.8
Meropenem	4,339	0.0	0.1	0.0	0.0	921	0.1	0.3	0.1	0.2
Klebsiella aerogenes										
Piperacillin–tazobactam	78	9.0	16.7	–†	33.3	51	11.8	27.5	–†	43.1
Ceftriaxone	78	1.3	29.5	1.3	29.5	51	0.0	39.2	0.0	39.2
Ceftazidime	78	3.8	25.6	6.4	29.5	51	2.0	37.3	0.0	39.2

Species and antimicrobial	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
	No.	I	R	S-IE	R	No.	I	R	S-IE	R
Cefepime	78	1.3§	0.0	2.6	0.0	51	3.9§	0.0	3.9	3.9
Gentamicin	78	0.0	2.6	–†	2.6	51	0.0	2.0	–†	2.0
Tobramycin	78	2.6	0.0	–†	2.6	51	2.0	0.0	–†	2.0
Amikacin	78	0.0	0.0	–†	0.0	51	0.0	0.0	–†	0.0
Ciprofloxacin	78	1.3	2.6	1.3	2.6	51	0.0	3.9	0.0	3.9
Meropenem	78	0.0	0.0	0.0	0.0	51	0.0	5.9	3.9	2.0
Klebsiella oxytoca										
Amoxicillin–clavulanic acid (2:1 ratio)	168	3.6	4.8	–*	–*	90	5.6	12.2	–*	–*
Piperacillin–tazobactam	196	1.0	5.6	–†	7.7	99	3.0	13.1	–†	19.2
Cefuroxime	26	0.0	0.0	100.0	0.0	9	n/a	n/a	n/a	n/a
Ceftriaxone	196	0.0	5.1	0.0	5.1	100	1.0	7.0	1.0	7.0
Ceftazidime	196	0.0	0.0	0.0	0.0	100	1.0	1.0	1.0	2.0
Cefepime	196	0.0§	0.0	0.5	0.0	100	0.0§	1.0	1.0	1.0
Gentamicin	196	0.0	0.5	–†	0.5	101	0.0	2.0	–†	2.0
Tobramycin	196	0.5	0.0	–†	0.5	100	2.0	0.0	–†	2.0
Amikacin	196	0.0	0.0	–†	0.0	100	0.0	0.0	–†	0.0
Ciprofloxacin	196	0.5	0.5	0.5	0.5	101	0.0	1.0	0.0	1.0
Meropenem	196	0.0	0.0	0.0	0.0	99	0.0	2.0	2.0	0.0
Klebsiella pneumoniae complex										
Amoxicillin–clavulanic acid (2:1 ratio)	859	3.7	2.0	–*	–*	371	6.7	5.9	–*	–*
Piperacillin–tazobactam	962	1.0	1.5	–†	6.3	424	1.9	6.1	–†	14.2
Cefazolin	860	–*	7.6	92.4	7.6	375	–*	16.0	84.0	16.0
Cefuroxime	91	1.1	5.5	93.4	6.6	47	10.6	6.4	83.0	17.0
Ceftriaxone	966	0.1	4.8	0.1	4.8	426	0.0	10.8	0.0	10.8
Ceftazidime	966	0.7	2.9	1.6	3.6	426	1.4	7.7	2.6	9.2
Cefepime	966	0.8§	1.7	2.0	2.1	426	1.2§	1.9	6.3	2.6
Gentamicin	966	0.2	2.6	–†	2.8	426	0.7	4.0	–†	4.7
Tobramycin	961	2.1	1.0	–†	3.1	422	3.8	2.4	–†	6.4
Amikacin	966	0.0	0.1	–†	0.1	426	0.0	0.0	–†	0.5
Ciprofloxacin	965	1.8	6.3	1.8	6.3	426	2.8	11.3	2.8	11.3
Meropenem	966	0.2	0.6	0.1	0.5	426	0.2	0.5	0.0	0.5
Proteus mirabilis										
Ampicillin	266	0.4	16.2	–†	16.5	57	1.8	14.0	–†	15.8
Amoxicillin–clavulanic acid (2:1 ratio)	227	5.7	3.5	–*	–*	51	5.9	2.0	–*	–*
Piperacillin–tazobactam	265	0.0	0.0	–†	0.0	57	0.0	0.0	–†	0.0
Cefuroxime	38	0.0	5.3	94.7	5.3	6	n/a	n/a	n/a	n/a
Ceftriaxone	266	0.4	1.1	0.4	1.1	57	1.8	1.8	1.8	1.8
Ceftazidime	266	0.4	0.8	0.8	1.1	57	0.0	0.0	0.0	0.0
Cefepime	266	0.4§	0.8	0.4	0.8	57	1.8§	0.0	3.5	0.0
Gentamicin	266	1.1	2.3	–†	4.9	57	1.8	0.0	–†	5.3
Tobramycin	266	1.1	2.3	–†	4.1	57	1.8	0.0	–†	1.8
Amikacin	266	0.0	0.4	–†	1.9	57	0.0	0.0	–†	0.0
Ciprofloxacin	266	0.8	4.9	0.8	4.9	57	0.0	0.0	0.0	0.0

Species and antimicrobial	Community-onset					Hospital-onset				
		CLSI, %		EUCAST, %			CLSI, %		EUCAST, %	
	No.	I	R	S-IE	R	No.	I	R	S-IE	R
Meropenem	266	0.0	0.0	0.0	0.0	57	0.0	0.0	0.0	0.0
Pseudomonas aeruginosa										
Piperacillin–tazobactam	468	6.6	4.1	89.3	10.7	364	11.0	8.8	80.2	19.8
Ceftazidime	471	3.4	3.0	93.6	6.4	366	8.2	7.9	83.9	16.1
Cefepime	472	1.9	1.5	96.6	3.4	366	5.2	4.6	90.2	9.8
Tobramycin	470	0.2	0.2	–†	0.4	357	0.3	0.6	–†	1.1
Amikacin	471	0.2	0.0	–†	0.2	365	0.3	0.5	–†	0.8
Ciprofloxacin	472	3.6	3.6	92.8	7.2	364	8.5	5.2	86.3	13.7
Meropenem	471	5.1	2.1	6.2	1.1	365	3.8	10.7	6.0	8.5
Salmonella species (non-typhoidal)										
Ampicillin	89	0.0	5.6	–†	5.6	7	n/a	n/a	–†	n/a
Amoxicillin–clavulanic acid (2:1 ratio)	81	1.2	0.0	–*	–*	6	n/a	n/a	–*	–*
Piperacillin–tazobactam	89	0.0	0.0	–†	0.0	7	n/a	n/a	–†	n/a
Ceftriaxone	89	0.0	3.4	0.0	3.4	7	n/a	n/a	n/a	n/a
Ceftazidime	89	0.0	3.4	0.0	3.4	7	n/a	n/a	n/a	n/a
Cefepime	89	1.1§	1.1	2.2	1.1	7	n/a	n/a	n/a	n/a
Ciprofloxacin**	89	3.4	11.2	–†	14.6	8	n/a	n/a	–†	n/a
Meropenem	89	0.0	0.0	0.0	0.0	7	n/a	n/a	n/a	n/a
Serratia marcescens										
Piperacillin–tazobactam	85	1.2	0.0	–†	1.2	127	0.8	0.0	–†	0.8
Ceftriaxone	114	0.0	3.5	0.0	3.5	143	0.7	2.8	0.7	2.8
Ceftazidime	114	0.9	1.8	0.9	2.6	143	0.0	1.4	0.0	1.4
Cefepime	114	0.0§	0.9	0.9	0.9	143	0.7§	0.7	0.0	1.4
Gentamicin	114	0.0	1.8	–†	1.8	143	0.0	2.1	–†	2.8
Tobramycin	113	15.9	0.9	–†	30.1	142	16.2	1.4	–†	32.4
Amikacin	114	0.0	0.0	–†	0.0	143	0.0	0.0	–†	0.0
Ciprofloxacin	114	0.9	3.5	0.9	3.5	143	2.1	1.4	2.1	1.4
Meropenem	114	0.0	1.8	0.9	0.9	143	0.0	1.4	0.7	0.7

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate; R = resistant; S-IE = susceptible, increased exposure; n/a = not applicable, insufficient numbers (<10) to calculate percentage; No. = number of isolates

* No guidelines for indicated species
† No category defined
§ Includes sensitive, dose dependent category for CLSI
# The cefazolin concentration range available on the Vitek card used restricts the ability to accurately identify susceptible and intermediate (CLSI) categories
** The ciprofloxacin concentration range available on the Vitek® card used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. Results of gradient test strips or perfloxacin 5 µg disc when available, were provided

3.8. Multi-drug resistance

The most problematic pathogens are those with multiple acquired resistances. The definitions proposed by Magiorakos et al.[5], where multi-drug resistance was defined as resistance to one or more agent in three or more antimicrobial categories, were applied in this survey. Antimicrobials were excluded from the count if natural resistance mechanisms are present in that species.

Only isolates for which the full range of antimicrobial categories was tested were included for determination of multi-drug resistance. EUCAST breakpoints were primarily used in the analysis.

Multiple acquired resistances for key species are shown in Tables 9 to 12. The agents included for each species are listed in the notes after each table. For other common species, refer to Appendix D.

Table 9: Multiple acquired resistance in *Enterobacter cloacae* complex, by state and territory, AGAR, 2022

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)				
		0	1	2	%	3	4	5	6	%
NSW	169	90	16	42	87.6	6	9	3	3	12.4
Vic	97	61	8	21	92.8	3	2	1	1	7.2
Qld	86	49	17	16	95.3	0	2	1	1	4.7
SA	22	10	2	8	–*	0	1	1	0	–*
WA	51	43	3	3	96.1	2	0	0	0	3.9
Tas	17	12	0	4	–*	1	0	0	0	–*
NT	9	3	2	3	–*	0	0	1	0	–*
ACT	16	11	2	2	–*	0	1	0	0	–*
Total	**467**	**279**	**50**	**99**	**91.6**	**12**	**15**	**7**	**5**	**8.4**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable, insufficient numbers (<30) to calculate percentage

Notes:
1. Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Enterobacter cloacae* complex includes *E. bugandensis* (*n* = 5), *E. asburiae* (*n* = 4), *E. hormaechei* (*n* = 4), and *E. ludwigii* (*n* = 1).

Table 10: Multiple acquired resistance in *Escherichia coli*, by state and territory, AGAR, 2022

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)							
		0	1	2	%	3	4	5	6	7	8	9	%
NSW	1,738	758	291	239	74.1	135	139	114	36	19	7	0	25.9
Vic	1,051	475	209	144	78.8	87	57	53	18	6	1	1	21.2
Qld	706	327	131	107	80.0	43	39	44	8	6	1	0	20.0
SA	435	188	80	75	78.9	29	26	25	5	5	2	0	21.1
WA	692	267	126	128	75.3	56	58	28	22	5	2	0	24.7
Tas	200	118	35	28	90.5	9	5	4	1	0	0	0	9.5
NT	169	46	16	34	56.8	21	17	25	8	2	0	0	43.2
ACT	190	83	35	27	76.3	20	11	11	2	1	0	0	23.7
Total	**5,181**	**2262**	**923**	**782**	**76.6**	**400**	**352**	**304**	**100**	**44**	**13**	**1**	**23.4**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), non-extended-spectrum cephalosporins (cefazolin or cefuroxime), and penicillins (ampicillin).

Table 11: Multiple acquired resistance in *Klebsiella pneumoniae* complex isolates, by state and territory, AGAR, 2022

State or territory	Total	Number of categories (non-MDR)				Number of categories (MDR)						
		0	1	2	%	3	4	5	6	7	8	%
NSW	429	324	35	29	90.4	13	9	6	10	3	0	9.6
Vic	282	220	23	21	93.6	7	5	0	3	1	2	6.4
Qld	225	175	26	12	94.7	5	2	2	2	0	1	5.3
SA	82	67	7	3	93.9	2	2	1	0	0	0	6.1
WA	212	175	7	17	93.9	3	5	1	4	0	0	6.1
Tas	43	38	0	0	88.4	1	3	1	0	0	0	11.6
NT	51	33	3	4	78.4	2	2	2	4	0	1	21.6
ACT	42	34	4	0	90.5	0	1	1	1	1	0	9.5
Total	**1,366**	**1066**	**105**	**86**	**92.0**	**33**	**29**	**14**	**24**	**5**	**4**	**8.0**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories

Notes:
1. Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and non-extended-spectrum cephalosporins (cefazolin or cefuroxime).
2. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 116) and *K. quasipneumoniae* (*n* = 3).

Table 12: Multiple acquired resistance in *Pseudomonas aeruginosa*, by state and territory, AGAR, 2022

State or territory		Number of categories (non- MDR)				Number of categories (MDR)			
	Total	0	1	2	%	3	4	5	%
NSW	258	199	27	24	96.9	5	2	1	3.1
Vic	146	106	13	13	90.4	9	5	0	9.6
Qld	152	122	15	12	98.0	0	2	1	2.0
SA	76	57	5	9	93.4	2	3	0	6.6
WA	111	99	5	4	97.3	1	2	0	2.7
Tas	34	26	5	1	94.1	1	1	0	5.9
NT	13	11	1	1	–*	0	0	0	–*
ACT	30	27	2	1	100.0	0	0	0	0.0
Total	**820**	**647**	**73**	**65**	**95.7**	**18**	**15**	**2**	**4.3**

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable, insufficient numbers (<30) to calculate percentage

Note: Antimicrobial categories (agents) are aminoglycosides (tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftazidime), fluoroquinolones (ciprofloxacin)

Nationally, 53.8% of all *E. coli* isolates were resistant to at least one of five key antimicrobial groups (aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems; Table 13). For *K. pneumoniae* complex isolates, 10.9% were resistant to at least one antimicrobial group (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems; Table 14). For *P. aeruginosa,* 21.1% were resistant to at least one antimicrobial group (piperacillin-tazobactam, fluoroquinolones, ceftazidime, aminoglycosides and carbapenems; Table 15).

Table 13: Resistance combinations among *Escherichia coli* tested against aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems, Australia, AGAR, 2022

Resistance pattern	Number	% of total*
Fully susceptible	2,425	46.2
Single resistance	1,801	34.3
Aminopenicillins	1,677	31.9
Fluoroquinolones	107	2.0
Aminoglycosides	16	0.3
Third-generation cephalosporins	1	0.0
Resistance to two antimicrobial groups	456	8.7
Aminopenicillins + third-generation cephalosporins	217	4.1
Aminopenicillins + fluoroquinolones	143	2.7
Aminopenicillins + aminoglycosides	96	1.8
Resistance to three antimicrobial groups	420	8.0
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	214	4.1
Aminopenicillins + third-generation cephalosporins + aminoglycosides	104	2.0
Aminopenicillins + fluoroquinolones + aminoglycosides	102	1.9
Resistance to four antimicrobial groups	150	2.9
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	148	2.8
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + carbapenems	2	<0.1
Resistance to five antimicrobial groups	2	<0.1
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	2	<0.1

Note: Only data from isolates tested against all five antimicrobial groups are included (*n* = 5,254).

Table 14: Resistance combinations among *Klebsiella pneumoniae* complex tested against fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems, Australia, AGAR, 2022

Resistance pattern	Number	% of total
Fully susceptible	1,240	89.1
Single resistance	72	5.2
Fluoroquinolones	40	2.9
Third-generation cephalosporins	23	1.7
Aminoglycosides	9	0.6
Resistance to two antimicrobial groups	41	2.9
Third-generation cephalosporins + fluoroquinolones	26	1.9
Third-generation cephalosporins + aminoglycosides	9	0.6
Fluoroquinolones + aminoglycosides	6	0.4
Resistance to three antimicrobial groups	32	2.3
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	31	2.2
Third-generation cephalosporins + aminoglycosides + carbapenems	1	<0.1
Resistance to four antimicrobial groups	0	0.0
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	6	0.4

Notes:
1. Only data from isolates tested against all four antimicrobial groups are included (*n* = 1,391).
2. *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 121) and *K. quasipneumoniae* (*n* = 3).

Table 15: Resistance combinations among *Pseudomonas aeruginosa* tested against piperacillin–tazobactam, ceftazidime, fluoroquinolones, aminoglycosides and carbapenems, Australia, AGAR, 2022

Resistance pattern	Number	% of total
Fully susceptible	647	78.9
Single resistance	73	8.9
Fluoroquinolones	39	4.8
Piperacillin-tazobactam	26	3.2
Ceftazidime	5	0.6
Carbapemems	3	0.4
Resistance to two antimicrobial groups	65	7.9
Piperacillin-tazobactam + ceftazidime	47	5.7
Piperacillin-tazobactam + fluoroquinolones	10	1.2
Fluoroquinolones + carbapenems	3	0.4
Ceftazidime + carbapenems	2	0.2
Aminoglycosides + carbapenems	1	0.1
Ceftazidime + fluoroquinolones	1	0.1
Piperacillin-tazobactam + carbapenems	1	0.1
Resistance to three antimicrobial groups	18	2.2
Piperacillin-tazobactam + ceftazidime + fluoroquinolones	8	1.0
Piperacillin-tazobactam + ceftazidime + carbapenems	5	0.6
Piperacillin-tazobactam + fluoroquinolones + carbapenems	4	0.5
Piperacillin-tazobactam + fluoroquinolones + aminoglycosides	1	0.1
Resistance to four antimicrobial groups	15	1.8
Piperacillin-tazobactam + ceftazidime + aminoglycosides + carbapenems	13	1.6
Piperacillin-tazobactam + ceftazidime + fluoroquinolones + carbapenems	2	0.2
Resistance to five antimicrobial groups	2	0.2
Piperacillin-tazobactam + ceftazidime + fluoroquinolones + aminoglycosides + carbapenems	2	0.2

Note: Only data from isolates tested against all five antimicrobial groups are included (*n* = 820).

Multi-drug resistance by onset setting and 30-day all-cause mortality

Multi-drug resistances by onset setting (community or hospital) and 30-day all-cause mortality for the most common species are shown in Table 16.

There was no significant association between multidrug resistance and 30-day all-cause mortality or onset setting.

Table 16: Multi-drug resistance, by onset setting and 30-day all-cause mortality, AGAR, 2022

Species	Category	Total		Community onset		Hospital onset	
		Number	Deaths, % (n)	Number	Deaths,% (n)	Number	Deaths, % (n)
Escherichia coli	Total	3,619	11.5 (415)	2,939	11.1 (325)	680	13.2 (90)
	Non-MDR (≤2)	2,765	11.0 (305)	2,286	10.6 (243)	479	12.9 (62)
	MDR (>2)	854	12.9 (110)	653	12.6 (82)	201	13.9 (28)
Enterobacter cloacae complex	Total	360	12.5 (45)	184	9.8 (18)	176	15.3 (27)
	Non-MDR (≤2)	330	12.1 (40)	174	10.3 (18)	156	14.1 (22)
	MDR (>2)	30	16.7 (5)	10	0.0 (0)	20	25.0 (5)
Klebsiella pneumoniae complex	Total	1,001	12.8 (128)	688	12.2 (84)	313	14.1 (44)
	Non-MDR (≤2)	922	12.9 (119)	648	11.9 (77)	274	15.3 (42)
	MDR (>2)	79	11.4 (9)	40	17.5 (7)	39	5.1 (2)
Pseudomonas aeruginosa	Total	611	18.5 (113)	343	18.7 (64)	268	18.3 (49)
	Non-MDR (≤2)	581	18.4 (107)	337	18.7 (63)	244	18.0 (44)
	MDR (>2)	30	20.0 (6)	6	16.7 (1)	24	20.8 (5)

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories. The agents included for each species are listed in the notes after each table (Tables 9-12)

Note: *Enterobacter cloacae* complex includes *E. bugandensis* (*n* = 5), *E. asburiae* (*n* = 4), *E. hormaechei* (*n* = 3), and *E. ludwigii* (*n* = 1). *Klebsiella pneumoniae* complex includes *K. variicola* (*n* = 93) and *K. quasipneumoniae* (*n* = 3).

3.9. Whole genome sequencing

This section describes the resistance mechanisms of gram-negative organisms identified by WGS. The benefits of this method include increased accuracy in detecting the genetic mechanisms for AMR and clarifying the underlining epidemiology.

All referred gram-negative isolates were sequenced and analysed for antimicrobial resistance mechanisms.

3.9.1. Extended-spectrum β-lactamases

Gram-negative organisms carrying ESBL genes are important internationally, especially in hospital practice. Initially, ESBLs were more common in *Klebsiella* species than in *E. coli*. The emergence of specific types of ESBLs (CTX-M enzymes) in *E. coli* from the community is part of a global epidemic.[6-8] It is unclear what is driving the community expansion of CTX-M ESBLs in Australia, as third-generation cephalosporins are not widely used in that setting; it is thought to be driven by cross-resistance and co-resistance to agents used in community practice. There is also increasing recognition that ESBLs are becoming established in long-term care facilities in Australia.[9]

ESBLs are important because they compromise the efficacy of third-generation cephalosporins, which have been an important therapeutic alternative for infections in patients presenting from the community. ESBL-producing isolates often have co-resistance to other non-β-lactam agents. This can result in delays in the use of effective empirical therapy. The lack of available oral options for treatment can result in unnecessary hospitalisation and, in the setting of bacteraemia, increased mortality risk.

Most ESBL-producing isolates will be detected using the CLSI/EUCAST ceftriaxone 'susceptible' breakpoint of 1 mg/L. The CLSI 'susceptible' breakpoint of 4 mg/L for ceftazidime is less reliable. Isolates with ceftriaxone and/or ceftazidime MICs above 1 mg/L were referred and underwent sequencing.

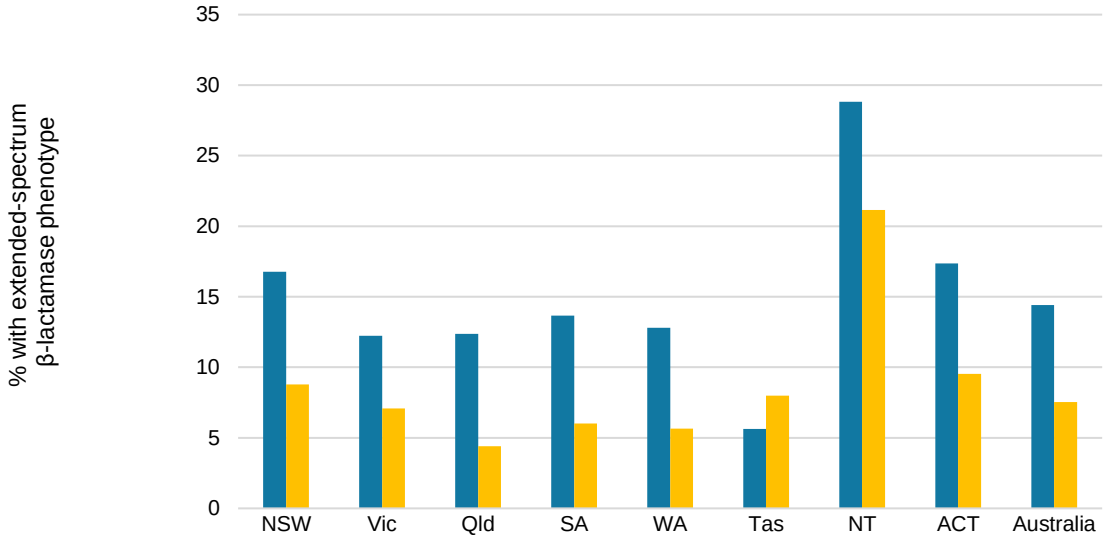
Neither ceftriaxone nor ceftazidime testing will identify ESBL production in *Enterobacter* species because of their intrinsic chromosomal AmpC β-lactamase. Cefepime MICs of greater than 0.25 mg/L suggest that an *Enterobacter* isolate of this genus harbours an ESBL.[10] However, due to the cefepime concentration range available on the susceptibility cards, isolates with a cefepime MIC of greater than 1 mg/L were referred and underwent sequencing.

Sequences of all referred isolates were screened for the presence of β-lactamase genes using methods outlined in Appendix B.

E. coli and *K. pneumoniae* complex isolates resistant to ceftriaxone and/or ceftazidime (MIC > 1 mg/L), and their variation across states and territories, are shown in Figure 5.

The percentage of *E. coli* with an ESBL phenotype was highest in the Northern Territory (28.8%, 49/170) and lowest in Tasmania (5.6%, 13/231). The percentage of *K. pneumoniae* complex with an ESBL phenotype ranged from 21.2% (11/52) in the Northern Territory, to 4.4% (10/227) in Queensland.

Figure 5. Percentage of *Escherichia coli* and *Klebsiella pneumoniae* complex with extended-spectrum β-lactamase phenotype, by state and territory, and nationally, AGAR, 2022



	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
E. coli, %	16.8	12.2	12.4	13.7	12.8	5.6	28.8	17.4	14.4
K. pneumoniae complex, %	8.8	7.1	4.4	6.0	5.7	8.0	21.2	9.5	7.5
E. coli (n = 5,261)	297	129	88	60	89	13	49	33	758
K. pneumoniae complex (n = 1,392)	39	20	10	5	12	4	11	4	105

Note: Extended spectrum β-lactamase phenotype defined as ceftriaxone or ceftazidime MIC > 1 mg/L

An ESBL phenotype was significantly more prevalent among HO than CO episodes of *E. coli* (158/921 [17.2%] vs 600/4340 [13.8%], $P < 0.01$) and *K. pneumoniae* complex bacteraemia (54/426 [12.7%] vs 51/966 [5.3%], $P < 0.01$).

An ESBL phenotype was more common among *E. coli* (758/5261, 14.4%) than *K. pneumoniae* complex isolates (105/1392, 7.5%) (Figure 5). For 57 *E. cloacae* complex isolates with cefepime MIC >1 mg/L, 24 (42.1%; 4.4% overall) contained a non-intrinsic β-lactamase gene(s): ESBL only (*n* = 14), ESBL + carbapenemase (*n* = 8), or carbapenemase only (*n* = 2) (Table 17).

The vast majority (94.4%, 17/18) of *K. oxytoca* isolates with a ceftriaxone-resistant phenotype are presumably hyperproducers of OXY, the natural chromosomal β-lactamase in this species, with characteristic resistance to piperacillin–tazobactam and borderline resistance to cefepime, but susceptibility to ceftazidime (data not shown).[11, 12] This pattern is not typical of other types of gram-negative β-lactamases.

Plasmid-borne AmpC and/or carbapenemase genes were also detected in isolates that had an ESBL phenotype but no ESBL genes.

Table 17: β-lactamase genes detected in *Enterobacterales* with extended-spectrum β-lactamase phenotype, AGAR, 2022

β-lactamase mechanism	*Escherichia coli*	*Klebsiella pneumoniae* complex	*Enterobacter cloacae* complex	*Proteus mirabilis*	*Klebsiella oxytoca*	*Salmonella* spp.†
Total	5,261	1,392	475	323	296	133
ESBL phenotype*, % (n)	14.4 (758)	7.5 (105)	12.0 (57)	2.5 (8)	6.1 (18)	4.5 (6)
β-lactamase genes confirmed/number tested (%)	683/723 (94.5)	91/103 (88.3)	24/57 (42.1)	4/6 (66.7)	1/14 (7.1)	6/6 (100.0)
ESBL	560	75	14	3	0	6
ESBL, AmpC	17	1	0	0	0	0
ESBL, AmpC, Carb	0	1	0	0	0	0
ESBL, Carb	4	3	8	0	0	0
AmpC	99	7	0	1	1	0
AmpC, Carb	1	1	0	0	0	0
Carb	2	3	2	0	0	0
Not detected	40	12	33	2	13	0
Not determined§	35	2	0	2	4	0

AmpC = plasmid-borne *ampC*; Carb = carbapenemase; ESBL = extended-spectrum β-lactamase

* ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L; for *E. cloacae* complex, cefepime MIC > 1 mg/L
† Non-typhoidal (n = 96), typhoidal (n = 37)
§ Isolate not available for confirmation

The β-lactamase genes confirmed in *Enterobacterales* with an ESBL phenotype are shown in Table 18. *bla*$_{\text{CTX-M}}$ types continue to be the dominant β-lactamase genes in *E. coli*. Of 683 with confirmed β-lactamase gene(s), 578 (84.6%) had one or more *bla*$_{\text{CTX-M}}$ genes, either *bla*$_{\text{CTX-M}}$ group 1 (*n* = 295), *bla*$_{\text{CTX-M}}$ group 9 (*n* = 282), or a CTX-M group 1/9/1 hybrid (*n* = 1). CTX-M group 1 types were dominant in Victoria, South Australia, and the Australian Capital Territory. CTX-M group 9 types were more prevalent in Queensland, Western Australia, and Tasmania.

Among *K. pneumoniae* complex isolates with confirmed β-lactamase genes, 73 of 91 (80.2%) contained a *bla*$_{\text{CTX-M}}$ gene: *bla*$_{\text{CTX-M}}$ group 1 (*n* = 65), *bla*$_{\text{CTX-M}}$ group 9 (*n* = 6) or *bla*$_{\text{CTX-M}}$ group 1 + *bla*$_{\text{CTX-M}}$ group (*n* = 1) (Table 18).

Table 18: β-lactamase genes among *Enterobacterales* with extended-spectrum β-lactamase phenotype, by state and territory, AGAR, 2022

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Escherichia coli	1,771	1,054	711	439	695	231	170	190	5,261
ESBL phenotype*, % (*n*)	16.8 (297)	12.2 (129)	12.4 (88)	13.7 (60)	12.8 (89)	5.6 (13)	28.8 (49)	17.4 (33)	14.4 (758)
Confirmed β-lactamase genes/number tested	251/ 270	120/ 128	82/ 86	53/ 58	85/ 87	12/ 13	48/ 48	32/ 33	683/ 723
ESBL types	198	113	61	48	75	12	46	28	581
CTX-M-types	197	112	60	48	75	12	46	28	578
group 1	96	61	24	29	35	4	25	21	295
group 9	101	50	36	19	40	8	21	7	282
group 1/9/1 hybrid	0	1	0	0	0	0	0	0	1
SHV (ESBL types)	1	1	0	0	0	0	0	0	2
TEM (ESBL types)	0	0	1	0	0	0	0	0	1
Plasmid-borne AmpC	62	8	23	6	11	1	3	3	117
CMY-2-like	31	5	10	0	3	0	1	2	52
DHA-1	31	3	13	6	7	1	2	1	64
CMY-2-like + DHA	0	0	0	0	1	0	0	0	1
Carbapenemases	4	1	0	0	1	0	0	1	7
NDM-5	2	1	0	0	1	0	0	0	4
NDM-5 + OXA-181	1	0	0	0	0	0	0	0	1
IMP-4	0	0	0	0	0	0	0	1	1
OXA-181	1	0	0	0	0	0	0	0	1
Klebsiella pneumoniae complex	444	282	227	83	212	50	52	42	1,392
ESBL phenotype*, % (*n*)	8.8 (39)	7.1 (20)	4.4 (10)	6.0 (5)	5.7 (12)	8.0 (4)	21.2 (11)	9.5 (4)	7.5 (105)
Confirmed β-lactamase genes/number tested	33/37	18/20	7/10	4/5	10/12	4/4	11/11	4/4	91/103
ESBL types	26	18	6	3	9	4	11	3	80
CTX-M-types	25	15	6	2	9	4	10	2	73
group 1	24	11	5	2	9	4	10	0	65
group 9	1	4	1	0	0	0	0	0	6
group 1 + group 9	0	0	0	0	0	0	0	2	2
SHV (ESBL types)	2	3	1	1	0	1	1	3	12
PER	0	1	0	0	0	0	0	0	1
Plasmid-borne AmpC	6	1	1	1	1	0	0	0	10
DHA-1	5	0	1	1	1	0	0	0	8
CMY-2-like	1	1	0	0	0	0	0	0	2
Carbapenemases	2	3	1	0	0	0	1	1	8
IMP-4	2	1	0	0	0	0	1	1	5
NDM-1	0	1	1	0	0	0	0	0	2
NDM-1 + OXA-181	0	1	0	0	0	0	0	0	1

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Enterobacter cloacae complex	170	98	88	22	51	19	9	18	475
ESBL phenotype*, % (*n*)	15.3 (26)	13.3 (13)	6.8 (6)	31.8 (7)	2.0 (1)	10.5 (2)	11.1 (1)	5.6 (1)	12.0 (57)
Confirmed β-lactamase genes/number tested (%)	13/26	5/13	2/6	1/7	1/1	1/2	1/1	0/1	24/57
ESBL types	11	5	2	1	1	1	1	0	22
CTX-M-types	5	3	1	1	1	0	1	0	12
group 1	5	3	1	1	0	0	1	0	11
group 9	0	0	0	0	1	0	0	0	1
SHV (ESBL types)	4	2	2	0	0	1	0	0	9
VEB	2	0	0	0	0	0	0	0	2
Carbapenemases	7	1	2	0	0	0	0	0	10
IMP-4	7	1	1	0	0	0	0	0	9
NDM-1	0	0	1	0	0	0	0	0	1

ESBL = extended-spectrum β-lactamase; n/a = Insufficient numbers (<10) to calculate percentage

* ESBL phenotype = ceftriaxone and/or ceftazidime MIC > 1 mg/L; for *E. cloacae* complex, cefepime MIC > 1 mg/L

Note: Isolates may possess more than one type of β-lactamase gene.

bla$_{\text{CTX-M}}$ genes were detected in 79.9% (578/723) of *E. coli* with an ESBL phenotype (Table 19). In the *bla*$_{\text{CTX-M-1}}$ group, *bla*$_{\text{CTX-M-15}}$ accounted for 89.2% (263/295). In the *bla*$_{\text{CTX-M-9}}$ group, *bla*$_{\text{CTX-M-27}}$ and *bla*$_{\text{CTX-M-14}}$ were the major genotypes, accounting for 78.4% (221/282) and 18.1% (51/282), respectively.

Table 19: *Escherichia coli*, CTX-M variants, ESBL phenotype, sequence type, AGAR, 2022

		Phenotype		Sequence type						
CTX-M variant	Number	ESBL	Non-ESBL	131	1193	69	-*	73	38	Other types (*n* = 93)
Not detected	221	145	76	13	14	35	12	10	8	129
CTX-M-1 group	296	295	2	120	23	12	18	33	7	84
CTX-M-15	261	260	1	114	16	9	13	33	7	69
CTX-M-55	22	21	1	5	6	2	2	0	0	7
CTX-M-3	7	7	0	0	0	0	3	0	0	4
CTX-M-1	2	2	0	0	1	0	0	0	0	1
CTX-M-15-like†	2	2	0	0	0	1	0	0	0	1
CTX-M-15, CTX-M-189	1	1	0	1	0	0	0	0	0	0
CTX-M-62	1	1	0	0	0	0	0	0	0	1
CTX-M-182	1	1	0	0	0	0	0	0	0	1
CTX-M-9 group	283	282	1	171	27	5	22	5	27	26
CTX-M-27	221	220	1	146	24	3	21	1	14	12
CTX-M-14a	47	47	0	19	2	2	1	4	6	13
CTX-M-24	7	7	0	5	0	0	0	0	2	0
CTX-M-14b	4	4	0	0	0	0	0	0	4	0
CTX-M-27-like§	1	1	0	0	0	0	0	0	1	0
CTX-M-65	1	1	0	0	0	0	0	0	0	1
CTX-M-134	1	1	0	1	0	0	0	0	0	0
CTX-M-240	1	1	0	0	1	0	0	0	0	0
CTX-M group 1/9/1 hybrid	1	1	0	0	1	0	0	0	0	0
CTX-M-64	1	1	0	0	1	0	0	0	0	0
	802	723	79	304	65	52	52	48	42	239

ESBL = extended-spectrum β-lactamase

* Not available
† CTX-M-15-like (*n* = 2): one has 2 SNPs at 214T to A (Cys to Ser) and 239C to T (Ala to Val); and another with 2 SNPs at 208G to C (Ala to Pro) and 724G to A (Gly to Ser)
§ CTX-M-27-like: 1 SNP. 352G to A (Gly to Ser)

In the *bla*$_{CTX-M}$-positive isolates, *bla*$_{SHV}$- or *bla*$_{TEM}$-type ESBL genes were not detected. Among 145 *bla*$_{CTX-M}$-negative isolates with an ESBL phenotype, 99 harboured one or more pAmpC type genes only (*bla*$_{DHA-1}$ [56], *bla*$_{DHA-27}$ [1], *bla*$_{CMY-2}$ [38], *bla*$_{CMY-4}$ [1], *bla*$_{CMY-42}$ [1], *bla*$_{CMY-141}$ [1], *bla*$_{CMY-42}$ + *bla*$_{DHA-1}$ [1]). Three harboured only a *bla*$_{SHV}$ or *bla*$_{TEM}$ ESBL gene (*bla*$_{SHV-12}$ [2], *bla*$_{TEM-207}$ [1]); two harboured only carbapenemase gene(s) alone (*bla*$_{IMP-4}$ [1]; *bla*$_{NDM-5}$ + *bla*$_{OXA-181}$ [1]); and one harboured both pAmpC and carbapenemase gene (*bla*$_{CMY-146}$ + *bla*$_{OXA-181}$). β-lactam resistance mechanisms were not detected in the remaining 40 isolates.

Half (49.9%, 290/581) of the ESBL-producing *E. coli* with confirmed ESBL genes belong to sequence type 131 (ST131) (Table 20). The fluoroquinolone-resistant subclade, H30R, was the most prevalent subclade of ST131 (52.4%, 152/290). Within ST131, all isolates that identified as H30Rx (subclade C2) (*n* = 87) carried *bla*$_{CTX-M-15}$, a finding reported globally.[13-15] Two-thirds (65.9%, 145/220) of isolates with *bla*$_{CTX-M-27}$ were ST131; 86 belonged to H41 subclade A; 45 belonged to H30R subclade C1-M27, 11 belonged to H99 and 3 to other *fimH* alleles.

ST1193 has recently been identified as an emerging multidrug-resistant clone.[16, 17] In the 2022 survey, ST1193 was the second most prevalent ST among *E. coli* with an ESBL phenotype (57/723, 7.9%). All 57 ST1193 isolates were ciprofloxacin resistant. All of these isolates harboured either ESBL (*bla*$_{CTX-M}$ [49]), pAmpC (*bla*$_{DHA-1}$ [6] or (*bla*$_{CMY-42}$ [1]) alone, or both ESBL + pAmpC (*bla*$_{CTX-M-27}$ + *bla*$_{CMY-2}$ [1]) genes.

Table 20: ESBL-producing *Escherichia coli*, ST131, *fimH* allele, H30Rx, AGAR, 2022

ESBL type	ST131								Non-ST131
			H30						
	Number	All	H41*	H30Rx	H30R	H99	H89	Others†	
CTX-M-15	260	114	20	87	3	1	0	3	146
CTX-M-27	220	145	86	0	45	11	0	3	75
CTX-M-14a	47	19	4	0	14	0	0	1	28
CTX-M-55	21	5	2	0	2	0	0	1	16
CTX-M-3	7	0	0	0	0	0	0	0	7
CTX-M-24	7	5	0	0	0	0	5	0	2
CTX-M-14b	4	0	0	0	0	0	0	0	4
CTX-M-1	2	0	0	0	0	0	0	0	2
CTX-M-15-like	2	0	0	0	0	0	0	0	2
CTX-M-15, CTX-M-189	1	1	1	0	0	0	0	0	0
CTX-M-27-like	1	0	0	0	0	0	0	0	1
CTX-M-62	1	0	0	0	0	0	0	0	1
CTX-M-64	1	0	0	0	0	0	0	0	1
CTX-M-65	1	0	0	0	0	0	0	0	1
CTX-M-134	1	1	0	0	1	0	0	0	0
CTX-M-182	1	0	0	0	0	0	0	0	1
CTX-M-240	1	0	0	0	0	0	0	0	1
SHV-12	2	0	0	0	0	0	0	0	2
TEM-207	1	0	0	0	0	0	0	0	1
	581	290	113	87	65	12	5	8	291

ESBL = extended-spectrum β-lactamase

* Includes H41-like (*n* = 1)
† H22 (*n* = 4), H54 (*n* = 2), unknown (*n* = 2)

3.9.2. Plasmid-borne AmpC β-lactamases

Plasmid-borne *ampC* β-lactamase genes have emerged internationally as a potential gram-negative resistance problem. They are the result of mobilisation of natural chromosomally located genes from common and uncommon species of *Enterobacterales* onto transmissible plasmids, and transmission into more common pathogens. There are currently six separate groups of plasmid-encoded AmpC β-lactamases. Like ESBLs, these enzymes confer resistance to the important third-generation cephalosporins, such as ceftriaxone and ceftazidime. Routine phenotypic detection methods have not yet been developed. Nevertheless, it is possible to exploit a special feature of these enzymes: their ability to inactivate the cephamycins, represented by cefoxitin. *Enterobacter* species naturally possess a chromosomally encoded AmpC enzyme.

All referred isolates were examined for the presence of plasmid-borne *ampC* (*bla*$_{CMY-2}$-like, *bla*$_{DHA}$, *bla*$_{FOX}$, *bla*$_{MOX}$, *bla*$_{ACT/MIR}$, *bla*$_{ACC}$) genes using WGS methods outlined in Appendix B.

The proportions of *E. coli* and *K. pneumoniae* complex isolates with a cefoxitin MIC > 8 mg/L (non-wild type) remain low (5.3% and 5.0% respectively) (Table 21). A little over one-third (108/265, 40.8%) of *E. coli* and 15.6% (10/64) of *K. pneumoniae* complex isolates with cefoxitin MIC > 8 mg/L that were available for confirmation contained one or more plasmid-borne *ampC* genes (Table 21). In most cases the plasmid-borne *ampC* gene type was *bla*$_{DHA}$, found in 57.4% (62/108) of *E. coli* and 80.0% (8/10) of *K. pneumoniae* complex isolates

Table 21: Number of isolates with presumptive plasmid-borne AmpC β-lactamase production, by state and territory, AGAR, 2022

Species	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Escherichia coli	1,771	1,053	711	439	695	231	170	190	5,260
Cefoxitin MIC > 8 mg/L (%)	123 (6.9)	47 (4.5)	39 (5.5)	17 (3.9)	31 (4.5)	6 (2.6)	5 (2.9)	10 (5.3)	278 (5.3)
Confirmed/number tested	54/115	6/46	23/37	6/15	11/31	1/6	3/5	4/10	108/265
bla$_{DHA-1}$*	27	2	14	6	7	1	1	2	60
bla$_{DHA-6}$	0	0	0	0	0	0	1	0	1
bla$_{DHA-27}$	1	0	0	0	0	0	0	0	1
bla$_{CMY-2}$	21	4	9	0	2	0	1	2	39
bla$_{CMY-4}$	2	0	0	0	0	0	0	0	2
bla$_{CMY-42}$	1	0	0	0	0	0	0	0	1
bla$_{CMY-141}$	1	0	0	0	0	0	0	0	1
bla$_{CMY-146}$	1	0	0	0	0	0	0	0	1
Other *bla*$_{CMY-2}$-like	0	0	0	0	1	0	0	0	1
bla$_{CMY-42}$ + $_{DHA-1}$	0	0	0	0	1	0	0	0	1
Klebsiella pneumoniae complex	444	282	227	83	212	50	52	42	1,392
Cefoxitin MIC > 8 mg/L (%)	24 (5.4)	17 (6.0)	8 (3.5)	4 (4.8)	12 (5.7)	0 (0.0)	3 (5.8)	1 (2.4)	69 (5.0)
Confirmed/number tested	6/23	1/16	1/6	1/3	1/12	0/0	0/3	0/1	10/64
bla$_{DHA-1}$	5	0	1	1	1	0	0	0	8
bla$_{CMY-6}$	0	1	0	0	0	0	0	0	1
bla$_{CMY-13}$	1	0	0	0	0	0	0	0	1

MIC = minimum inhibitory concentration

* Includes DHA-1-like (*n* = 1): 1 SNP, 721G to T (Gly to Cys)

Of cefoxitin non-wild type (MIC > 8 mg/L) isolates that did not have a plasmid-encoded *ampC* gene, one or more carbapenemase genes were detected in six of 157 (3.8%) *E. coli* (*bla*$_{IMP-5}$ [4], *bla*$_{NDM-5}$ + *bla*$_{OXA-181}$ [1], *bla*$_{IMP-4}$ [1]), and six of 54 (11.1%) *K. pneumoniae* complex (*bla*$_{IMP-4}$ [5],

bla$_{NDM-7}$ [1]). Eleven *E. coli* with a wild type cefoxitin MIC (≤ 8 mg/L) contained pAmpC types (*bla*$_{CMY-2}$ [5], *bla*$_{CMY-4}$ [2], *bla*$_{DHA-1}$ [4]), and one *K. pneumoniae* complex with cefoxitin MIC ≤ 8 mg/L contained *bla*$_{CMY-70}$ (data not shown).

3.9.3. Carbapenem resistance

Only 0.4% (37/8,742) of *Enterobacterales* had a meropenem MIC > 2 mg/L; an additional 28 had meropenem MIC between 1 and 2 mg/L. Meropenem resistance (MIC > 8 mg/L) was at 4.3% (36/836) for *P. aeruginosa*, and 1.9% (2/106) for *Acinetobacter* species (Table 22).

Among meropenem-resistant (MIC >8 mg/L) isolates that were available, carbapenemase genes were found in 91.7% (22/24) of *Enterobacterales*, 2.9% (1/34) *P. aeruginosa*, and all (2/2) *Acinetobacter* species (Table 22). Carbapenemase genes were found in two *Enterobacterales* with meropenem MIC of 2 mg/L, *K. pneumoniae* (*bla*$_{NDM-1}$ + *bla*$_{OXA-181}$), and *E. coli* (*bla*$_{OXA-244}$), and one *E. coli* (*bla*$_{OXA-181}$), with MIC of 0.5 mg/L.

Table 22: Number of isolates with carbapenemase genes, organism group, meropenem MIC, AGAR, 2022

	***Acinetobacter* (*n* = 106)**			***Enterobacterales* (*n* = 8,742)**				***Pseudomonas* (*n* = 836)**		
	Meropenem MIC (mg/L)			Meropenem MIC (mg/L)				Meropenem MIC (mg/L)		
	≤2	4-8	>8	≤0.5	1-2	4-8	>8	≤2	4-8	>8
Number	104	0	2	8,677	28	12	25	749	51	36
Confirmed/number tested	0/0	–*	2/2	1/1,142	2/27	4/11	22/24	0/3	0/11	1/34
Carbapenemase type†										
Class B	0	0	0	0	0	3	22	0	0	1
bla$_{IMP-4}$	0	0	0	0	0	2	16	0	0	0
bla$_{NDM-1}$	0	0	0	0	0	0	3	0	0	1
bla$_{NDM-5}$	0	0	0	0	0	1	3	0	0	0
Class D	0	0	2	1	1	0	0	0	0	0
bla$_{OXA-23}$	0	0	2	0	0	0	0	0	0	0
bla$_{OXA-181}$	0	0	0	1	0	0	0	0	0	0
bla$_{OXA-244}$	0	0	0	0	1	0	0	0	0	0
Class B + class D	0	0	0	0	1	1	0	0	0	0
bla$_{NDM-1}$ + *bla*$_{OXA-181}$	0	0	0	0	1	0	0	0	0	0
bla$_{NDM-5}$ + *bla*$_{OXA-181}$	0	0	0	0	0	1	0	0	0	0

MIC = minimum inhibitory concentration

* not applicable

† Carbapenemase molecular class: class B (metallo-β-lactamases - IMP, NDM); class D (oxacillinases – OXA-23, OXA-181, OXA-244)

Note: No Class A carbapenemases (KPC) were detected in 2022

Thirty-two (0.3%) isolates from 31 patients were found to harbour a carbapenemase gene (Table 23). Overall prevalence of carbapenemase genes among *Enterobacterales* was 0.3% (29/8773), although for *E. cloacae* complex isolates it was 2.1% (10/477). *bla*$_{IMP-4}$ accounted for 62.1% (18/29) of all CPE in 2022. Half of the *bla*$_{IMP-4}$ genes were found in *E. cloacae* complex isolates (9/18, 50.0%). Other types detected in *Enterobacterales* were *bla*$_{NDM}$ (*n* = 7), *bla*$_{NDM}$ + *bla*$_{OXA-181}$ (*n* = 2), *bla*$_{OXA-181}$ (*n* = 1), and *bla*$_{OXA-244}$ (*n* = 1) genes.

In the 2022 survey among *Acinetobacter* species isolates only 1.6% (2/126), both *Acinetobacter baumannii* complex, harboured a carbapenemase gene; *bla*$_{OXA-23}$. Only one of 840 (0.1%) *P. aeruginosa* isolates carried a carbapenemase gene (*bla*$_{NDM-1}$).

Table 23: Carbapenemase-producing organisms, carbapenemase genes, AGAR, 2022

Species	Total	Carbapenemase type, number								
		IMP-4	NDM-1	NDM-5	OXA-23	OXA-181	OXA-244	NDM-1, OXA-181	NDM-5, OXA-181	% (*n*)
Enterobacterales	8,773	18	3	4	0	1	1	1	1	0.3 (29)
Escherichia coli	5,273	1	0	4	0	1	1	0	1	0.2 (8)
Klebsiella pneumoniae complex*	1,395	5	2	0	0	0	0	1	0	0.6 (8)
Enterobacter cloacae complex†	477	9	1	0	0	0	0	0	0	2.1 (10)
Serratia marcescens	257	3	0	0	0	0	0	0	0	1.2 (3)
Pseudomonas aeruginosa	840	0	1	0	0	0	0	0	0	0.1 (1)
Acinetobacter	126	0	0	0	2	0	0	0	0	1.6 (2)
Acinetobacter baumannii complex	70	0	0	0	2	0	0	0	0	2.8 (2)
All species	9,739	18	4	4	2	1	1	1	1	0.3 (32)

* *K. pneumoniae* (*n* = 7: $bla_{\text{IMP-4}}$ [5], $bla_{\text{NDM-1}}$ [1], $bla_{\text{NDM-1}}$ + $bla_{\text{OXA-181}}$ [1]); *K. variicola* (*n* = 1: $bla_{\text{NDM-1}}$)
† *E. hormaechei* (*n* = 9: $bla_{\text{IMP-4}}$ [8], $bla_{\text{NDM-1}}$ [1]); *E. cloacae* (*n* = 1, $bla_{\text{IMP-4}}$)

Isolates carrying carbapenemase genes were detected in 18 hospitals from six states and territories. CPE infections are particularly notable in New South Wales (15/2195, 0.5%) and Victoria (7/1789, 0.4%), compared to other states and territories (Table 24). A little over one-half (10/18, 55.6%) of the hospitals had one carbapenemase-producing isolate only.

Table 24: Carbapenemase genes, organism group, state and territory, AGAR, 2022

Organism group and carbapenemase	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Total species, *n*	3,210	1,960	1,398	785	1,325	426	296	339	9,739
Acinetobacter	23	25	26	12	15	9	12	4	126
Carbapenemase, % (*n*)	0.0 (0)	0.0 (0)	3.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	8.3 (1)	0.0 (0)	1.6 (2)
$bla_{\text{OXA-23}}$	0	0	1	0	0	0	1	0	2
Enterobacterales	2,915	1,789	1,218	697	1,197	381	271	305	8,773
Carbapenemase, % (*n*)	0.5 (15)	0.4 (7)	0.3 (3)	0.0 (0)	0.1 (1)	0.0 (0)	0.7 (1)	0.6 (2)	0.3 (29)
$bla_{\text{IMP-4}}$	10	4	1	0	0	0	1	2	18
$bla_{\text{NDM-5}}$	2	1	0	0	1	0	0	0	4
$bla_{\text{NDM-1}}$	0	1	2	0	0	0	0	0	3
$bla_{\text{NDM-1}}$ + $bla_{\text{OXA-181}}$	0	1	0	0	0	0	0	0	1
$bla_{\text{NDM-5}}$ + $bla_{\text{OXA-181}}$	1	0	0	0	0	0	0	0	1
$bla_{\text{OXA-181}}$	1	0	0	0	0	0	0	0	1
$bla_{\text{OXA-244}}$	1	0	0	0	0	0	0	0	1
Pseudomonas aeruginosa	272	146	154	76	113	36	13	30	840
Carbapenemase, % (*n*)	0.4 (1)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	0.1 (1)
$bla_{\text{NDM-1}}$	1	0	0	0	0	0	0	0	1
Overall prevalence, % (n)	0.5 (16)	0.4 (7)	0.3 (4)	0.0 (0)	0.1 (1)	0.0 (0)	0.7 (2)	0.6 (2)	0.3 (32)

3.9.4. Fluoroquinolone resistance

Multiple resistance mechanisms against quinolones have been described. Resistance is most commonly due to mutations in the quinolone resistance-determining region (QRDR) of DNA gyrase (*gyrA*, *gyrB*) and/or topoisomerase IV (*parC*, *parE*). Transmissible plasmid-mediated quinolone resistance (PMQR) has emerged in *Enterobacterales*. PMQR determinants include *qnr* genes (*qnrA, qnrB, qnrC, qnrD, qnrE, qnrS, qnrVC*)*; aac(6')-Ib-cr*, coding for a variant aminoglycoside acetyltransferase enzyme, and genes coding for efflux pumps (*qepA*, *oqxAB*).[18, 19] *oqxAB* genes are intrinsic in *Klebsiella* and *Enterobacter*.

Salmonella species

Ciprofloxacin resistance (MIC > 0.06 mg/L) among non-typhoidal species was 13.4% (13/97 confirmed). For the typhoidal species, 84.2% (32/38) were resistant, comprising 28/34 (82.4%) *S*. Typhi and all *S*. Paratyphi A (*n* = 4) (Table 25).

Table 25: *Salmonella* species, ciprofloxacin minimum inhibitory concentrations, AGAR, 2022

	Ciprofloxacin minimum inhibitory concentration (mg/L)							
Organism	**≤0.06**	**0.125**	**0.25**	**0.5**	**1**	**2**	**≥4**	**Total**
Salmonella species (non-typhoidal)	84	1	1	3	3	3	2	99
Salmonella species (typhoidal)	6	0	6	8	12	0	6	36
S. Typhi	6	0	6	7	9	0	6	34
S. Paratyphi A	0	0	0	1	3	0	0	4
Total	90	1	7	11	15	3	8	135

Notes:

1. MICs determined using MIC strips on Salmonella where Vitek® MIC ≤0.25 mg/L.
2. For some laboratories using EUCAST interpretative criteria, a perfloxacin disc was used to screen for ciprofloxacin resistance. If susceptible to a 5 mg/L disc, the isolate was recorded as MIC≤ 0.06 mg/L (susceptible).

All typhoidal isolates that were resistant to ciprofloxacin harboured a mutation in the QRDR of *gyrA*, either in codon 83 (*n* = 30) codon 87 (*n* = 1), known mutations conferring quinolone resistance (Table 26).[20]

ESBL genes were also confirmed in six *Salmonella* isolates with QRDR mutations: $bla_{\text{CTX-M-15}}$ (*n* = 3, typhoidal species) $bla_{\text{CTX-M-55}}$ (*n* = 3, non-typhoidal species).

Table 26: Fluroquinolone resistance determinants in ciprofloxacin-resistant *Salmonella* species, AGAR, 2022

Species	Mutations in QRDR			PMQR genes	Total
	gyrA	*parC*	parE		
Salmonella (non-typhoidal)					11
	–*	T57S	–*	*qnrB19*	3
	S83Y	–*	–*	–*	2
	S83Y	T57S	–*	*qnrS1*	2
	S83F	T57S	–*	–*	1
	D87Y	–*	–*	–*	1
	S83F, D87N	S80I	–*	–*	1
	S83F, D87Y	T57S, S80I	–*	–*	1
Salmonella (typhoidal)					31
S. Typhi (*n* = 28)	S83F	–*	–*	–*	19
	S83F	–*	–*	*qnrS1*	3
	S83F, D87N	S80I	–*	–*	2
	D87N	–*	L416F	–*	1
	S83F	S80I	–*	–*	1
	S83Y	–*	–*	–*	1
	S83Y	E84G	–*	–*	1
S. Paratyphi A (*n* = 3)	S83F	T57S	–*	–*	3

PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

* Not detected

Notes:
1. Fluoroquinolone resistant determinants include mutations in either the QRDR of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[21], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*).
2. Mutations in *gyrB* were not detected.

Escherichia coli

Nationally, 17.4% (917/5,259) of *E. coli* had a ciprofloxacin MIC >0.25 mg/L, ranging from 8.2% (19/231) in Tasmania to 24.7% in the Northern Territory (42/170; Table 27). A subset of 801 *E. coli* (15.2% of total) was referred and underwent WGS. This included 723 with an ESBL phenotype and 494 with ciprofloxacin MIC >0.25 mg/L (Table 27).

Table 27: *Escherichia coli*, ciprofloxacin susceptibility, ESBL phenotype, AGAR, 2022

		Ciprofloxacin MIC (mg/L)				
Subset	Phenotype	≤0.25	0.5	>0.5	Total	% of total
Total	ESBL	35.0 (265)	14.6 (111)	50.4 (382)	758	14.4
	non-ESBL	90.6 (4,077)	1.9 (85)	7.5 (339)	4,501	85.6
	Total	82.6 (4,342)	3.7 (196)	13.7 (721)	5,259	
WGS	ESBL	254	105	364	723	
	non-ESBL	53	0	25	78	
	Total	307	105	389	801	

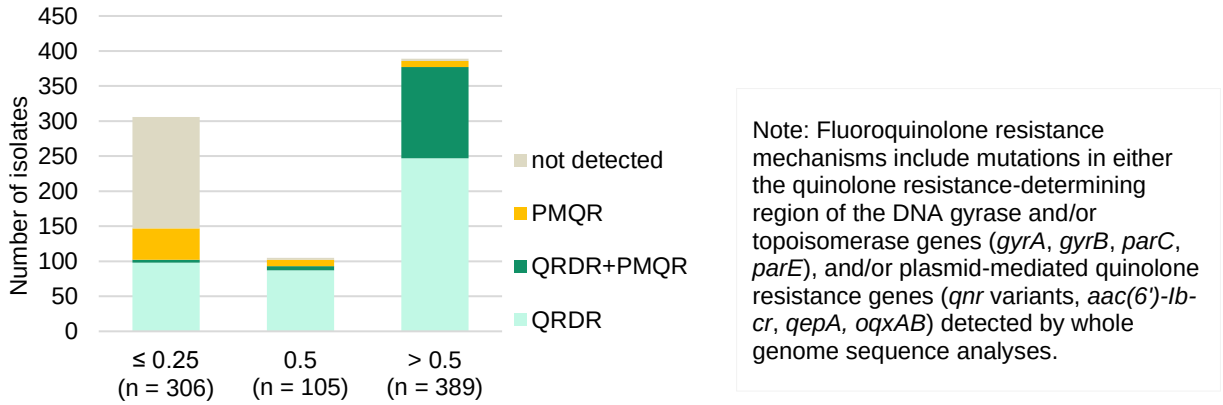
ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; n/a = not applicable; WGS = whole genome sequencing

Note: ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L.

Almost all (488/494, 98.8%) of the *E. coli* subset that had ciprofloxacin MIC > 0.25 mg/L harboured fluoroquinolone resistance determinants (Figure 6). The vast majority (93.4%, 456/488) of this group harboured a QRDR mutation in codon 83 of *gyrA*. A substantial majority (82.5%, 311/377) of isolates resistant to ciprofloxacin (MIC >0.5 mg/L) also had a second mutation in *gyrA* (codon 87), and 88.6% (334/377) showed at least one mutation in *parC* (Table 28).

PMQR genes (*qnr* variants) alone were more common in ciprofloxacin susceptible isolates. Of 63 *E. coli* with confirmed *qnr*, most had *qnrB* (*n* = 40, 63.5%), while some had *qnrS* (*n* = 21, 33.3%) or *qnrB* + *qnrS* (*n* = 2) (data not shown).

Figure 6: *Escherichia coli* (*n* = 800), fluoroquinolone resistance mechanisms, ciprofloxacin MIC, AGAR, 2022



MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

A substantial majority (68.4%, 266/389) of the ciprofloxacin resistant *E. coli* belonged to either ST131 (*n* = 202, 51.9%) or ST1193 (*n* = 64, 16.5%), both with reported distinguishing *parE* mutations (I529L and L416F, respectively).[22] Almost one-quarter (24.2%, 94/389) harboured *aac(6')-Ib-cr* (Table 28), almost all (95.7%, 90/94) of which harboured $bla_{\text{CTX-M-15}}$ (*n* = 89) or $bla_{\text{CTX-M-65}}$ (*n* = 1) (data not shown). Just over one half (87/165, 52.7%) of the ciprofloxacin resistant isolates with $bla_{\text{CTX-M-15}}$ belonged to the ST131-H30Rx clone (data not shown).

Table 28: Fluoroquinolone resistance determinants in *Escherichia coli*, AGAR, 2022

QRDR mutations				Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*	*PMQR*	≤0.25	0.5	>0.5	Total
–*	–*	–*	–*	159	3	3	165
–*	–*	–*	*qnr*	45	9	9	63
–*	–*	I355T	–*	1	0	0	1
–*	–*	I355T	*qnr*	1	0	0	1
–*	–*	I529L	–*	12	0	0	12
–*	–*	I529L	*aac(6')–*Ib–*cr*, *qnr*	0	0	1	1
–*	–*	I529L	*qnr*	1	0	0	1
–*	S57T	I355T	–*	1	0	0	1
–*	S80I	L416F	–*	0	0	3	3
–*	S80I	S458A	–*	0	0	1	1
–*	S80I, E84V	–*	–*	0	0	4	4
–*	S80I, E84V	–*	*aac(6')–*Ib–*cr*	0	0	4	4
–*	T57S	–*	–*	1	0	0	1
D87N	–*	–*	–*	2	0	0	2
D87Y	–*	–*	–*	1	0	1	2
D87Y	S57T	–*	–*	3	0	0	3
S83A	–*	–*	*qnr*	2	1	1	4
S83L	–*	–*	–*	1	0	0	1
S83L	–*	–*	–*	44	23	7	74
S83L	–*	–*	*aac(6')–*Ib–*cr*	0	0	1	1
S83L	–*	–*	*qnr*	0	5	11	16
S83L	–*	D476N	–*	1	0	0	1
S83L	–*	I529L	–*	29	61	12	102
S83L	–*	I529L	*qnr*	0	0	1	1
S83L	–*	I529L, S458A	–*	1	0	1	2
S83L	–*	I529L	–*	0	2	2	4
S83L	–*	S458A	–*	0	0	5	5
S83L	E84G	–*	–*	0	0	1	1
S83L	S57T	–*	–*	1	0	0	1
S83L	S80I	–*	–*	0	0	5	5
S83L	S80I	–*	*qnr*	0	0	3	3
S83L	S80I, E84V	I529L	–*	0	0	1	1
S83L	S80R	–*	–*	0	0	1	1
S83L, D87G	S80I	–*	–*	0	0	1	1
S83L, D87N	S57T, S80I	–*	–*	0	0	1	1
S83L, D87N	S57T, S80I	S458A	–*	0	0	1	1
S83L, D87N	S57T, S80I	S458A	*aac(6')–*Ib–*cr*	0	0	2	2
S83L, D87N	S80I	–*	–*	1	0	5	6
S83L, D87N	S80I	–*	*qnr*	0	0	2	2
S83L, D87N	S80I	E460D	–*	0	0	6	6
S83L, D87N	S80I	L416F	–*	0	0	51	51
S83L, D87N	S80I	L416F	*aac(6')–*Ib–*cr*	0	0	12	12
S83L, D87N	S80I	L416F	*qnr*	0	0	6	6
S83L, D87N	S80I	L445H	–*	0	0	1	1
S83L, D87N	S80I	S458A	–*	0	1	16	17
S83L, D87N	S80I	S458A	*aac(6')–*Ib–*cr*	0	0	12	12
S83L, D87N	S80I	S458A	*qnr*	0	0	3	3
S83L, D87N	S80I, E84G	–*	–*	0	0	1	1
S83L, D87N	S80I, E84V	–*	–*	0	0	2	2
S83L, D87N	S80I, E84V	I529L	–*	0	0	113	113
S83L, D87N	S80I, E84V	I529L	*aac(6')–*Ib–*cr*	0	0	60	60
S83L, D87N	S80I, E84V	I529L	*qnr*	0	0	6	6
S83L, D87N	S80R	–*	*qnr*	0	0	1	1
S83L, D87V	S80I	–*	*qnr*	0	0	1	1
S83L, D87Y	S80I	–*	–*	0	0	1	1
S83L, D87Y	S80I	–*	*aac(6')–*Ib–*cr*	0	0	1	1
S83L, D87Y	S80I	S458A	–*	0	0	2	2
S83L, D87Y	S80I	S458A	*aac(6')–*Ib–*cr*	0	0	1	1
S83L, D87Y	S80I	S458A	*qnr*	0	0	1	1

QRDR mutations			PMQR	Ciprofloxacin MIC (mg/L)			
gyrA	*parC*	*parE*		≤0.25	0.5	>0.5	Total
S83L, D87Y	S80I, E84V	I529L	–*	0	0	2	2
Total				307	105	389	801

MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

* Not detected

Notes:
1. Fluoroquinolone resistant determinants include mutations in either the QRDR of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[21], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA, oqxAB*) detected by whole genome sequence analysis.
2. Bold formatting highlights **ST131** (blue) and **ST1193** (red) isolates.
3. No mutations in *gyrB* were detected.

Klebsiella pneumoniae complex

Nationally, 9.9% (139/1,401) of *K. pneumoniae* complex isolates had a ciprofloxacin MIC >0.25 mg/L, ranging from 4.8% in South Australia (4/83) to 23.1% in the Northern Territory (12/52) (Table 29). A subset of 147 *K. pneumoniae* complex (10.6% of total) was referred and underwent WGS. This included 103 with an ESBL phenotype and 85 with ciprofloxacin MIC >0.25 mg/L (Table 29).

Table 29: *Klebsiella pneumoniae* complex, ciprofloxacin susceptibility, ESBL phenotype, AGAR, 2022

		Ciprofloxacin MIC (mg/L)				
Subset	Phenotype	≤0.25	0.5	>0.5	Total	% of total
Total	ESBL	26.7 (28)	11.4 (12)	61.9 (65)	105	7.5
	non-ESBL	95.3 (1,225)	1.3 (17)	3.4 (44)	1,286	92.5
	Total	90.1 (1,253)	2.1 (29)	7.8 (109)	1,391	
WGS	ESBL	27	12	64	103	
	non-ESBL	35	4	5	44	
	Total	62	16	69	147	

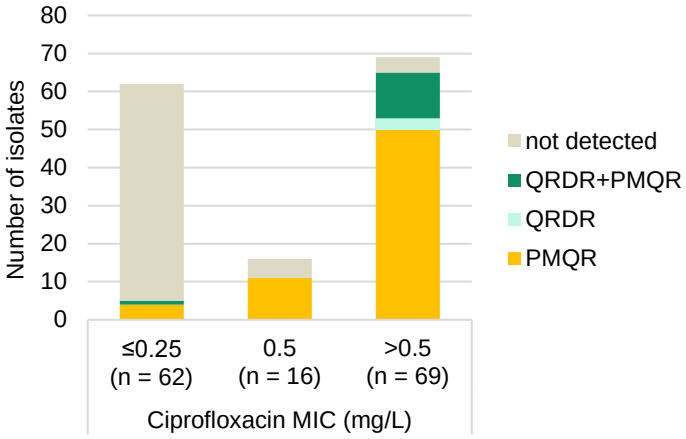
ESBL = extended-spectrum β-lactamase; MIC = minimum inhibitory concentration; n/a = not applicable; WGS = whole genome sequencing

Note: ESBL phenotype = ceftriaxone or ceftazidime MIC > 1 mg/L.

Of the *K. pneumoniae* complex subset that had ciprofloxacin MIC >0.25 mg/L, 89.4% (76/85) harboured fluoroquinolone resistance determinants (Figure 7). PMQR genes either alone (71.8%, 61/85) or in combination with QRDR mutations in codon 83 of *gyrA* (14.1%, 12/85) were prevalent; only 3/85 had *gyrA* mutations alone. One *K. pneumoniae* complex harboured a *parE* mutation (ciprofloxacin MIC > 0.5 mg/L (Table 30).

In *K. pneumoniae* complex isolates, when PMQR genes (*qnr* variants) were found alone (39/65, 60.0%) they were usually in isolates with ciprofloxacin MIC >0.25 mg/L (37/39, 94.9%). In 39 *K. pneumoniae* complex isolates with confirmed *qnr*, most had *qnrS* (*n* = 27, 69.2%), while some had *qnrB* (*n* = 11) or *qnrA* (*n* = 1).

Figure 7: *Klebsiella pneumoniae* complex (*n* = 147), fluoroquinolone resistance mechanisms, ciprofloxacin MIC, AGAR, 2022



Note: Fluoroquinolone resistance mechanisms include mutations in either the quinolone resistance-determining region of the DNA gyrase or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*), and/or plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*) as detected by whole genome sequence analyses.

MIC = minimum inhibitory concentration; PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

Table 30: Fluroquinolone resistance determinants in *Klebsiella pneumoniae* complex, AGAR, 2022

QRDR mutations			Ciprofloxacin MIC (mg/L)			
gyrA	parE	PMQR	≤0.25	0.5	>0.5	Total
–*	–*	–*	57	5	4	66
–*	–*	*aac(6')-Ib-cr*	2	0	1	3
–*	–*	*aac(6')-Ib-cr*, *qnr*	0	0	23	23
–*	–*	qnr	2	11	26	39
–*	I529L	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
D87Y	–*	–*	0	0	1	1
S83F	–*	*qnr*	0	0	1	1
S83F, D87A	–*	*aac(6')-Ib-cr*, *qnr*	0	0	2	2
S83I	–*	–*	0	0	1	1
S83I	–*	*aac(6')-Ib-cr*	0	0	2	2
S83I	–*	*aac(6')-Ib-cr*, *qnr*	0	0	1	1
S83I	–*	*qnr*	0	0	1	1
S83Y	–*	–*	0	0	1	1
S83Y	–*	*aac(6')-Ib-cr*	1	0	4	5
Total			62	16	69	147

PMQR = plasmid-mediated quinolone resistance; QRDR = quinolone resistance-determining region

* Not detected

Notes:

1. Fluoroquinolone resistant determinants include mutations in either the QRDR of the DNA gyrase and/or topoisomerase genes (*gyrA*, *gyrB*, *parC*, *parE*) identified by PointFinder[21], and/or presence of plasmid-mediated quinolone resistance genes (*qnr* variants, *aac(6')-Ib-cr*, *qepA*) detected by whole genome sequence analysis.
2. Mutations in *gyrB* or p*arC* were not detected.

Pseudomonas aeruginosa

Of 49 *P. aeruginosa* isolates referred for sequencing eight harboured QRDR mutations, in codon 83 of *gyrA* (T83I, *n* = 6; T83A, *n* = 1). One isolate with a T83I mutation also had a second mutation in codon 87 (S87L). The ciprofloxacin MIC for all these isolates was ≥ 2 mg/L. No PMQR genes were detected.

3.9.5. Plasmid-mediated colistin determinants

Four *E. cloacae* complex isolates with the *bla*$_{IMP-4}$ carbapenemase gene (*E. hormaechei*, *n* = 3; *E. cloacae*, *n* = 1) also harboured *mcr-9.1*.

Fourteen additional isolates (*E. cloacae* complex, *n* = 13; *K. pneumoniae*, *n* = 1) that did not carry a carbapenemase gene had either *mcr-9* (*n* = 8) or *mcr-10* (*n* = 6). *mcr-9* has recently been found among several species of *Enterobacterales*. It is not associated with a resistant phenotype[23], but is typically carried on HI2 plasmids.[24, 25]

3.9.6. Ribosomal methyltransferases

Simultaneous resistance to gentamicin, tobramycin and/or amikacin is often due to ribosomal methyltransferases (RMT), which are frequently coproduced with ESBL and carbapenemases.[26, 27]

In the 2022 survey, three *Enterobacterales* were resistant to amikacin (MIC > 32 mg/L), gentamicin (MIC > 8 mg/L) and tobramycin (MIC > 8 mg/L). RMT genes were detected in all three; one *E. coli* with r*mtB1*, one *E. coli* with *armA* and one *K. pneumoniae* complex isolate with *rmtC*. All also carried a *bla*$_{CTX-M}$ gene.

Two *A. baumannii* complex isolates that carried *bla*$_{OXA-23}$ also harboured *armA*. One P*. aeruginosa* that carried *bla*$_{NDM-1}$ also harboured *rmtB4*.

3.10. Trend analysis (2013–2022)

Trend data are available for *Enterobacterales* for the 10-year period 2013 to 2022. *Acinetobacter* species and *P. aeruginosa* were introduced into the program in 2015.

EUCAST interpretive criteria have been used throughout, with the notable exception of amoxicillin–clavulanic acid. Ninety percent of the pathology services used Vitek® cards which have the CLSI formulation (2:1 ratio) for interpretation for susceptibility for this agent.

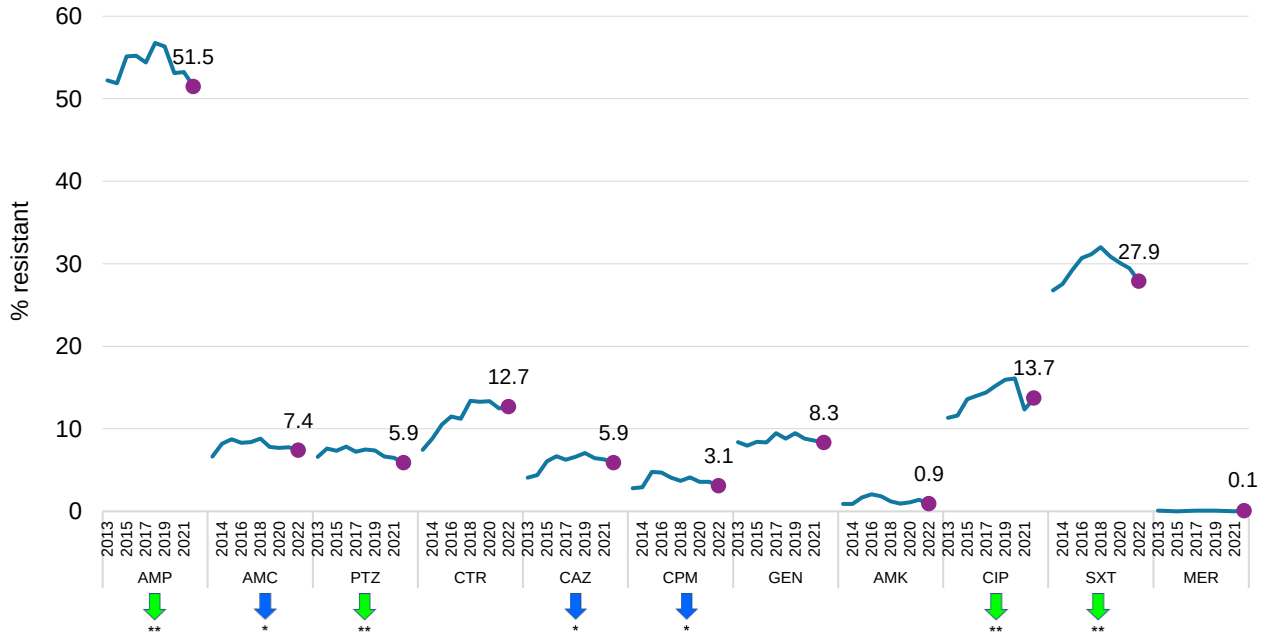
Escherichia coli

National

The percentage of resistant *E. coli* in 2022 was similar to 2021 for all antimicrobial agents tested, except for ciprofloxacin, where a 11.1% increase in resistance was seen relative to 2021 (606/4910, 12.3% in 2021, 721/5259, 13.7% in 2022; $P = 0.0421$) (Figure 8).

Rates of resistance to key antimicrobial agents over the past five years (2018–2022) decreased for ampicillin (X^2 for linear trend = 36.82, $P < 0.01$), trimethoprim-sulfamethoxazole (X^2 for linear trend = 22.48, $P < 0.01$), ciprofloxacin (X^2 for linear trend = 17.47, $P < 0.01$), and piperacillin-tazobactam (X^2 for linear trend = 12.91, $P < 0.01$) (Figure 8).

Figure 8. *Escherichia coli* resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



AMC = amoxicillin–clavulanic acid (2:1 ratio); AMK = amikacin; AMP = ampicillin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; SXT = trimethoprim-sulfamethoxazole

Notes:

1. Percentage resistance determined using EUCAST 2023 breakpoints for all years. Numbers adjacent to filled circles are those for 2022.
2. Arrows indicate antimicrobial agents for which there was a significant decrease in resistance over the past five years (2018 to 2022). Green ($P < 0.01$, **); blue ($0.01 < P < 0.05$, *).

State and territory

In 2022, fluoroquinolone resistance in *E. coli* increased in three states and territories relative to 2021, most notably in New South Wales (2021, 12.1%; 2022, 16.4%, up 35.4%, $P < 0.01$) and South Australia (2021, 8.5%; 2022, 14.6%, up 71.3%, $P < 0.01$). There was an increase in third-generation cephalosporin resistance in the Northern Territory (2021, 13.4%; 2022, 28.8%, up 115%, $P < 0.01$), and an increase in aminoglycoside resistance in South Australia (2021, 8.1%; 2022, 12.3%, up 52.5%, $P = 0.0368$).

There were significantly decreasing trends in fluoroquinolone resistance in *E. coli* over the past five years (2018-2022) in Victoria (X^2 for linear trend = 17.05, $P = <0.01$), Western Australian (X^2 for linear trend = 10.45, $P = 0.0012$) and the Australian Capital Territory (X^2 for linear trend = 7.438, $P = 0.0064$) (Table 31).

There was a significantly decreasing trend in third-generation cephalosporin resistance in *E. coli* over the past five years (2018-2022) in Victoria (X^2 for linear trend = 16.91, $P < 0.01$) (Table 32).

Over the past five years (2018-2022) aminoglycoside resistance in *E. coli* decreased in Victoria (X^2 for linear trend = 19.74, $P < 0.01$) (Table 33).

Table 31: *Escherichia coli*, percentage resistant to ciprofloxacin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	6.3 (79)	7.6 (79)	7.6 (79)	10.7 (168)	5.7 (174)	7.6 (184)	12.9 (201)	8.0 (201)	10.6 (218)	6.9 (231)	↔
Qld	8.1 (652)	7.1 (742)	8.7 (691)	9.0 (811)	12.9 (858)	10.3 (868)	10.4 (817)	11.6 (628)	8.6 (686)	10.0 (711)	↔
ACT	13.6 (118)	12.5 (168)	10.7 (149)	13.6 (154)	12.0 (158)	**17.8** (157)	**20.5** (185)	**15.2** (198)	**13.6** (206)	**10.0** (190)	▼**
Vic	11.7 (530)	16.2 (722)	14.4 (727)	15.7 (709)	15.6 (794)	**18.1** (770)	**18.3** (919)	**20.0** (899)	**13.2** (1,085)	**13.1** (1,053)	▼**
WA	13.9 (524)	12.7 (510)	16.2 (650)	15.7 (677)	16.2 (770)	**20.5** (801)	**17.3** (736)	**17.5** (776)	**16.2** (740)	14.0 (695)	▼**
SA	10.6 (379)	10.9 (386)	9.0 (454)	13.3 (429)	8.3 (288)	11.6 (405)	13.9 (440)	9.8 (479)	8.5 (470)	14.6 (439)	↔
NT	10.3 (78)	8.2 (97)	9.5 (137)	9.8 (153)	15.6 (141)	12.5 (160)	20.0 (205)	20.8 (197)	17.0 (224)	15.3 (170)	↔
NSW	13.2 (555)	11.8 (781)	17.7 (1,107)	17.3 (993)	16.3 (1,170)	15.8 (1,224)	16.9 (1,379)	17.5 (1,492)	12.1 (1,281)	16.4 (1,770)	↔
Australia	11.3 (2,915)	11.6 (3,485)	13.6 (3,994)	14.0 (4,094)	**14.4** (4,353)	**15.2** (4,569)	**16.0** (4,882)	**16.1** (4,870)	**12.3** (4,910)	**13.7** (5,259)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P < 0.01$, **), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years.

Table 32: *Escherichia coli*, percentage resistant to ceftriaxone and/or ceftazidime (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	1.3 (80)	10.1 (79)	0.0 (79)	6.5 (168)	5.2 (174)	7.6 (184)	7.0 (201)	6.0 (201)	6.0 (218)	5.2 (231)	↔
Qld	5.4 (652)	7.1 (742)	6.1 (691)	8.1 (811)	9.4 (858)	11.5 (868)	8.4 (817)	8.9 (628)	10.6 (686)	11.0 (711)	↔
Vic	11.1 (530)	13.0 (722)	12.5 (727)	13.7 (709)	14.2 (794)	**17.1** (770)	**16.9** (922)	**17.0** (899)	**13.5** (1,086)	**11.5** (1,054)	▼**
WA	6.3 (524)	6.3 (510)	9.7 (650)	11.7 (677)	11.5 (771)	15.6 (801)	12.2 (736)	12.5 (776)	14.4 (741)	12.1 (695)	↔
SA	5.5 (379)	6.2 (386)	7.5 (454)	12.3 (431)	4.8 (289)	9.1 (405)	12.5 (440)	9.2 (479)	11.9 (471)	12.5 (439)	↔
NSW	11.2 (555)	10.0 (781)	15.4 (1,107)	15.1 (993)	14.4 (1,170)	13.5 (1,224)	15.4 (1,379)	15.7 (1,493)	14.1 (1,281)	14.6 (1,771)	↔
ACT	5.1 (118)	8.9 (168)	10.7 (149)	9.7 (154)	12.0 (158)	12.7 (157)	16.7 (186)	13.1 (198)	13.1 (206)	16.8 (190)	↔
NT	9.0 (78)	9.3 (97)	8.8 (137)	9.2 (153)	9.2 (141)	17.5 (160)	16.1 (205)	19.8 (197)	13.4 (224)	28.8 (170)	↔
Australia	7.7 (2,916)	9.0 (3,485)	10.7 (3,994)	11.8 (4,096)	11.6 (4,355)	13.6 (4,569)	13.5 (4,886)	13.6 (4,871)	12.9 (4,913)	13.1 (5,261)	↔

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P < 0.01$, **), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years.

Table 33: *Escherichia coli*, percentage resistant to gentamicin and/or tobramycin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	2.5 (80)	8.9 (79)	2.5 (79)	6.0 (168)	3.4 (174)	3.8 (184)	7.0 (201)	4.5 (201)	3.2 (218)	3.9 (231)	↔
Vic	11.9 (530)	10.9 (722)	10.2 (727)	9.3 (709)	12.8 (794)	**10.5** (770)	**12.9** (922)	**11.8** (899)	**7.7** (1,086)	**6.7** (1,054)	▼**
ACT	14.4 (118)	10.7 (168)	5.4 (149)	7.1 (154)	13.3 (158)	8.9 (157)	11.3 (186)	10.1 (198)	9.2 (206)	7.4 (190)	↔
Qld	7.2 (652)	8.1 (742)	7.7 (691)	8.1 (811)	9.7 (858)	7.7 (868)	8.4 (817)	8.3 (628)	7.6 (686)	7.5 (711)	↔
WA	9.2 (524)	7.8 (511)	11.8 (650)	14.8 (677)	12.2 (771)	13.0 (801)	9.6 (736)	9.7 (776)	11.6 (741)	8.8 (695)	↔
NSW	11.0 (555)	9.5 (781)	11.4 (1,107)	9.0 (993)	10.4 (1,170)	10.8 (1,225)	10.4 (1,379)	9.7 (1,493)	10.1 (1,281)	9.5 (1,769)	↔
SA	6.9 (378)	6.5 (386)	9.0 (454)	10.7 (431)	6.6 (289)	9.6 (405)	9.3 (440)	8.1 (479)	8.1 (471)	12.3 (439)	↔
NT	14.1 (78)	15.5 (97)	11.7 (137)	12.4 (153)	12.8 (141)	16.9 (160)	18.5 (205)	20.8 (197)	17.4 (224)	22.9 (170)	↔
Australia	9.4 (2,915)	9.1 (3,486)	9.9 (3,994)	9.9 (4,096)	10.7 (4,355)	10.3 (4,570)	10.6 (4,886)	10.0 (4,871)	9.3 (4,913)	8.9 (5,259)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ ($P<0.01$, **), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years

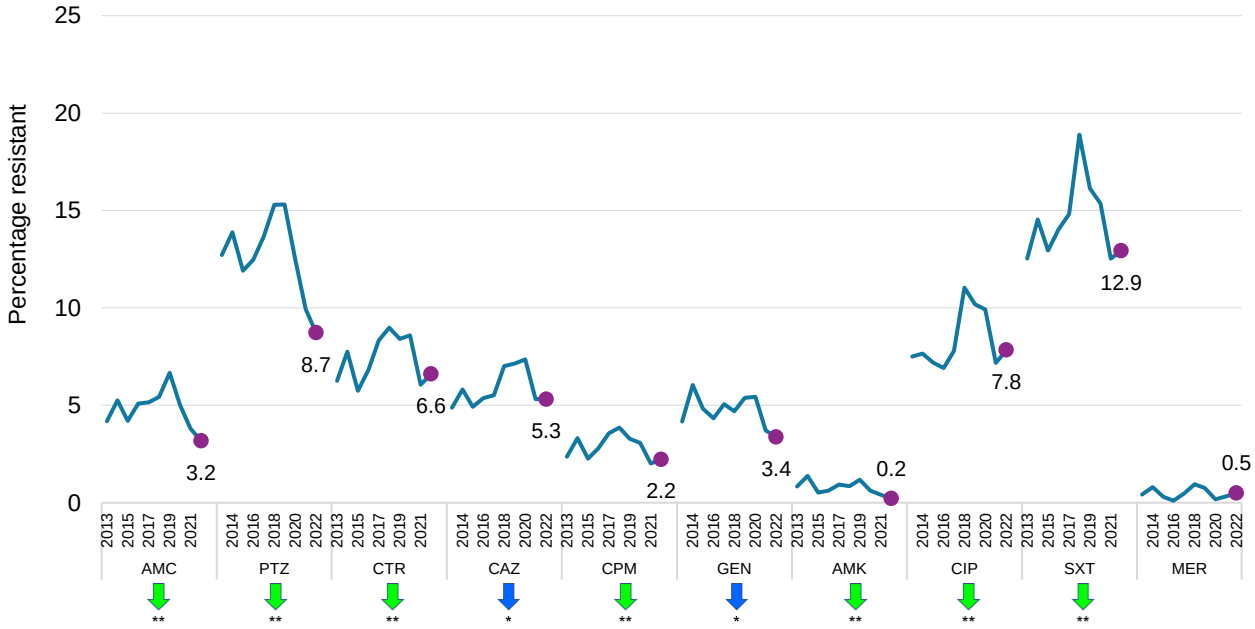
Klebsiella pneumoniae complex

National

The percentage of resistant *K. pneumoniae* complex isolates in 2022 was similar to that seen in 2021 (Figure 9).

Over the past five years (2018–2022), there was a significant decreasing trend in resistance to piperacillin-tazobactam (X^2 for linear trend = 40.27, $P < 0.01$), amoxicillin-clavulanic acid (X^2 for linear trend = 13.66, $P < 0.01$), trimethoprim-sulfamethoxazole (X^2 for linear trend = 23.00, $P < 0.01$), ciprofloxacin (X^2 for linear trend = 13.08, $P < 0.01$), cefepime (X^2 for linear trend = 8.994, $P < 0.01$), ceftriaxone (X^2 for linear trend = 8.848, $P < 0.01$), and amikacin (X^2 for linear trend = 8.553, $P < 0.01$) (Figure 9).

Figure 9. *Klebsiella pneumoniae* complex resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



AMC = amoxicillin–clavulanic acid (2:1 ratio); AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin–tazobactam; SXT = trimethoprim-sulfamethoxazole

Notes:

1. Percentage resistance determined using EUCAST 2023 breakpoints for all years. Numbers adjacent to filled circles are those for 2022.
2. Arrows indicate antimicrobial agents for which there was a significant decrease in resistance over the past five years (2018 to 2022). Green ($P < 0.01$, **); blue ($0.01 < P < 0.05$, *).

By state and territory

Four states and territories (Western Australia, Tasmania, Northern Territory and the Australian Capital Territory) had an increase in fluoroquinolone (Table 34), third-generation cephalosporin (Table 35), and aminoglycoside resistance (Table 36) in *K. pneumoniae* complex isolates in 2022, relative to 2021. The only notable change was a decline in fluoroquinolone resistance South Australia (2021, 9.6%; 2022, 2.4%; down 75.0%; $P = 0.047$).

Over the past five years (2018-2022), Victoria was the only state with significantly decreasing trends in fluoroquinolone (X^2 for linear trend = 37.54, $P < 0.01$), third generation cephalosporin (X^2 for linear trend = 30.99, $P < 0.01$), and aminoglycoside (X^2 for linear trend = 43.07, $P < 0.01$) resistance in *K. pneumoniae* complex isolates (Tables 34-36).

Table 34: *Klebsiella pneumoniae* complex, percentage resistant to ciprofloxacin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
SA	13.3 (75)	5.4 (74)	4.7 (85)	7.4 (81)	2.8 (71)	8.8 (91)	15.7 (89)	9.9 (81)	9.6 (114)	2.4 (83)	↔
Qld	5.8 (207)	5.3 (208)	6.3 (189)	4.2 (189)	6.1 (246)	5.6 (270)	5.2 (249)	6.5 (185)	8.0 (201)	5.7 (227)	↔
Vic	12.4 (145)	10.3 (174)	11.9 (177)	13.3 (180)	17.6 (199)	**24.3** (214)	**17.0** (212)	**17.7** (209)	**7.3** (260)	**7.4** (282)	▼**
Tas	7.1 (14)	11.1 (9)	5.6 (18)	5.6 (36)	0.0 (30)	11.8 (34)	7.8 (51)	6.7 (30)	4.5 (44)	8.0 (50)	↔
NSW	3.5 (113)	9.3 (205)	7.2 (236)	8.4 (226)	5.5 (293)	9.3 (301)	10.4 (347)	10.2 (371)	8.6 (337)	8.4 (443)	↔
WA	4.8 (124)	4.7 (149)	5.9 (187)	2.8 (181)	6.3 (159)	7.5 (186)	5.0 (160)	2.6 (189)	3.9 (204)	8.5 (212)	↔
ACT	4.5 (22)	7.7 (26)	5.7 (35)	5.3 (38)	7.7 (39)	8.3 (36)	8.3 (36)	13.2 (38)	4.3 (46)	11.9 (42)	↔
NT	10.5 (19)	16.1 (31)	4.3 (47)	2.6 (38)	6.7 (30)	13.5 (37)	15.6 (45)	16.2 (37)	6.1 (33)	17.3 (52)	↔
Australia	7.5 (719)	7.6 (876)	7.2 (974)	6.9 (969)	7.8 (1,067)	**11.0** (1,169)	**10.2** (1,189)	**9.9** (1,140)	**7.2** (1,239)	**7.8** (1,391)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ (P<0.01, **), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years.

Table 35: *Klebsiella pneumoniae* complex, percentage resistant to ceftriaxone and/or ceftazidime (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Qld	6.3 (207)	4.3 (208)	3.7 (189)	3.7 (189)	3.3 (246)	5.9 (270)	4.4 (249)	3.8 (185)	2.5 (201)	3.5 (227)	↔
SA	2.7 (75)	4.1 (74)	3.5 (85)	7.4 (81)	5.6 (72)	9.9 (91)	9.0 (89)	7.4 (81)	6.1 (114)	4.8 (83)	↔
WA	4.0 (124)	4.0 (149)	3.7 (187)	5.5 (181)	5.7 (159)	4.3 (186)	4.4 (160)	3.7 (189)	3.9 (204)	5.2 (212)	↔
Vic	13.1 (145)	10.9 (174)	10.7 (177)	13.9 (180)	19.6 (199)	**19.2** (214)	**16.0** (212)	**16.7** (210)	**5.0** (260)	**6.4** (282)	▼**
Tas	7.1 (14)	11.1 (9)	5.6 (18)	5.6 (36)	3.3 (30)	11.8 (34)	7.8 (51)	6.7 (30)	4.5 (44)	8.0 (50)	↔
NSW	2.7 (113)	12.1 (206)	7.6 (236)	9.7 (226)	7.5 (293)	8.9 (302)	9.8 (348)	9.2 (371)	12.2 (337)	8.1 (444)	↔
ACT	0.0 (22)	11.5 (26)	2.9 (35)	2.6 (38)	10.3 (39)	5.6 (36)	11.1 (36)	7.9 (38)	4.3 (46)	9.5 (42)	↔
NT	15.8 (19)	6.5 (31)	6.4 (47)	2.6 (38)	6.7 (30)	13.5 (37)	15.6 (45)	27.0 (37)	15.2 (33)	21.2 (52)	↔
Australia	6.4 (719)	7.8 (877)	6.1 (974)	7.6 (969)	8.3 (1,068)	**9.6** (1,170)	**9.2** (1,190)	**9.1** (1,141)	**6.7** (1,239)	**6.9** (1,392)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ (P<0.01, **), ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years.

Table 36: *Klebsiella pneumoniae* complex, percentage resistant to gentamicin and/or tobramycin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
Tas	7.1 (14)	11.1 (9)	11.1 (18)	2.8 (36)	3.3 (30)	8.8 (34)	5.9 (51)	6.7 (30)	0.0 (44)	2.0 (50)	↔
Qld	3.9 (207)	4.3 (208)	4.2 (189)	3.7 (189)	3.3 (246)	3.0 (270)	2.4 (249)	2.7 (185)	3.5 (201)	2.2 (227)	↔
SA	5.3 (75)	1.4 (74)	5.9 (85)	3.7 (81)	4.2 (72)	7.7 (91)	7.9 (89)	3.7 (81)	6.1 (114)	2.4 (83)	↔
WA	3.2 (124)	2.7 (149)	3.2 (187)	5.0 (181)	3.8 (159)	3.8 (186)	3.1 (160)	2.1 (189)	2.5 (204)	3.3 (212)	↔
Vic	11.0 (145)	9.8 (174)	7.9 (177)	10.0 (180)	15.6 (199)	**18.7** (214)	**14.2** (212)	**11.0** (210)	**4.6** (260)	**3.5** (282)	▼**
NSW	2.7 (113)	11.2 (206)	8.1 (236)	6.2 (226)	5.5 (293)	5.0 (302)	9.5 (348)	8.9 (371)	5.9 (337)	5.6 (444)	↔
ACT	0.0 (22)	7.7 (26)	2.9 (35)	2.6 (38)	7.7 (39)	8.3 (36)	11.1 (36)	5.3 (38)	4.3 (46)	11.9 (42)	↔
NT	15.8 (19)	16.1 (31)	10.6 (47)	2.6 (38)	6.7 (30)	16.2 (37)	13.3 (45)	24.3 (37)	9.1 (33)	13.5 (52)	↔
Australia	5.4 (719)	7.1 (877)	6.2 (974)	5.6 (969)	6.6 (1,068)	**7.6** (1,170)	**7.9** (1,190)	**7.1** (1,141)	**4.5** (1,239)	**4.5** (1,392)	▼**

* Chi-square test for trend for past five years (2018–2022), **bold** text significant decrease ▼ (P<0.01, **), ↔ no significant difference

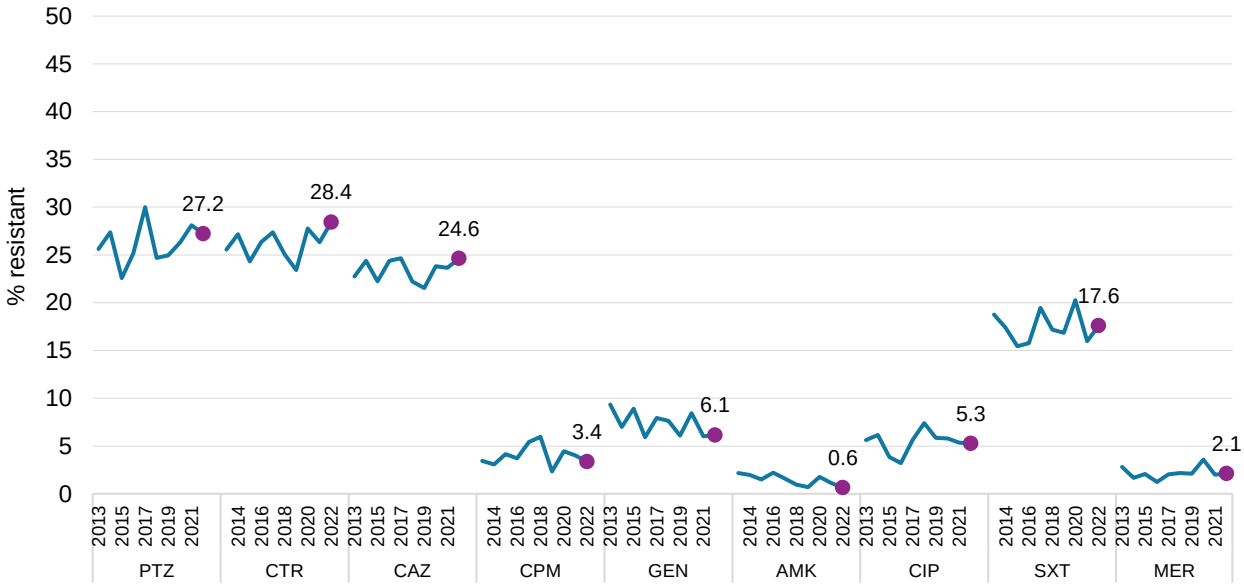
Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years

Enterobacter cloacae complex

National

For *E. cloacae* complex isolates, the percentage resistance to all key antimicrobials in 2022 was similar to 2021. There were no significant trends of increasing or decreasing resistance in *E. cloacae* complex isolates over the past five-year period (2018–2022) (Figure 10).

Figure 10. *Enterobacter cloacae* complex resistance to key antimicrobials (EUCAST), bloodstream isolates, AGAR, 2013–2022



AMK = amikacin; CAZ = ceftazidime; CIP = ciprofloxacin; CPM = cefepime; CTR = ceftriaxone; EUCAST = European Committee on Antimicrobial Susceptibility Testing; GEN = gentamicin; MER = meropenem; PTZ = piperacillin-tazobactam; SXT = trimethoprim-sulfamethoxazole

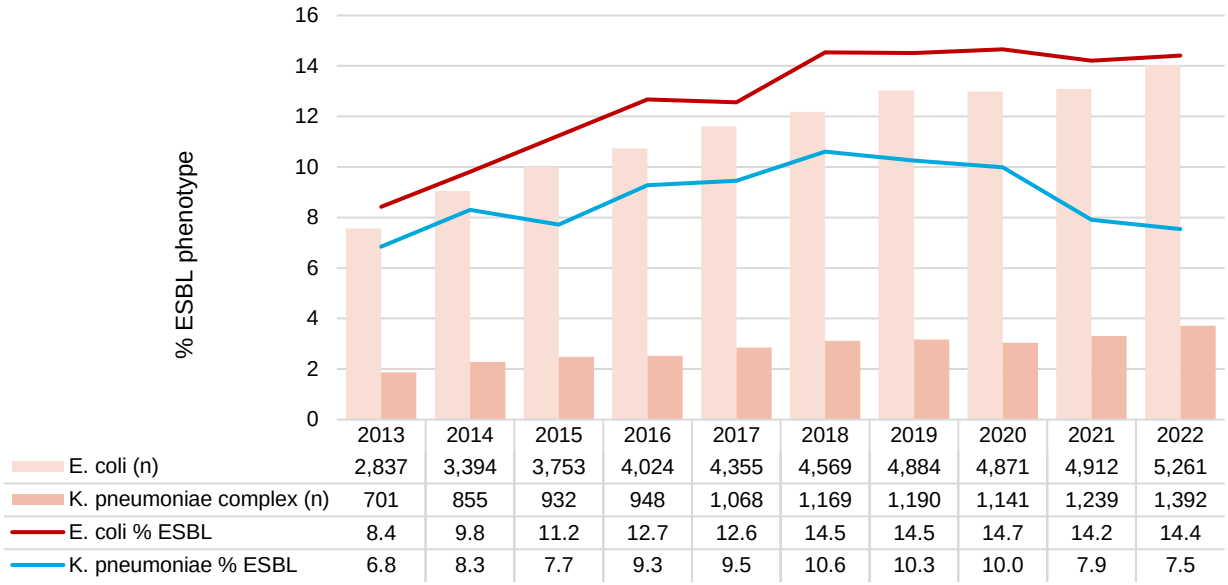
Notes: Percentage resistance determined using EUCAST 2023 breakpoints for all years. Filled circles indicate values for 2022.

Extended-spectrum β-lactamases

The frequency of *E. coli* with an ESBL phenotypes increased from 8.4% in 2013 to 14.4% in 2018 and has remained at steady at 14% since 2019. For *K. pneumoniae* complex isolates, the frequency of an ESBL phenotypes was lower than that observed among *E. coli* and increased from 6.8% in 2013 to 10% in 2018 to 2020, decreasing to 7.9% in 2021 and 7.5% in 2022 (Figure 11).

ESBL-type β-lactamase genes (alone or with other *bla* genes) continue to be the dominant β-lactam resistance mechanism among *E. coli* and *K. pneumoniae* complex isolates with an ESBL phenotype, with considerable regional variation noted.

Figure 11. Ten-year trend in percent *Escherichia coli* and *Klebsiella pneumoniae* complex isolates with extended spectrum β-lactamase phenotype, AGAR, 2013–2022



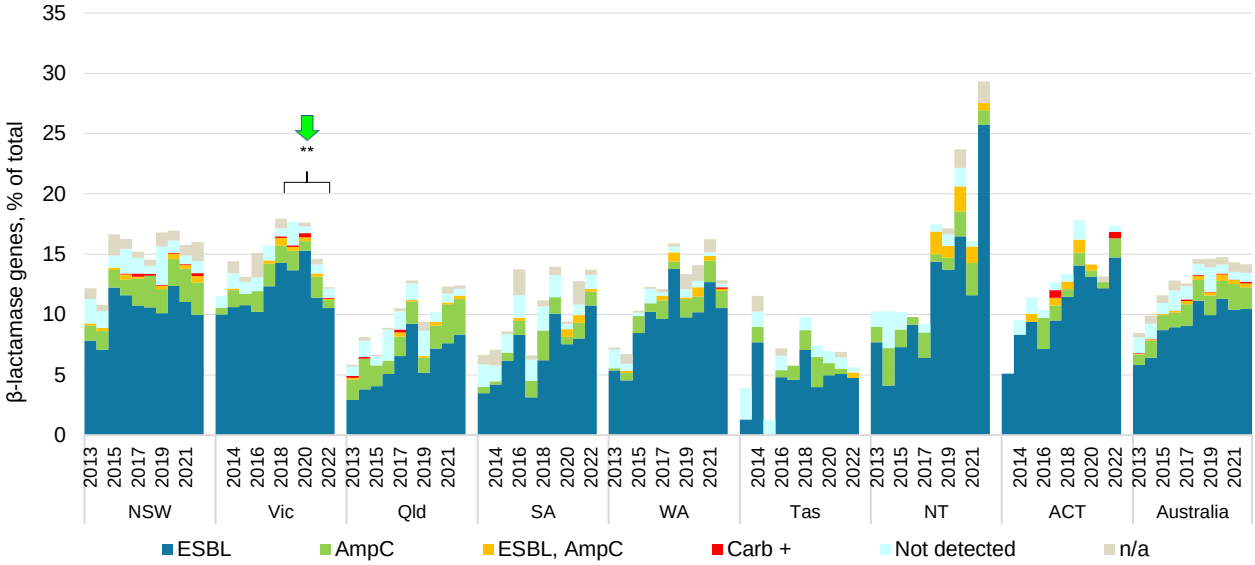
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
E. coli (n)	2,837	3,394	3,753	4,024	4,355	4,569	4,884	4,871	4,912	5,261
K. pneumoniae complex (n)	701	855	932	948	1,068	1,169	1,190	1,141	1,239	1,392
E. coli % ESBL	8.4	9.8	11.2	12.7	12.6	14.5	14.5	14.7	14.2	14.4
K. pneumoniae % ESBL	6.8	8.3	7.7	9.3	9.5	10.6	10.3	10.0	7.9	7.5

ESBL = extended-spectrum β-lactamase

Overall, in the 2022 survey, there was no change in the proportion of *E. coli* with confirmed ESBL genes relative to 2021 (2021: 524/4873, 10.8%; 2022: 566/5206, 10.8%). However, in the Northern Territory, the proportion of confirmed ESBL genes doubled (2021,12.9%; 2022, 26.3%, $P < 0.01$) (Figure 12). In *K. pneumoniae* complex isolates, the proportion of confirmed ESBL genes overall in 2022 increased by 19.2% relative to 2021 (2021: 57/1235, 4.6%; 2022: 77/1396, 5.5%).

Over the past five years (2018-2022), a significantly decreasing trend in the proportion of *E. coli* with confirmed ESBL-genes was seen in Victoria (X_2 for linear trend = 10.39, $P < 0.01$) (Figure 12). Victoria also had a significantly decreasing trend (X_2 for linear trend = 21.95, $P < 0.01$) for *K. pneumoniae* complex isolates (Figure 13).

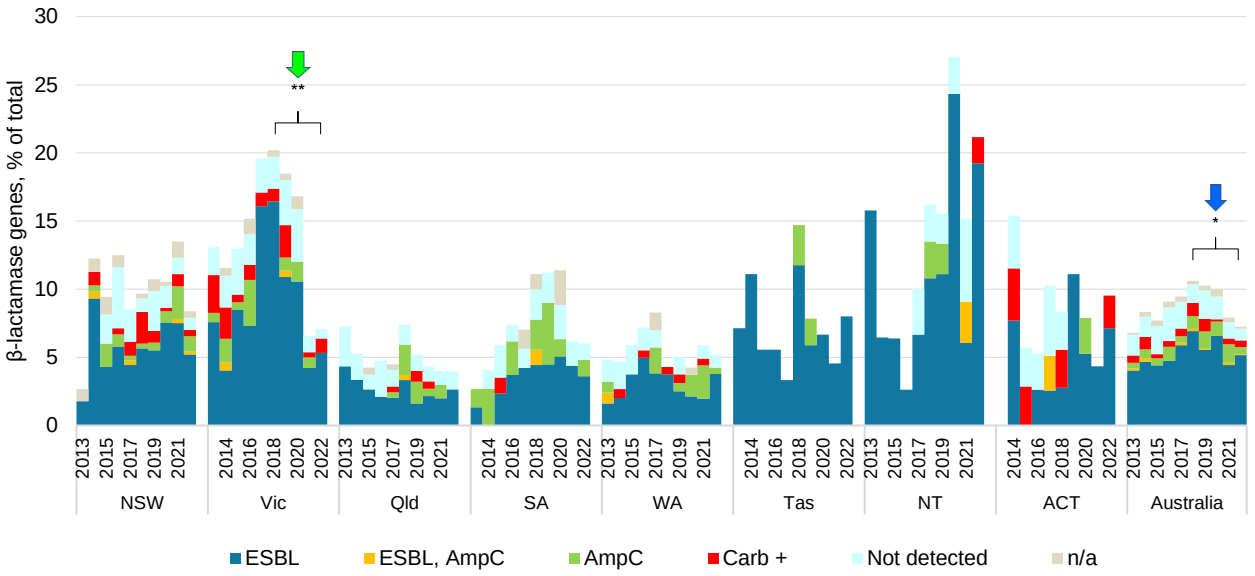
Figure 12. Proportion of β-lactamase genes in *Escherichia coli*, by state and territory, and nationally, AGAR, 2013–2022



AmpC = plasmid-borne AmpC; Carb+ = carbapenemase with or without other β-lactamase genes; ESBL = extended spectrum β-lactamase; n/a = isolate not available for confirmation by WGS

Notes:
1. β-lactamase genes (ESBL-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Green arrow indicates a significant decrease ($P < 0.01$, **) over the past five years (2018 to 2022) seen in Victoria only.

Figure 13. Proportion of β-lactamase genes in *Klebsiella pneumoniae* complex isolates by state and territory, and nationally, AGAR, 2013–2022



AmpC = plasmid-borne AmpC; Carb+ = carbapenemase with or without other β-lactamase genes; ESBL = extended spectrum β-lactamase; n/a = isolate not available for confirmation by WGS

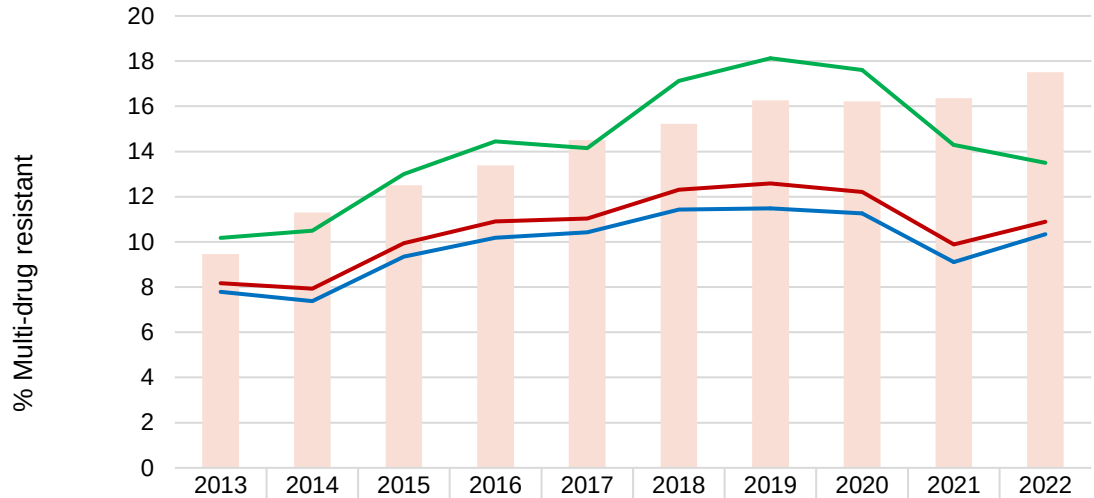
Notes:
1. β-lactamase genes (ESBL-types, AmpC, carbapenemase) detected among isolates with an ESBL phenotype.
2. Arrows indicate states and territories where there was a significant decrease in proportion of β-lactamase genes over the past five years (2018 to 2022); green ($P < 0.01$, **), blue ($0.01 < P < 0.05$, *)

Multi-drug resistance

In *E. coli*, the frequency of MDR to five key antimicrobial groups (aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) increased from 8.2% in 2013 to 11.0% in 2017, remained steady at 12% from 2018 to 2020, and decreased to 9.9% in 2021 and 10.9% in 2022. It was highest among HO isolates (Figure 14). Although the rate of MDR among CO isolates increased in 2022 (10.3%) compared to 2021 (9.1%), the increase was not statistically significant.

For *K. pneumoniae* complex isolates, the frequency of MDR to fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems was more variable (Figure 15). For HO isolates, the highest frequency was observed from 2018 and 2019 (10.6%–11.2%). It fell sharply in 2020 to 5.4% and was 4.2% in 2021 and 4.0% in 2022. There was little change in frequency among CO isolates; the lowest rate was observed in 2021 (2.0%), down from 4.6% in 2018. It was 2.2% in 2022.

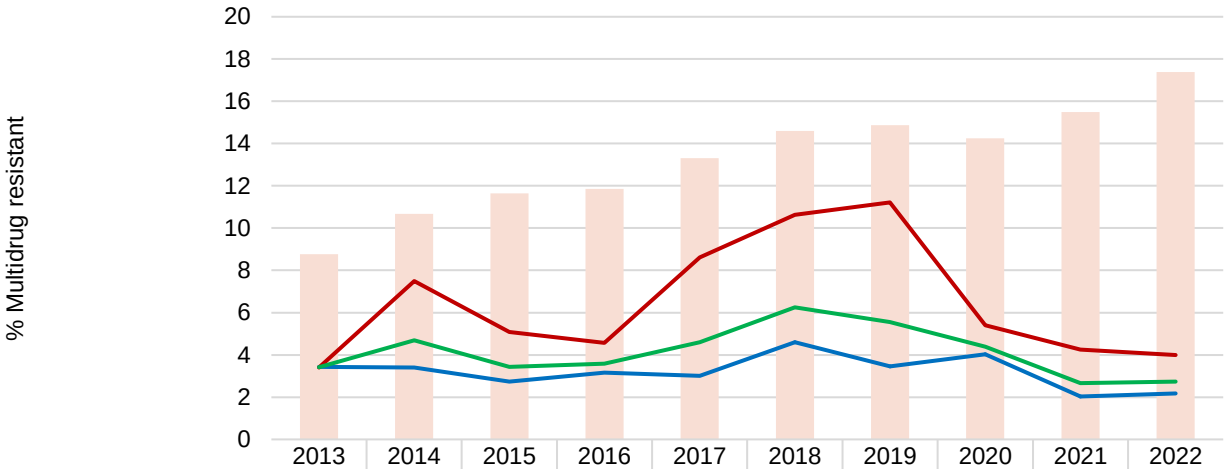
Figure 14. Ten-year trend in percent multi-drug resistance among *Escherichia coli*, by onset, AGAR, 2013 to 2022



	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Isolates, n	2,838	3,392	3,751	4,016	4,352	4,566	4,878	4,865	4,907	5,254
Community onset	7.8	7.4	9.3	10.2	10.4	11.4	11.5	11.3	9.1	10.3
Hospital onset	10.2	10.5	13.0	14.5	14.1	17.1	18.1	17.6	14.3	13.5
Overall	8.2	7.9	9.9	10.9	11.0	12.3	12.6	12.2	9.9	10.9

Notes:
1. Multi-drug resistance was defined as resistance to one or more agent in three or more antimicrobial categories.
2. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), and penicillins (ampicillin).

Figure 15. Ten-year trend in percent multi-drug resistance among *Klebsiella pneumoniae* complex isolates by onset, AGAR, 2013 to 2022



	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Isolates, n	701	854	932	948	1,065	1,168	1,189	1,140	1,239	1,391
Community onset	3.4	3.4	2.7	3.2	3.0	4.6	3.5	4.0	2.0	2.2
Hospital onset	3.4	7.5	5.1	4.6	8.6	10.6	11.2	5.4	4.2	4.0
Overall	3.4	4.7	3.4	3.6	4.6	6.3	5.6	4.4	2.7	2.7

Notes:
1. Multi-drug resistance was defined as resistance to one or more agent in three or more antimicrobial categories.
2. Antimicrobial categories (agents) were aminoglycosides (gentamicin or tobramycin), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin).

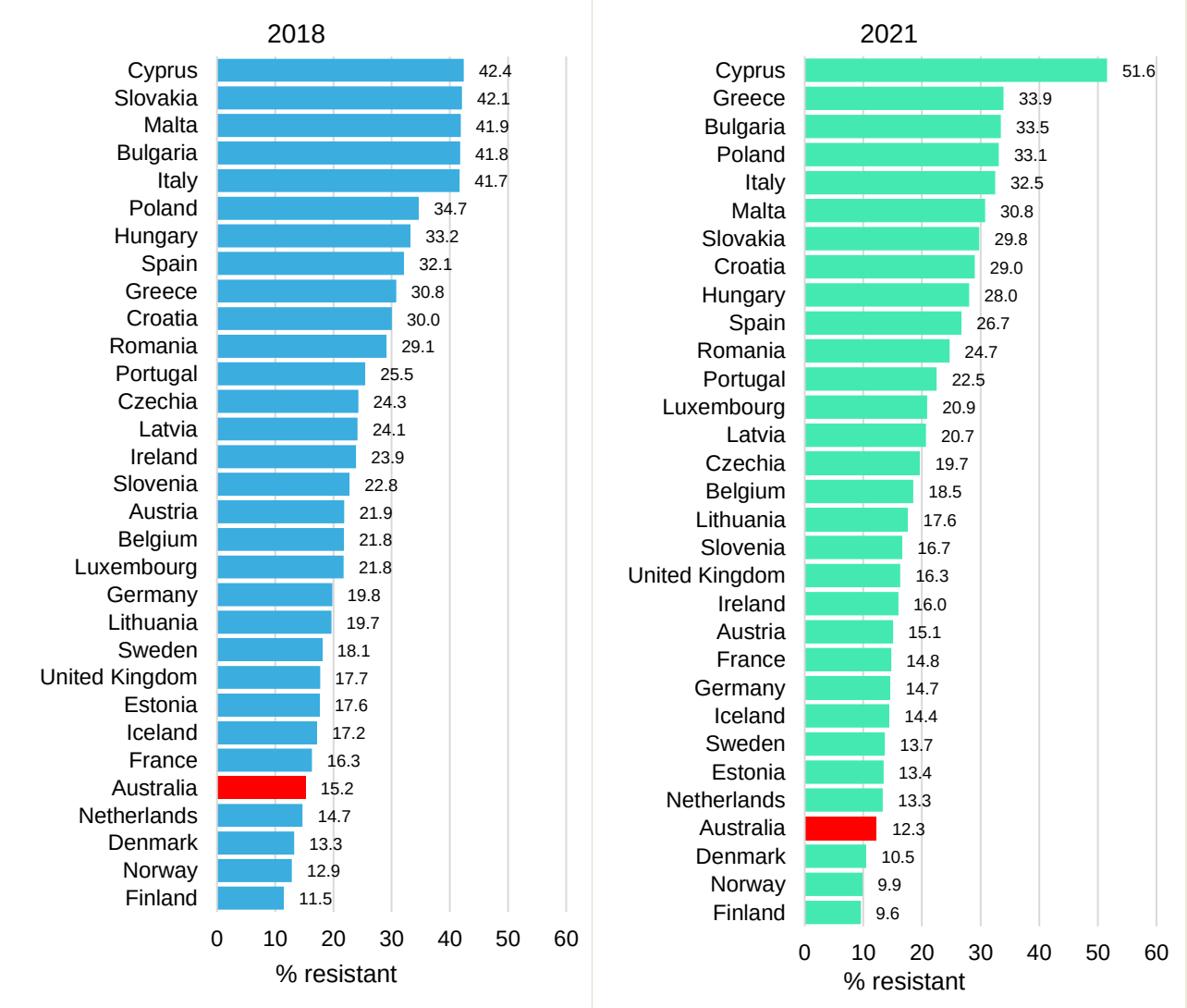
4. International comparisons

Data from AGAR can be compared with data from the European Antimicrobial Resistance Surveillance Network (EARs-Net) program[28], and the World Health Organization (WHO) Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network[29], as all these surveillance systems review resistance in bacterial pathogens isolated from blood cultures. Data from 2022 was not available at the time of this report.

Rates of resistance to fluoroquinolones in *E. coli* and *K. pneumoniae* (represented by resistance to ciprofloxacin) remain low in Australia compared with most European countries (Figures 16 and 17). Australia ranked fifth lowest in rates of resistance to fluoroquinolones in *E. coli* compared with European countries in 2018 (15.2%), it was fourth lowest in 2021 (12.3%); in 2022 the rate was 13.7%. For *K. pneumoniae*, Australia ranked fourth lowest in 2018 (11.0%) and 2021 (7.2%); in 2022, the rate was 7.9%.

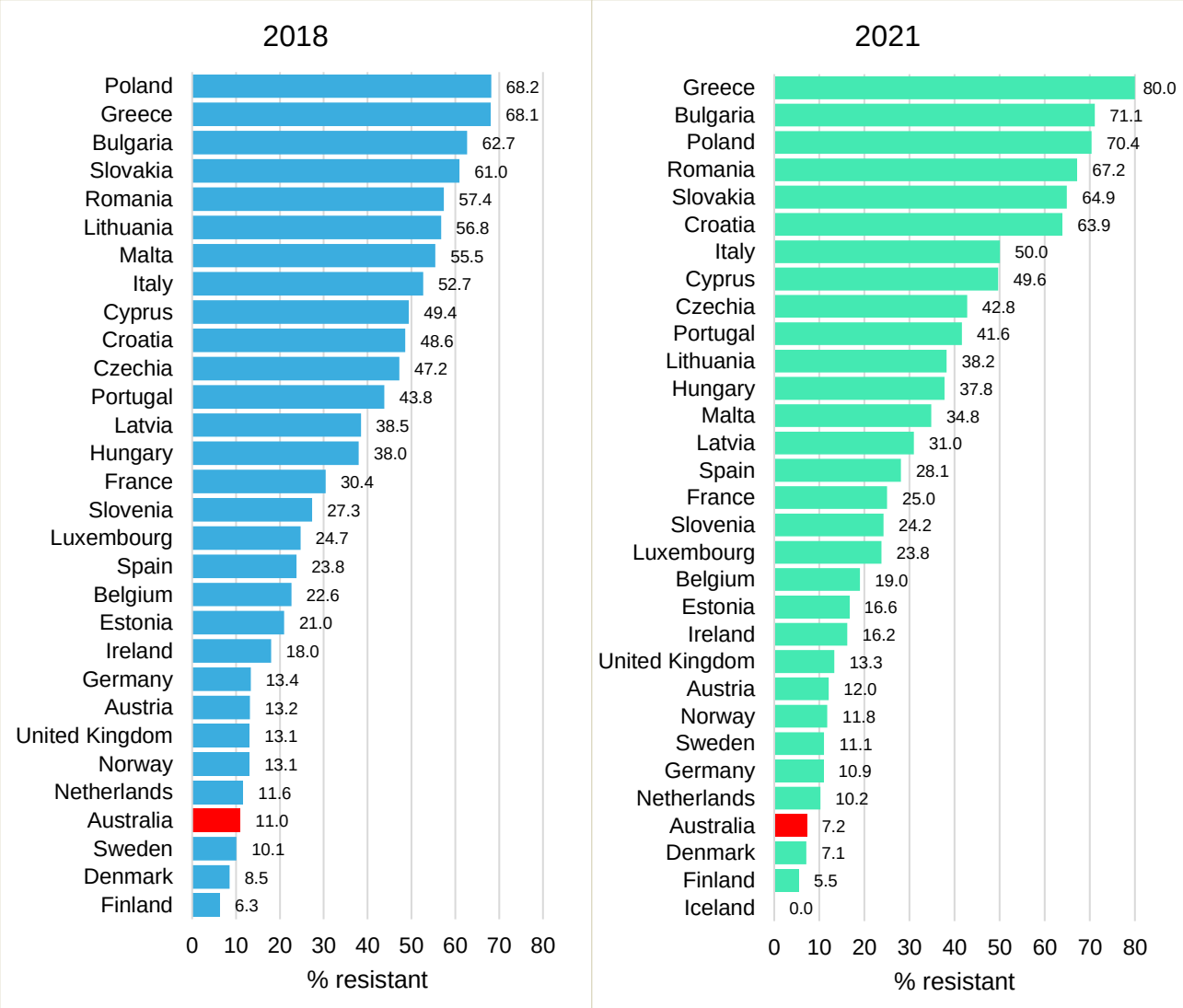
Australia now ranks towards the middle in rates of resistance to third-generation cephalosporins in *E. coli* compared to European countries. Third-generation cephalosporin resistance in *K. pneumoniae* is low by comparison (Figures 18 and 19).

Figure 16: Comparison of *Escherichia coli* rates of resistance to ciprofloxacin in Australia (AGAR), European countries and the United Kingdom, blood culture isolates, 2018 and 2021



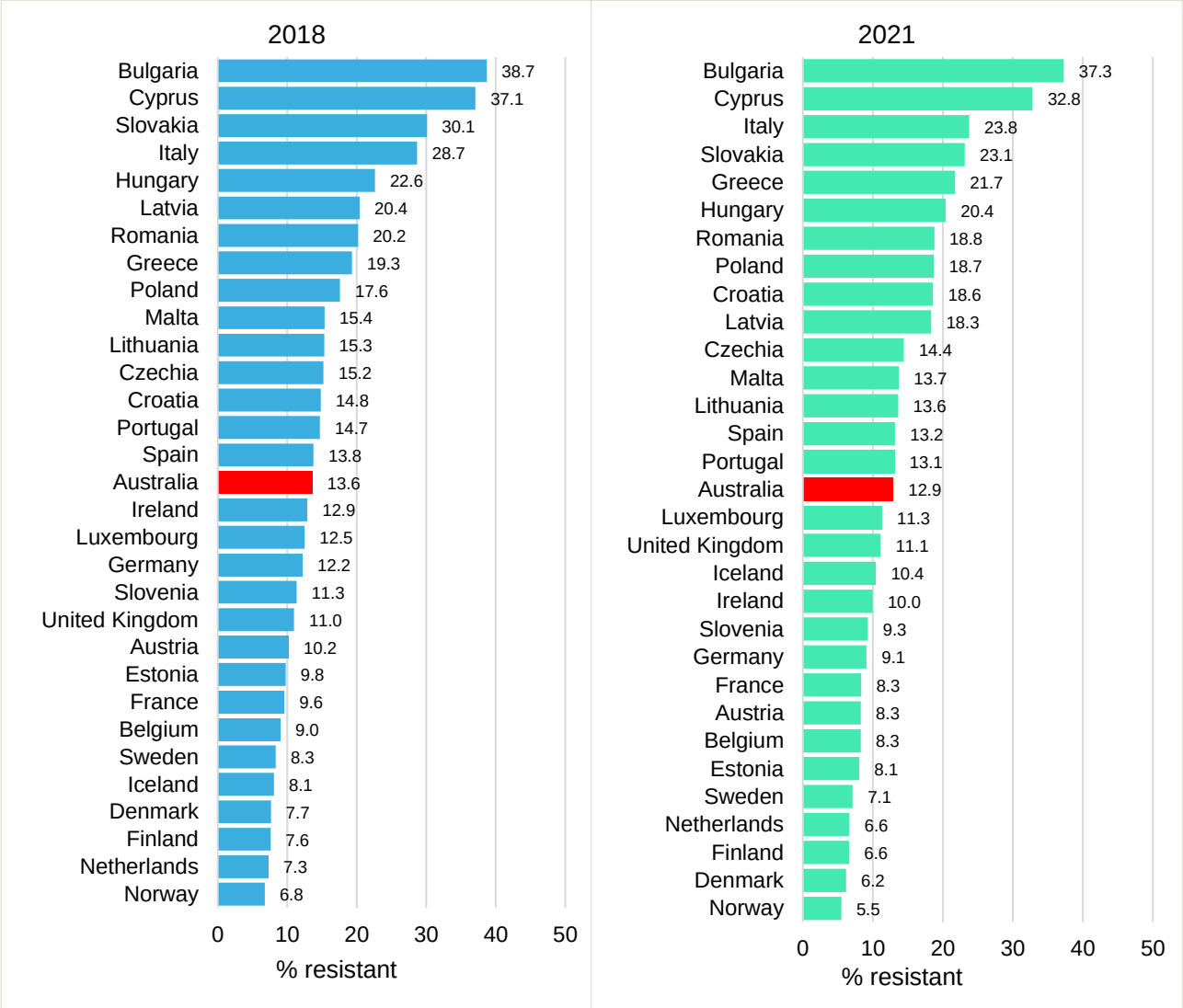
Source: EARS-Net (Europe)[30, 31], CAESAR (United Kingdom)[29]

Figure 17: Comparison of *Klebsiella pneumoniae* rates of resistance to ciprofloxacin in Australia (AGAR), European countries and the United Kingdom, blood culture isolates, 2018 and 2021



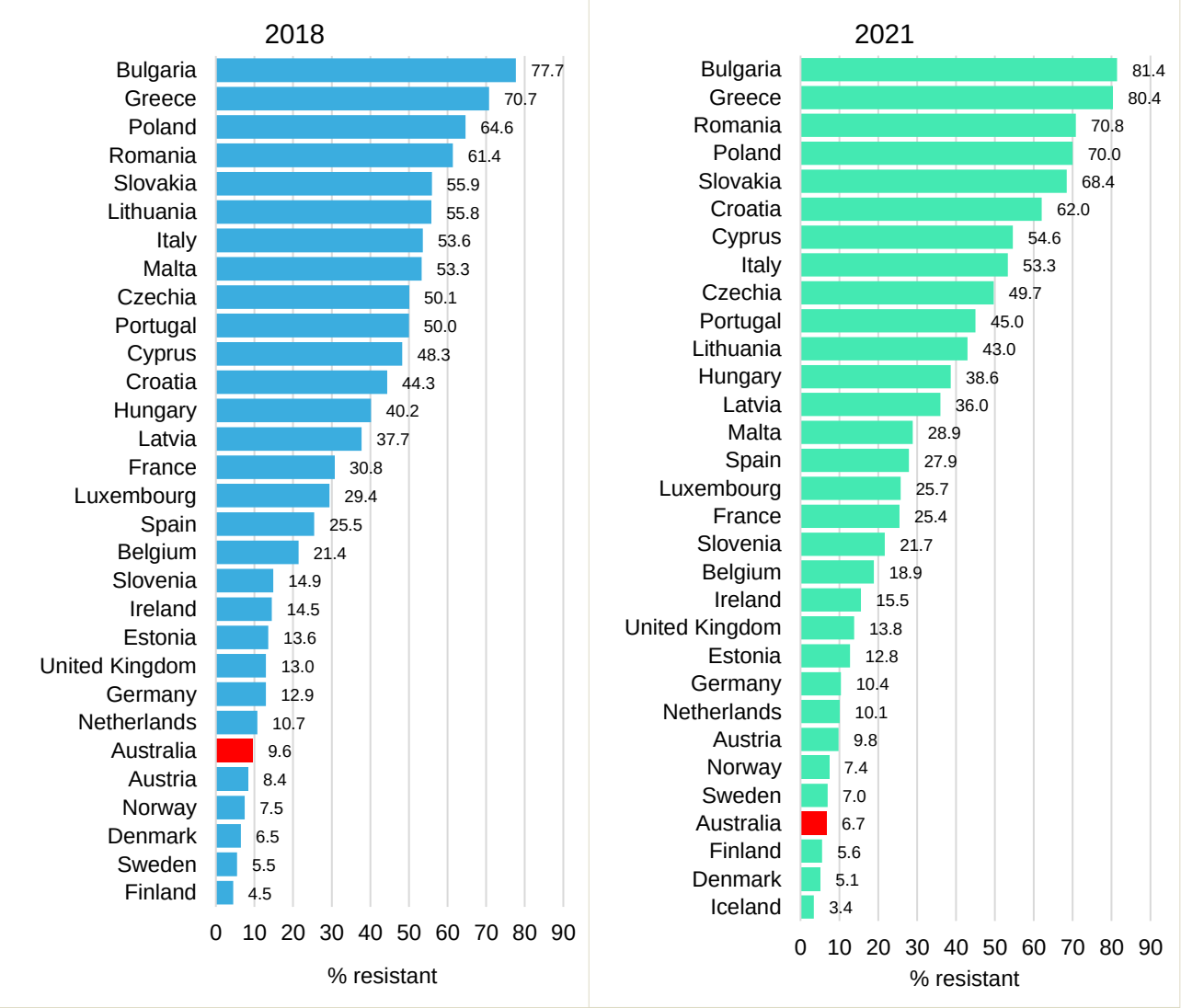
Source: EARS-Net (Europe)[30, 31], CAESAR (United Kingdom)[29]

Figure 18: Comparison of *Escherichia coli* rates of resistance to third-generation cephalosporins in Australia (AGAR), European countries and the United Kingdom, blood culture isolates, 2018 and 2021



Source: EARS-Net (Europe)[30, 31], CAESAR (United Kingdom)[29]

Figure 19: Comparison of *Klebsiella pneumoniae* rates of resistance to third-generation cephalosporins in Australia (AGAR), European countries, and the United Kingdom, blood culture isolates, 2018 and 2021



Source: EARS-Net (Europe)[30, 31], CAESAR (United Kingdom)[29]

5. Limitations of the study

Although this study is considered comprehensive in its coverage of Australia, and the methods follow international standards, the data and their interpretation have a number of limitations:

- The data are not denominator controlled, and there is currently no consensus on an appropriate denominator for such surveys; hospital size, patient throughput, patient complexity and local antibiotic use patterns all influence the types of resistance that are likely to be observed.
- Although data have been collected from 44 large hospitals, or for north-west Western Australia from 11 regional or district hospitals, it is not yet clear how representative the sample is of Australia as a whole, because the proportion of the population that is served by the laboratories that participate in AGAR is not accurately known. Further, it is likely that the proportion of the population served differs in each state and territory.
- Because of the formulation of amoxicillin–clavulanic acid in the Vitek® cards used, interpretation using EUCAST guidelines for this agent was limited to data available from Phoenix™ cards. Only 9% of the laboratories used cards that contained the EUCAST formulation.
- Concentration ranges of some antimicrobial agents in both the Vitek® and Phoenix™ cards limit accurate identification of 'susceptible' for some combinations of antimicrobial agents and species.
- Data are classified into HO- and CO infections; healthcare-associated CO infections may be included in the CO group.
- Association of resistance genes with relevant mobile genetic element/s (for example, plasmid/s) is not included in this report.

6. Discussion and conclusions

AGAR data show that in 2022 onset of episodes of bacteraemia in Australia continues to be overwhelmingly in the community. For the GnSOP bacteraemia program, the most frequent predisposing clinical manifestations were urinary tract infection for CO episodes and febrile neutropenia and urinary tract infection for HO episodes. Strategies to reduce blood stream infections should take this information on clinical manifestation (sources of bacteraemia) into account.

Previous AGAR reports had shown a longitudinal trend of increasing *E. coli* resistance to key anti-gram-negative antimicrobial agents, such as ceftriaxone and ciprofloxacin.[32, 33] Resistance to both agents stabilised in 2018 to 2020 (ceftriaxone 13.3%–13.4%, ciprofloxacin 15.2%–16.1%); the level of resistance declined to 12.5% and 12.3% respectively in 2021. In 2022, the level of resistance remained stable (12.7% and 13.7%). The steady rise in resistance to fluoroquinolones is more striking in HO bacteraemia, with a change from 13.7% to 19.8% between 2013 and 2018, to 21.3% in 2019, and to 21.8% in 2020. In 2021 the level of resistance fell to 16.7%, and it increased slightly to 17.8% in 2022. In *K. pneumoniae* complex, rates of resistance to ciprofloxacin were lower than for *E. coli*. Resistance in this species peaked in 2018-2019 at 11.0%-10.2%, falling to 7.2% in 2021, and was 7.8% in 2022.

A little over a decade ago, ciprofloxacin-resistance rates were consistently between 1% and 4%.[32, 33] Despite this concerning increase, the percentage of fluoroquinolone-resistant *E. coli* in Australia remains low in comparison to most European countries and the United Kingdom.[29, 30] Because fluoroquinolone resistance is often linked to cephalosporin resistance caused by ESBLs of the CTX-M type, fluoroquinolone use alone may not be solely responsible for the increase. It is possible that the high use of oral cephalosporins in the community is driving this resistance.

The proportion of *E. coli* with an ESBL phenotype in 2022 was similar to 2021 (2021: 698/4912, 14.2%; 2022: 758/5261, 14.4%). For *K. pneumoniae* complex, the proportion with an ESBL phenotype was also similar to the previous year (2021: 98/1239, 7.9%; 2022: 105/1392, 7.5%). A

substantial majority of (600/758, 79.2%) of ESBL-producing *E. coli* bacteraemias were CO. This indicates that a substantial reservoir of resistance exists in the community, known to be particularly in the elderly population and in long-term residential care settings.[34] In *E. coli* rates of resistance to ceftriaxone in HO bacteraemia rose from 13.0% in 2016 to 20.2% in 2019. Rates fell to 18.8% in 2020, 17.8% in 2021, and to 15.2% in 2022. CO ceftriaxone resistance has remained steady (11.1% in 2016, 11.9% in 2019, 12.4% in 2020, 11.5% in 2021, and 12.1% in 2022).

To date, carbapenemase-producing *Enterobacterales* (CPE) remain relatively uncommon in patients with bacteraemia (0.2% of *E. coli* and 0.6% of *K. pneumoniae* complex isolates). The overall low rates of CPE bacteraemia are encouraging, but some organisms harbour carbapenemase genes more commonly; namely 2.1% of *E. cloacae* complex isolates (3.5% HO; 0.8% CO) in 2022. Examining previous and current AGAR surveys, most CPEs are endemic in origin.[35, 36] Eighteen of the 29 (62.1%) CPEs had $bla_{\text{IMP-4}}$, with reports predominately from New South Wales (10/18, 55.6%). Nine (31.0%) bla_{NDM} genes were reported from four states and territories. Eighteen of the participating hospitals had at least one isolate with a carbapenemase gene. This reinforces the importance of infection control programs and adherence to carbapenemase management guidelines to limit transmission of CPE.[37] There were no reports of $bla_{\text{KPC-2}}$.

No mobile colistin resistance genes other than *mcr-9* or *mcr-10* were detected in any isolates referred for WGS (*n* = 1,233). *mcr-9* has recently been found among several species of *Enterobacterales*. It is not associated with a colistin resistant phenotype[23], but is typically found on IncHI2 plasmids that may carry a carbapenemase gene.[24, 25]

Bacteraemia episodes contributed to increased length of hospital stay; the average length of stay in all Australian public hospitals in 2020–2021 was 5.0 days without a hospital-acquired complication (HAC), and 20.6 days with a HAC.[38] In 2022, where data were available for episodes of bacteraemia caused by GnSOP isolates, a little over one-half (5,042/8,894, 56.7%) had a length of stay seven days or more.

In this survey multidrug resistance did not appear to play a contributory role in the rates of all-cause mortality for patients with *E. coli*, *K. pneumoniae* complex, *E. cloacae* complex, or *P. aeruginosa* bacteraemia.

It should be noted that outbreaks of multidrug-resistant organisms occur in hospitals and other institutional care settings, and substantial transmission occurs before invasive blood stream infections develop. AGAR data may therefore underestimate local or regional spread of multidrug-resistant organisms and may not assist with early detection of sentinel resistances, such as certain CPEs. AGAR bacteraemia data need to be assessed with other sources of information to provide broader insights into antimicrobial resistance in Australia. The AURA Surveillance System enables these assessments via Australian Passive AMR Surveillance (APAS) and National Alert System for Critical Antimicrobial Resistances (CARAlert) data, which complement AGAR data.

The impact of COVID-19 on antimicrobial resistance remains unclear and may be due to a number of contributing factors. A combination of COVID-19 related travel restrictions on incoming travellers throughout much of 2020 and 2021, and an increasing awareness of and utilization of antimicrobial stewardship as part of the National Safety and Quality Health Service Standards[39] implementation and accreditation Australia-wide, may have reduced some resistance particularly for ESBLs.

Pharmaceutical Benefits Scheme data indicate that the COVID-19 pandemic had a profound impact on antimicrobial use in 2020, with a 40% drop in antimicrobials dispensed between March and April in 2020, with use remaining at this lower level for the rest of the year.[35]

It is also possible that a reduction in elective surgery and, related to this, post-surgical blood stream infections may have occurred during 2020 and 2021.

Future AGAR surveys will help determine if the observed reduction in resistance rates is sustained.

It is clear that ongoing AGAR surveillance remains core to Australia's response to the problem of increasing AMR. AGAR data contribute to understanding AMR in Australian human health settings, and to informing the national response to AMR.

Abbreviations

Abbreviation	Term
AGAR	Australian Group on Antimicrobial Resistance
APAS	Australian Passive AMR Surveillance
ASA	Australian Society for Antimicrobials
AURA	Antimicrobial Use and Resistance in Australia
CI	confidence interval
CLSI	Clinical and Laboratory Standards Institute
CO	community onset
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECOFF	epidemiological cut-off value
ESBL	extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
GnSOP	Gram-negative Sepsis Outcome Program
HO	hospital onset
MDR	Multidrug-resistant
MIC	minimum inhibitory concentration
PCR	polymerase chain reaction
PMQR	plasmid mediated quinolone resistance
QRDR	quinolone resistant determining region
RMT	ribosomal methyltransferase
WGS	whole genome sequencing
WHO	World Health Organization

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Participating members of AGAR in 2022:

Hospitals	AGAR members
Alfred Hospital, Vic	Adam Jenney and Jacqueline Williams
Alice Springs Hospital, NT	James McLeod
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Canberra Hospital, ACT	Peter Collignon and Susan Bradbury
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Concord Hospital, NSW	Thomas Gottlieb and John Huynh
Dandenong Hospital, Vic	Tony Korman and Kathryn Cisera
Fiona Stanley Hospital, WA	Denise Daley
Flinders Medical Centre, SA	Kelly Papanaoum and Xiao Chen,
Gold Coast University Hospital, Qld	Petra Derrington and Cheryl Curtis
Gosford Hospital, NSW	Gabrielle O'Kane and Nola Hitchick
Greenslopes Private Hospital, Qld	Jennifer Robson and Marianne Allen
John Hunter Hospital, NSW	Hemalatha Varadhan and Bree Harris
Joondalup Hospital, WA	Shalinie Perera and Ian Meyer
Launceston General Hospital, Tas	Pankaja Kalukottege and Brooke Woolley
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Monash Medical Centre, Vic	Tony Korman and Despina Kotsanas
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Royal Prince Alfred Hospital, NSW	Sebastiaan van Hal and Thomas Le
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St Vincent's Hospital, Melbourne, Vic	Amy Crowe and Lisa Brenton
St Vincent's Hospital, Sydney, NSW	David Lorenz
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Westmead Hospital, NSW	Jon Iredell and Elena Martinez
Wollongong Hospital, NSW	Peter Newton and Melissa Hoddle
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Reference laboratories

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Appendix A. Study design

Fifty-five hospitals participated in the 2022 survey, 48 adult and seven children's hospitals. All states and territories were represented. The hospital peer group/type[40] represented were:

Principal referral hospitals (*n* = 27)
Public acute group A hospitals (*n* = 5
Children's hospitals (*n* = 6)
Private acute group A hospitals (*n* = 2)
Private acute group B hospitals (*n* = 1)
Combined Women's and children's hospitals (*n* = 1)
Regional and district hospitals from north-west regional Western Australia (*n* = 13)

- Public acute group C hospitals (*n* = 5)
- Public acute group D hospitals (*n* = 6)
- Very small hospitals (*n* = 2)

The 33 laboratories that serviced the hospitals participating in AGAR collected either all isolates from different patient episodes of bacteraemia or up to 200 isolates for the Gram-negative Surveillance Outcome Program. In patients with more than one isolate, a new episode was defined as a new positive blood culture more than two weeks after the initial positive culture.

An episode was defined as CO if the first positive blood culture was collected 48 h or less after admission, and as HO if collected greater than 48 h after admission.

All laboratories that participated in AGAR obtained basic laboratory information for each patient episode plus varying demographic information, depending on the level at which they are enrolled in the program, Bronze or Silver (Tables A1–A3). Bronze level laboratories provided date of collection, date of birth, sex, postcode and admission date. Silver level laboratories provided discharge date, device-related infection, principal clinical manifestation, outcome at seven and 30 days from blood culture date of collection, and date of death if appropriate.

In 2022, one hospital from Queensland was only able to participate for Quarter one, and three additional hospitals from New South Wales (*n* = 2) and Queensland (*n* = 1) contributed data.

Table A1: Level of participation of laboratories that contributed data on gram-negative* bacteraemia, by state and territory, 2022

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	13	2	11
Victoria	8	0	8
Queensland	7†	0	7†
South Australia	3	0	3
Western Australia	19§	2	17§
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	55	5	50

* *Enterobacterales*, *Acinetobacter* species and *Pseudomonas aeruginosa*
† One institution participated for Quarter 1 only
§ Includes 13 regional and district hospitals from north-west Western Australia

Appendix B. Methods

Species identification

Isolates were identified using the routine methods for each institution, either Vitek® or Phoenix™ automated Microbiology systems, and, if available, mass spectrometry (MALDI - TOF).

Susceptibility testing

Testing was performed using two commercial semi-automated methods: Vitek® 2 (bioMérieux) (*n* = 30) and Phoenix (BD) (*n* = 3), which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution. Commercially available Vitek® 2 (AST-N246, AST-N435 or AST-N410) or Phoenix (NMIC-422) cards were used by all participants throughout the survey period.

The CLSI M100[1] and the EUCAST v13.0[2] breakpoints from January 2023 were used in the analysis.

Clinical and outcome data

Device related infection
Device-related bacteraemia is defined as a bacteraemia derived from central (which includes portacaths, PICC lines) or peripheral (venous and arterial) intravascular devices, from catheter-associated urinary tract infection (including nephrostomy tubes and stents), or ventilator-associated respiratory tract infection or bacteraemias associated with biliary stents.

Principal clinical manifestation
For GnSOP surveys, the principal clinical manifestation for each patient episode is categorised as:

- Biliary tract infection (including cholangitis)
- Device-related infection with metastatic focus
- Device-related infection without metastatic focus
- Febrile neutropenia
- Intra-abdominal infection other than biliary tract
- No identifiable focus
- Osteomyelitis/septic arthritis
- Other clinical syndrome
- Skin and skin structure infection
- Urinary tract infection

Length of hospital stay following bacteraemia
Length of hospital stay following bacteraemia was calculated from the date of blood culture collection to patient discharge or death.

All-cause mortality
All-cause mortality refers to outcome (died, survived, unknown) at 7- and 30-days from blood culture date of collection.

Antimicrobials tested

The antimicrobials tested are shown in Table B1.

Table B1: Antimicrobials available on susceptibility testing cards and interpretive guidelines for CLSI and EUCAST

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v13.0†		
	S	SDD	I	R	S, SD	S, IE	R
Amikacin							
Acinetobacter spp.	≤16		32	≥64	≤8	–§	>8
Enterobacterales	≤16		32	≥64	≤8	–§	>8
Pseudomonas spp.	≤16		32	≥64	≤16	–§	>16
Amoxicillin–clavulanic acid (2:1 ratio)							
Enterobacterales	≤8/4		16/8	≥32/16	–#	–#	–#
Amoxicillin–clavulanic acid (fixed)**							
Enterobacterales	–#		–#	–#	≤8	–§	>8
Ampicillin							
Enterobacterales	≤8		16	≥32	≤8	–§	>8
Aztreonam (Phoenix card)							
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤0.001	0.002–16	>16
Cefazolin							
Enterobacterales	≤2‡		4‡	≥8	≤0.001	0.002–4	>4
Cefepime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤2	4–8	–§	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤0.001	0.002–8	>8
Cefalexin	–#		–#	–#	≤16	–§	>16
Cefuroxime (Phoenix card)							
Enterobacterales (parental)	≤8		16	≥32	≤0.001	0.002–8	>8
Enterobacterales (oral)	≤4		8–16	≥32	≤8	–§	>8
Cefoxitin							
Enterobacterales	≤8		16	≥32	–#	–#	–#
Ceftazidime							
Acinetobacter spp.	≤8		16	≥32	–#	–#	–#
Enterobacterales	≤4		8	≥16	≤1	2–4	>4
Pseudomonas spp.	≤8		16	≥32	≤0.001	0.002–8	>8
Ceftolozane–tazobactam							
Enterobacterales	≤2/4		4/4	≥8/4	≤2	–§	>2
Pseudomonas spp.	≤4/4		8/4	≥16/4	≤4	–§	>4
Ceftriaxone							
Acinetobacter spp.	≤8		16–32	≥64	–#	–#	–#
Enterobacterales	≤1		2	≥4	≤1	2	>2
Ciprofloxacin							
Acinetobacter spp.	≤1		2	≥4	≤0.001	0.002–1	>1
Enterobacterales	≤0.25		0.5	≥1	≤0.25	0.5	>0.5
Salmonella spp.§§	≤0.06		0.12–0.5	≥1	≤0.06	–§	>0.06

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v13.0†		
	S	SDD	I	R	S, SD	S, IE	R
Pseudomonas spp.	≤0.5		1	≥2	≤0.001	0.002–0.5	>0.5
Colistin (Phoenix card)							
Acinetobacter spp.	–[#]		≤2	≥4	≤2	–[§]	>2
Enterobacterales	–[#]		≤2	≥4	≤2	–[§]	>2
Pseudomonas spp.	–[#]		≤2	≥4	≤2	–[§]	>2
Ertapenem (Phoenix card)	≤0.5		1	≥2	≤0.5	–[§]	>0.5
Fosfomycin (Phoenix card)							
Enterobacterales	≤64		128	≥256	≤32	–[§]	>32
Gentamicin							
Acinetobacter spp.	≤4		8	≥16	≤4	–[§]	>4
Enterobacterales	≤4		8	≥16	≤2	–[§]	>2
Pseudomonas spp.	≤4		8	≥16	–[#]	–[#]	–[#]
Imipenem (Phoenix card)							
Acinetobacter spp.	≤2		4	≥8	≤2	4	>4
Enterobacterales	≤1		2	≥4	≤2	4	>4
Pseudomonas spp.	≤2		4	≥8	≤0.001	0.002–4	>4
Meropenem							
Acinetobacter spp.	≤2		4	≥8	≤2	4–8	>8
Enterobacterales	≤1		2	≥4	≤2	4–8	>8
Pseudomonas spp.	≤2		4	≥8	≤2	4–8	>8
Nitrofurantoin							
Enterobacterales	≤32		64	≥128	≤64[##]	–[§]	>64[##]
Norfloxacin							
Enterobacterales	≤4		8	≥16	≤0.5	–[§]	>0.5
Pseudomonas spp.	≤4		8	≥16	–[#]	–[#]	–[#]
Piperacillin–tazobactam							
Acinetobacter spp.	≤16/4		32/4–64/4	≥128/4	–[#]	–[#]	–[#]
Enterobacterales	≤16/4		32/4–64/4	≥128/4	≤8	–[§]	>8
Pseudomonas spp.	≤16/4		32/4–64/4	≥128/4	≤0.001	0.002–16	>16
Tetracycline							
Acinetobacter spp.	≤4		8	≥16	–[#]	–[#]	–[#]
Enterobacterales	≤4		8	≥16	–[#]	–[#]	–[#]
Ticarcillin–clavulanate							
Acinetobacter spp.	≤16/2		32/2–64/2	≥128/2	–[#]	–[#]	–[#]
Enterobacterales	≤16/2		32/2–64/2	≥128/2	≤8	16	>16
Pseudomonas spp.	≤16/2		32/2–64/2	≥128/2	≤0.001	0.002–16	>16
Tigecycline (Phoenix card)	–[#]		–[#]	–[#]	≤0.5	–[§]	>0.5
Tobramycin							
Acinetobacter spp.	≤4		8	≥16	≤4	–[§]	>4
Enterobacterales	≤4		8	≥16	≤2	–[§]	>2
Pseudomonas spp.	≤4		8	≥16	≤2	–[§]	>2
Trimethoprim							
Enterobacterales	≤8		–[§]	≥16	≤4	–[§]	>4
Trimethoprim–sulfamethoxazole							
Acinetobacter spp.	≤2/38		–[§]	≥4/76	≤2/38	4/76	>4/76
Enterobacterales	≤2/38		–[§]	≥4/76	≤2/38	4/76	>4/76

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate (CLSI); R = resistant; S = susceptible (CLSI); S, IE = susceptible, increased exposure (EUCAST); S, SD = sensitive, standard dosing (EUCAST); SDD = sensitive dose dependent (CLSI)

* The breakpoints selected to identify resistance are described in the *Performance Standards for Antimicrobial Susceptibility Testing. 33rd ed. CLSI supplement* M100, 2023
† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 13.1, 2023 (www.eucast.org)
§ No category defined
# No guidelines for indicated species
** For susceptibility testing purposes, EUCAST fixes the concentration of clavulanate at 2 mg/L, rather than the 2:1 ratio used in the CLSI guidelines. The EUCAST breakpoint is based in intravenous administration
‡ The cefazolin concentration range available on the current Vitek® card restricts the ability to identify the susceptible and intermediate categories (CLSI)
§§ The ciprofloxacin concentration range available on the cards used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. Either MIC strips or perflocaxin 5 ug disc were used to determine susceptibility on all *Salmonella* species where Vitek® MIC ≤0.25 mg/L
Breakpoints apply to *E. coli* only

Whole genome sequencing

E. coli, *Klebsiella* spp., and *Proteus* spp. and *Salmonella* spp. with ceftazidime or ceftriaxone MIC >1 mg/L, or cefoxitin MIC >8 mg/L; any other *Enterobacterales* with cefepime MIC >1 mg/L; all *Enterobacterales* with meropenem MIC >0.125 mg/L (>0.25 if tested using Vitek); all *Acinetobacter* isolates and *P. aeruginosa* with meropenem MIC ≥ 8 mg/L; all isolates with amikacin MIC >32 mg/L, and all isolates with colistin MIC > 4 mg/L were referred to a central laboratory (Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research) for WGS.

WGS was performed by the Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, CIDMLS, ICPMR, Westmead Hospital using the Illumina NextSeq™ 500 platform. Data were analysed using a modification of the Nullarbor bioinformatic pipeline[3], incorporating searching contigs against the NCBI AMRFinder database (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA313047) using ABRicate[41] and AMRFinder[42], followed by a custom AMR-specific pipeline which includes a read-based search using ARIBA[43] against the CARD[44] and NCBI databases. Ambiguities and potential multiple gene copies/variants were checked manually by mapping reads to reference genes from https://www.ncbi.nlm.nih.gov/pathogens/isolates#/refgene/ using Geneious Prime 2022.1.1 (https://www.geneious.com).. Reported chromosomal mutations were derived from ARIBA result tables (quinolone mutations) or its mapping-based reassemblies (all other mutations). Additional mutations in *gyr* and *par* genes identified by PointFinder[21] and potentially contributing to resistance were also examined manually. *fimH* type was predicted by FimTyper.[45] Detection of *H30-Rx* specific SNPs were carried out by *in silico* PCR.[46]

Quality control

Quality control strains used were those recommended by CLSI and EUCAST standards.

Data validation

Various checks were made to ensure that the data were valid. These included:

- Null values in the mandatory fields
- Missing MIC data
- Patient age if ≥100 years or <0 days
- Confirm dates when:
  - Specimen collected after patient discharged or died
  - Patient discharged or died before admitted
  - Patient admitted before born
  - Patient admitted more than two days after specimen collected
  - Patient admitted more than six months before specimen collected

Appendix C. Susceptibility to antimicrobial agents

Overall percentages of resistance or non-susceptibility for the indicator species of national priority[4] are shown in Table C1. For some antimicrobials, the concentration range tested did not distinguish between intermediate susceptibility (I) and resistant (R), and the term non-susceptible (NS) was used to describe these isolates.

Table C1: Activity of antimicrobial agents tested against isolates recovered from patients with Gram-negative blood stream infections, by state and territory, AGAR, 2022

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Amikacin										
Acinetobacter baumannii complex	n	6	6	21	3	4	3	8	1	52
	%R	n/a	n/a	0.0, 4.8	n/a	n/a	n/a	n/a	n/a	1.9, 3.8
Enterobacter cloacae complex	n	169	98	88	22	51	19	9	18	474
	%R	0.0, 0.0	0.0, 1.0	0.0, 1.1	0.0, 0.0	0.0, 0.0	0.0, 5.3	n/a	0.0, 0.0	0.0, 0.6
Escherichia coli	n	1,770	1,054	711	439	695	231	170	190	5,260
	%R	0.0, 1.0	0.1, 0.5	0.0, 0.7	0.0, 0.9	0.1, 1.2	0.0, 0.9	0.0, 3.5	0.0, 0.5	0.0, 0.9
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Klebsiella oxytoca	n	87	78	29	28	43	16	5	10	296
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0
Klebsiella pneumoniae complex	n	444	282	227	83	212	50	52	42	1,392
	%R	0.0, 0.2	0.4, 0.7	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, 0.2
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%R	0.9, 2.7	0.0, 1.4	0.0, 2.3	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.3, 1.5
Pseudomonas aeruginosa	n	271	145	153	76	113	35	13	30	836
	%R	0.7, 0.7	0.0, 0.7	0.0, 0.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.2, 0.5
Salmonella species (non-typhoidal)	n	17	18	16	0	18	12	8	3	92
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	n/a	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 0.0
Amoxicillin–clavulanic acid (2:1 ratio)†										
Escherichia coli	n	1,401	1,054	652	174	695	231	170	190	4,567
	%I	11.1, –§	8.5, –§	8.7, –§	10.9, –§	10.9, –§	6.9, –§	11.8, –§	10.0, –§	9.9, –§
	%R	8.6, –§	6.5, –§	7.4, –§	11.5, –§	6.8, –§	5.6, –§	5.3, –§	5.8, –§	7.4, –§
Klebsiella oxytoca	n	66	78	27	13	43	16	5	10	258

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%I	3.0, –[§]	5.1, –[§]	7.4, –[§]	0.0, –[§]	0.0, –[§]	6.3, –[§]	n/a	10.0, –[§]	4.3, –[§]
	%R	9.1, –[§]	6.4, –[§]	0.0, –[§]	7.7, –[§]	7.0, –[§]	18.8, –[§]	n/a	0.0, –[§]	7.4, –[§]
Klebsiella pneumoniae complex	n	348	282	210	34	212	50	52	42	1,230
	%I	5.5, –[§]	3.9, –[§]	3.3, –[§]	2.9, –[§]	4.7, –[§]	2.0, –[§]	11.5, –[§]	4.8, –[§]	4.6, –[§]
	%R	4.9, –[§]	3.2, –[§]	2.4, –[§]	2.9, –[§]	1.4, –[§]	2.0, –[§]	1.9, –[§]	4.8, –[§]	3.2, –[§]
Proteus mirabilis	n	86	69	42	14	48	9	4	6	278
	%I	5.8, –[§]	2.9, –[§]	2.4, –[§]	7.1, –[§]	10.4, –[§]	n/a	n/a	n/a	5.8, –[§]
	%R	2.3, –[§]	5.8, –[§]	2.4, –[§]	0.0, –[§]	2.1, –[§]	n/a	n/a	n/a	3.2, –[§]
Salmonella species (non-typhoidal)	n	13	16	15	0	18	12	10	3	87
	%I	0.0, –[§]	6.3, –[§]	0.0, –[§]	n/a	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	1.1, –[§]
	%R	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	0.0, –[§]
Salmonella species (typhoidal)	n	6	15	2	1	5	1	1	3	34
	%I	n/a	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	2.9, –[§]
	%R	n/a	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –[§]
Ampicillin										
Escherichia coli	n	1,768	1,053	711	439	695	231	170	190	5,257
	%I	1.1, –[#]	2.6, –[#]	0.8, –[#]	1.4, –[#]	1.4, –[#]	1.7, –[#]	0.6, –[#]	2.1, –[#]	1.5, –[#]
	%R	50.1, 51.2	47.4, 50.0	47.5, 48.4	51.3, 52.6	55.0, 56.4	36.8, 38.5	69.4, 70.0	50.5, 52.6	50.0, 51.5
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%I	0.0, –[#]	0.0, –[#]	0.0, –[#]	0.0, –[#]	4.2, –[#]	n/a	n/a	n/a	0.6, –[#]
	%R	17.7, 17.7	14.5, 14.5	7.0, 7.0	19.4, 19.4	18.8, 22.9	n/a	n/a	n/a	15.8, 16.4
Salmonella species (non-typhoidal)	n	21	16	16	0	18	12	10	3	96
	%I	0.0, –[#]	0.0, –[#]	0.0, –[#]	n/a	0.0, –[#]	0.0, –[#]	0.0, –[#]	n/a	0.0, –[#]
	%R	9.5, 9.5	12.5, 12.5	0.0, 0.0	n/a	5.6, 5.6	0.0, 0.0	0.0, 0.0	n/a	5.2, 5.2
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%I	n/a	0.0, –[#]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –[#]
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	18.9, 18.9
Cefazolin										
Escherichia coli	n	1,401	1,054	710	174	695	200	170	190	4,594
	%R	25.5, 25.5	18.8, 18.8	19.0, 19.0	21.8, 21.8	23.7, 23.7	10.5, 10.5	35.9, 35.9	24.7, 24.7	22.2, 22.2
Klebsiella oxytoca	n	59	78	30	13	43	15	5	10	253
	%R	59.3, 59.3	42.3, 42.3	40.0, 40.0	69.2, 69.2	86.0, 86.0	80.0, 80.0	n/a	60.0, 60.0	58.1, 58.1
Klebsiella pneumoniae complex	n	343	282	227	34	212	43	52	42	1,235
	%R	12.0,	9.6,	6.6,	11.8,	7.1,	11.6,	26.9,	9.5,	10.1,

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		12.0	9.6	6.6	11.8	7.1	11.6	26.9	9.5	10.1
Proteus mirabilis	n	75	69	43	14	48	6	4	6	265
	%R	17.3, 17.3	20.3, 20.3	14.0, 14.0	7.1, 7.1	22.9, 22.9	n/a	n/a	n/a	17.7, 17.7
Cefepime										
Acinetobacter baumannii	n	8	13	3	3	4	1	8	0	40
	%I	n/a	7.7, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	5.0, –[§]
	%R	n/a	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	7.5, –[§]
Enterobacter cloacae complex	n	170	98	88	22	51	19	9	18	475
	%SDD/I	6.5, 10.0	0.0, 9.2	1.1, 5.7	22.7, 31.8	0.0, 2.0	0.0, 5.3	n/a	0.0, 5.6	3.6, 8.6
	%R	1.2, 5.3	4.1, 4.1	1.1, 1.1	0.0, 0.0	0.0, 0.0	5.3, 5.3	n/a	0.0, 0.0	1.9, 3.4
Escherichia coli	n	1,771	1,054	711	439	695	231	170	190	5,261
	%SDD/I	3.0, 6.4	1.0, 5.8	0.8, 5.1	4.8, 5.2	1.4, 6.5	0.4, 3.5	4.1, 20.6	0.0, 12.1	2.1, 6.6
	%R	2.6, 3.8	1.9, 2.6	1.4, 1.8	4.3, 5.9	1.7, 2.4	0.9, 0.9	0.6, 4.1	1.1, 1.1	2.1, 3.1
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%SDD/I	2.6, 2.6	0.0, 6.9	0.0, 0.0	7.7, 0.0	0.0, 0.0	n/a	n/a	n/a	2.3, 3.1
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 7.7	0.0, 0.0	n/a	n/a	n/a	0.0, 1.6
Klebsiella oxytoca	n	86	78	30	28	43	16	5	10	296
	%SDD/I	0.0, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 6.3	n/a	0.0, 0.0	0.0, 0.7
	%R	0.0, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.3
Klebsiella pneumoniae complex	n	444	282	227	83	212	50	52	42	1,392
	%SDD/I	0.7, 3.4	0.7, 2.8	1.3, 0.9	0.0, 2.4	0.9, 3.3	4.0, 6.0	0.0, 15.4	2.4, 2.4	0.9, 3.3
	%R	2.9, 3.2	1.1, 1.8	0.9, 1.8	0.0, 0.0	0.5, 0.9	0.0, 2.0	3.8, 3.8	7.1, 7.1	1.7, 2.2
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%SDD/I	0.9, 1.8	0.0, 0.0	0.0, 0.0	3.2, 3.2	0.0, 0.0	n/a	n/a	n/a	0.6, 0.9
	%R	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.6, 0.6
Pseudomonas aeruginosa	n	271	146	154	76	113	35	13	30	838
	%I	3.0, 94.5	6.2, 89.0	1.9, 95.5	9.2, 86.8	0.9, 98.2	0.0, 94.3	0.0, 100.0	0.0, 100.0	3.3, 93.8
	%R	2.6, 5.5	4.8, 11.0	2.6, 4.5	3.9, 13.2	0.9, 1.8	5.7, 5.7	0.0, 0.0	0.0, 0.0	2.9, 6.2
Salmonella species (non-typhoidal)	n	21	16	16	0	18	12	10	3	96
	%SDD/I	0.0, 0.0	6.3, 6.3	0.0, 0.0	n/a	0.0, 5.6	0.0, 0.0	0.0, 0.0	n/a	1.0, 2.1
	%R	4.8, 4.8	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	1.0, 1.0
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%SDD/I	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0,	n/a	n/a	n/a	n/a	n/a	n/a	8.1, 8.1

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
			0.0							
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%SDD/I	0.0, 0.0	1.9, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	0.4, 0.4
	%R	1.0, 1.0	1.9, 3.8	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	0.8, 1.2
Cefoxitin										
Escherichia coli	n	1,771	1,053	711	439	695	231	170	190	5,260
	%R/ecoff	4.7, 6.9	2.4, 4.5	3.9, 5.5	2.5, 3.9	2.4, 4.5	0.9, 2.6	1.8, 2.9	2.6, 5.3	3.3, 5.3
Klebsiella oxytoca	n	86	78	30	28	43	16	5	10	296
	%R/ecoff	1.2, 2.3	1.3, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 6.3	n/a	0.0, 0.0	0.7, 1.4
Klebsiella pneumoniae complex	n	444	282	227	83	212	50	52	42	1,392
	%R/ecoff	3.6, 5.4	3.9, 6.0	2.6, 3.5	2.4, 4.8	3.8, 5.7	0.0, 0.0	3.8, 5.8	2.4, 2.4	3.3, 5.0
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%R/ecoff	0.9, 2.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.3, 1.2
Salmonella species (non-typhoidal)	n	21	16	16	0	18	12	10	3	96
	%R/ecoff	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 1.0
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%R/ecoff	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Ceftazidime										
Acinetobacter baumannii complex	n	8	13	21	3	4	1	8	1	59
	%I	n/a	7.7, –[§]	4.8, –[§]	n/a	n/a	n/a	n/a	n/a	11.9, –[§]
	%R	n/a	0.0, –[§]	4.8, –[§]	n/a	n/a	n/a	n/a	n/a	3.4, –[§]
Enterobacter cloacae complex	n	170	98	88	22	51	19	9	18	475
	%I	1.2, 5.3	1.0, 1.0	1.1, 1.1	0.0, 4.5	0.0, 3.9	5.3, 0.0	n/a	0.0, 16.7	1.1, 3.6
	%R	29.4, 30.6	25.5, 26.5	15.9, 17.0	50.0, 50.0	5.9, 5.9	26.3, 31.6	n/a	5.6, 5.6	23.6, 24.6
Escherichia coli	n	1,771	1,054	711	439	695	231	170	190	5,261
	%I	1.5, 7.6	0.1, 6.2	0.6, 6.6	2.3, 6.2	0.3, 6.5	0.4, 3.5	0.0, 20.6	1.1, 11.6	0.9, 7.3
	%R	6.1, 7.6	4.9, 5.0	4.4, 4.9	4.3, 6.6	4.5, 4.7	1.7, 2.2	7.1, 7.1	3.2, 4.2	5.0, 5.9
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%I	2.6, 7.7	3.4, 3.4	6.7, 0.0	0.0, 0.0	0.0, 5.6	n/a	n/a	n/a	3.1, 3.9
	%R	28.2, 30.8	34.5, 37.9	6.7, 13.3	53.8, 53.8	11.1, 11.1	n/a	n/a	n/a	30.2, 33.3
Klebsiella oxytoca	n	86	78	30	28	43	16	5	10	296
	%I	1.2, 1.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.3, 0.3
	%R	0.0, 1.2	1.3, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.3, 0.7
Klebsiella pneumoniae complex	n	444	282	227	83	212	50	52	42	1,392
	%I	1.4, 1.6	1.1, 2.5	0.9, 0.9	0.0, 3.6	0.0, 2.4	0.0, 0.0	3.8, 3.8	0.0, 0.0	0.9, 1.9

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	5.4, 6.8	2.8, 3.9	2.2, 3.1	2.4, 2.4	3.3, 3.3	8.0, 8.0	13.5, 17.3	9.5, 9.5	4.4, 5.3
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%I	0.9, 0.9	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.3, 0.6
	%R	1.8, 2.7	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.6, 0.9
Pseudomonas aeruginosa	n	270	146	154	76	113	35	13	30	837
	%I	5.9, 89.3	8.9, 83.6	3.9, 92.2	5.3, 82.9	3.5, 94.7	2.9, 91.4	7.7, 92.3	3.3, 96.7	5.5, 89.4
	%R	4.8, 10.7	7.5, 16.4	3.9, 7.8	11.8, 17.1	1.8, 5.3	5.7, 8.6	0.0, 7.7	0.0, 3.3	5.1, 10.6
Salmonella species (non-typhoidal)	n	21	16	16	0	18	12	10	3	96
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0
	%R	4.8, 4.8	6.3, 6.3	0.0, 0.0	n/a	5.6, 5.6	0.0, 0.0	0.0, 0.0	n/a	3.1, 3.1
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%I	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	8.1, 8.1
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%I	0.0, 1.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	0.4, 0.4
	%R	1.9, 1.9	3.8, 3.8	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	1.6, 1.9
Ceftriaxone										
Acinetobacter baumannii complex	n	6	18	21	2	4	3	8	1	63
	%I	n/a	72.2, –[§]	61.9, –[§]	n/a	n/a	n/a	n/a	n/a	68.2, –[§]
	%R	n/a	0.0, –[§]	4.8, –[§]	n/a	n/a	n/a	n/a	n/a	4.5, –[§]
Enterobacter cloacae complex	n	170	98	88	22	51	19	9	18	475
	%I	0.6, 0.6	0.0, 0.0	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.4, 0.4
	%R	35.9, 35.9	29.6, 29.6	18.2, 18.2	54.5, 54.5	9.8, 9.8	31.6, 31.6	n/a	16.7, 16.7	28.4, 28.4
Escherichia coli	n	1,771	1,054	711	439	695	231	170	190	5,261
	%I	0.2, 0.2	0.1, 0.1	0.0, 0.0	0.2, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
	%R	14.0, 14.0	11.2, 11.2	10.4, 10.4	12.3, 12.3	11.8, 11.8	5.2, 5.2	28.2, 28.2	16.3, 16.3	12.7, 12.7
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	7.7, 7.7	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
	%R	33.3, 33.3	37.9, 37.9	13.3, 13.3	46.2, 46.2	11.1, 11.1	n/a	n/a	n/a	33.3, 33.3
Klebsiella oxytoca	n	86	78	30	28	43	16	5	10	296
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.3, 2.3	0.0, 0.0	n/a	0.0, 0.0	0.3, 0.3
	%R	9.3, 9.3	3.8, 3.8	0.0, 0.0	3.6, 3.6	4.7, 4.7	12.5, 12.5	n/a	10.0, 10.0	5.7, 5.7
Klebsiella	n	444	282	227	83	212	50	52	42	1,392

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
pneumoniae complex	%I	0.2, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.1, 0.1
	%R	7.7, 7.7	6.4, 6.4	3.1, 3.1	4.8, 4.8	4.7, 4.7	8.0, 8.0	21.2, 21.2	9.5, 9.5	6.6, 6.6
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%I	0.9, 0.9	0.0, 0.0	0.0, 0.0	3.2, 3.2	0.0, 0.0	n/a	n/a	n/a	0.6, 0.6
	%R	3.5, 3.5	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	1.2, 1.2
Salmonella species (non-typhoidal)	n	21	16	16	0	18	12	10	3	96
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0
	%R	4.8, 4.8	6.3, 6.3	0.0, 0.0	n/a	5.6, 5.6	0.0, 0.0	0.0, 0.0	n/a	3.1, 3.1
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%I	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	8.1, 8.1
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%I	1.0, 1.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	0.4, 0.4
	%R	2.9, 2.9	5.8, 5.8	2.8, 2.8	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	3.1, 3.1
Ciprofloxacin										
Acinetobacter baumannii complex	n	9	18	19	3	4	3	8	1	65
	%I	n/a	0.0, 94.4	0.0, 94.7	n/a	n/a	n/a	n/a	n/a	0.0, 95.4
	%R	n/a	5.6, 5.6	5.3, 5.3	n/a	n/a	n/a	n/a	n/a	4.6, 4.6
Enterobacter cloacae complex	n	170	98	88	22	51	19	9	18	475
	%I	1.2, 1.2	1.0, 1.0	2.3, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	1.1, 1.1
	%R	6.5, 6.5	5.1, 5.1	4.5, 4.5	9.1, 9.1	0.0, 0.0	0.0, 0.0	n/a	5.6, 5.6	5.3, 5.3
Escherichia coli	n	1,770	1,053	711	439	695	231	170	190	5,259
	%I	4.1, 4.1	3.0, 3.0	4.4, 4.4	4.8, 4.8	2.6, 2.6	1.3, 1.3	9.4, 9.4	1.6, 1.6	3.7, 3.7
	%R	16.4, 16.4	13.1, 13.1	10.0, 10.0	14.6, 14.6	14.0, 14.0	6.9, 6.9	15.3, 15.3	10.0, 10.0	13.7, 13.7
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%I	0.0, 0.0	3.4, 3.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.8, 0.8
	%R	5.1, 5.1	0.0, 0.0	6.7, 6.7	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	3.1, 3.1
Klebsiella oxytoca	n	87	78	30	28	43	16	5	10	297
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.3, 2.3	0.0, 0.0	n/a	0.0, 0.0	0.3, 0.3
	%R	1.1, 1.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	2.3, 2.3	0.0, 0.0	n/a	0.0, 0.0	0.7, 0.7
Klebsiella pneumoniae complex	n	443	282	227	83	212	50	52	42	1,391
	%I	2.9, 2.9	1.1, 1.1	0.9, 0.9	2.4, 2.4	1.9, 1.9	2.0, 2.0	5.8, 5.8	2.4, 2.4	2.1, 2.1
	%R	8.4, 8.4	7.4, 7.4	5.7, 5.7	2.4, 2.4	8.5, 8.5	8.0, 8.0	17.3, 17.3	11.9, 11.9	7.8, 7.8

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%I	0.9, 0.9	1.4, 1.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.6, 0.6
	%R	6.2, 6.2	2.9, 2.9	0.0, 0.0	6.5, 6.5	4.2, 4.2	n/a	n/a	n/a	4.0, 4.0
Pseudomonas aeruginosa	n	271	146	152	76	113	35	13	30	836
	%I	6.6, 88.6	9.6, 87.0	6.6, 89.5	3.9, 88.2	2.7, 95.6	0.0, 94.3	0.0, 92.3	0.0, 96.7	5.7, 90.0
	%R	4.8, 11.4	3.4, 13.0	3.9, 10.5	7.9, 11.8	1.8, 4.4	5.7, 5.7	7.7, 7.7	3.3, 3.3	4.3, 10.0
Salmonella species (non-typhoidal)**	n	21	16	17	0	18	12	10	3	97
	%I	4.8, –[#]	6.3, –[#]	0.0, –[#]	n/a	5.6, –[#]	0.0, –[#]	0.0, –[#]	n/a	3.1, –[#]
	%R	14.3, 19.0	25.0, 31.3	0.0, 0.0	n/a	5.6, 11.1	0.0, 0.0	10.0, 10.0	n/a	10.3, 13.4
Salmonella species (typhoidal)**	n	9	16	2	1	5	1	1	3	38
	%I	n/a	18.8, –[#]	n/a	n/a	n/a	n/a	n/a	n/a	18.4, –[#]
	%R	n/a	56.3, 75.0	n/a	n/a	n/a	n/a	n/a	n/a	65.8, 84.2
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%I	1.0, 1.0	5.8, 5.8	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	1.6, 1.6
	%R	2.9, 2.9	3.8, 3.8	0.0, 0.0	n/a	2.9, 2.9	n/a	n/a	0.0, 0.0	2.3, 2.3
Gentamicin										
Acinetobacter baumannii complex	n	9	18	21	3	4	3	8	1	67
	%R	n/a	0.0, 0.0	4.8, 4.8	n/a	n/a	n/a	n/a	n/a	3.0, 3.0
Enterobacter cloacae complex	n	168	98	88	22	51	19	9	18	473
	%R	7.7, 7.7	4.1, 5.1	4.5, 5.7	4.5, 4.5	0.0, 2.0	15.8, 15.8	n/a	0.0, 0.0	5.5, 6.1
Escherichia coli	n	1,769	1,054	711	439	695	231	170	190	5,259
	%R	8.3, 8.8	6.1, 6.4	6.6, 7.0	10.7, 11.4	8.1, 8.5	3.0, 3.9	20.0, 20.0	6.8, 6.8	7.9, 8.3
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	2.3, 2.3
Klebsiella oxytoca	n	87	78	30	28	43	16	5	10	297
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	10.0, 10.0	1.0, 1.0
Klebsiella pneumoniae complex	n	444	282	227	83	212	50	52	42	1,392
	%R	3.6, 4.5	3.2, 3.2	2.2, 2.2	1.2, 1.2	1.4, 1.9	0.0, 0.0	7.7, 7.7	9.5, 9.5	3.0, 3.4
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%R	1.8, 7.1	1.4, 2.9	0.0, 4.7	6.5, 6.5	2.1, 4.2	n/a	n/a	n/a	1.9, 5.0
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%R	2.9, 2.9	0.0, 1.9	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	20.0, 20.0	1.9, 2.3
Meropenem										
Acinetobacter baumannii complex	n	9	18	21	3	4	3	8	1	67
	%I	n/a	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	0.0, 0.0

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
	%R	n/a	0.0, 0.0	4.8, 4.8	n/a	n/a	n/a	n/a	n/a	3.0, 3.0
Enterobacter cloacae complex	n	170	98	88	22	51	19	9	18	475
	%I	0.0, 1.2	1.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.2, 0.4
	%R	5.3, 4.1	1.0, 1.0	2.3, 2.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	2.5, 2.1
Escherichia coli	n	1,771	1,053	711	439	695	231	170	190	5,260
	%I	0.1, 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, 0.5	0.0, 0.1
	%R	0.2, 0.1	0.1, 0.1	0.0, 0.0	0.2, 0.2	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.5, 0.0	0.1, 0.1
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 1.6
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	7.7, 7.7	0.0, 0.0	n/a	n/a	n/a	2.3, 0.8
Klebsiella oxytoca	n	85	78	30	28	43	16	5	10	295
	%I	0.0, 1.2	0.0, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.7
	%R	1.2, 0.0	1.3, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.7, 0.0
Klebsiella pneumoniae complex	n	444	282	227	83	212	50	52	42	1,392
	%I	0.2, 0.0	0.4, 0.0	0.0, 0.0	0.0, 0.0	0.5, 0.0	0.0, 2.0	0.0, 0.0	0.0, 0.0	0.2, 0.1
	%R	0.5, 0.5	0.7, 0.7	0.4, 0.4	0.0, 0.0	0.0, 0.0	2.0, 0.0	1.9, 1.9	2.4, 2.4	0.6, 0.5
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	270	146	153	76	113	35	13	30	836
	%I	4.4, 6.7	3.4, 4.8	5.9, 6.5	6.6, 9.2	4.4, 6.2	0.0, 0.0	7.7, 7.7	3.3, 3.3	4.5, 6.1
	%R	6.3, 4.1	8.9, 7.5	3.9, 3.3	7.9, 5.3	4.4, 2.7	5.7, 5.7	0.0, 0.0	0.0, 0.0	5.9, 4.3
Salmonella species (non-typhoidal)	n	21	16	16	0	18	12	10	3	96
	%I	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%I	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 0.0
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%I	0.0, 0.0	0.0, 1.9	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	0.0, 0.8
	%R	1.0, 1.0	3.8, 1.9	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	1.6, 0.8
Nitrofurantoin										
Enterobacter cloacae	n	148	55	80	22	51	19	9	18	402

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
complex	%R	14.2, –[§]	3.6, –[§]	11.3, –[§]	9.1, –[§]	13.7, –[§]	10.5, –[§]	n/a	5.6, –[§]	11.4, –[§]
Escherichia coli	n	1,771	1,053	653	439	695	231	170	190	5,202
	%R	0.8, 0.8	0.4, 0.4	0.5, 0.5	0.5, 0.5	0.0, 0.0	0.0, 0.0	1.2, 1.2	1.1, 1.1	0.5, 0.5
Klebsiella aerogenes	n	33	20	15	13	18	7	3	5	114
	%R	33.3, –[§]	45.0, –[§]	20.0, –[§]	38.5, –[§]	33.3, –[§]	n/a	n/a	n/a	35.1, –[§]
Klebsiella oxytoca	n	76	50	27	28	43	16	5	10	255
	%R	2.6, –[§]	0.0, –[§]	3.7, –[§]	3.6, –[§]	0.0, –[§]	0.0, –[§]	n/a	0.0, –[§]	1.6, –[§]
Klebsiella pneumoniae complex	n	392	171	210	83	212	50	52	42	1,212
	%R	23.2, –[§]	31.0, –[§]	26.2, –[§]	22.9, –[§]	37.7, –[§]	20.0, –[§]	34.6, –[§]	19.0, –[§]	27.6, –[§]
Proteus mirabilis	n	96	61	42	31	48	9	4	0	291
	%R	83.3, –[§]	91.8, –[§]	95.2, –[§]	80.6, –[§]	89.6, –[§]	n/a	n/a	n/a	87.6, –[§]
Salmonella species (non-typhoidal)	n	14	10	15	0	18	12	10	1	80
	%R	0.0, –[§]	20.0, –[§]	0.0, –[§]	n/a	0.0, –[§]	0.0, –[§]	0.0, –[§]	n/a	2.5, –[§]
Salmonella species (typhoidal)	n	8	13	2	1	5	1	1	0	31
	%R	n/a	0.0, –[§]	n/a	n/a	n/a	n/a	n/a	n/a	0.0, –[§]
Serratia marcescens	n	80	42	34	7	35	8	4	10	220
	%R	100.0, –[§]	97.6, –[§]	100.0, –[§]	n/a	94.3, –[§]	n/a	n/a	90.0, –[§]	98.2, –[§]
Piperacillin–tazobactam										
Acinetobacter baumannii complex	n	9	13	20	3	4	1	8	1	59
	%R	n/a	7.7, –[§]	15.0, –[§]	n/a	n/a	n/a	n/a	n/a	10.2, –[§]
Enterobacter cloacae complex	n	170	97	86	22	51	17	9	18	470
	%R	22.4, 33.5	18.6, 24.7	14.0, 24.4	36.4, 45.5	5.9, 9.8	17.6, 17.6	n/a	5.6, 16.7	18.3, 27.2
Escherichia coli	n	1,765	1,051	707	437	693	231	169	190	5,243
	%R	3.7, 6.9	2.2, 5.0	2.5, 5.7	1.6, 3.9	3.2, 7.2	1.7, 3.9	1.8, 6.5	2.6, 4.2	2.8, 5.9
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%R	23.1, 41.0	24.1, 37.9	6.7, 13.3	23.1, 46.2	11.1, 22.2	n/a	n/a	n/a	20.9, 37.2
Klebsiella oxytoca	n	85	78	30	28	43	16	5	10	295
	%R	10.6, 10.6	10.3, 15.4	0.0, 3.3	0.0, 7.1	7.0, 9.3	18.8, 25.0	n/a	10.0, 10.0	8.1, 11.5
Klebsiella pneumoniae complex	n	442	282	225	82	212	50	51	42	1,386
	%R	4.3, 10.2	2.8, 8.2	2.7, 8.0	2.4, 4.9	1.9, 8.5	0.0, 2.0	0.0, 17.6	2.4, 7.1	2.9, 8.7
Proteus mirabilis	n	113	69	42	31	48	9	4	6	322
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	269	146	153	76	111	34	13	30	832
	%R	5.2, 14.1	9.6, 21.9	5.2, 12.4	10.5, 19.7	0.9, 7.2	11.8, 20.6	7.7, 7.7	3.3, 6.7	6.1, 14.7
Salmonella species	n	21	16	16	0	18	12	10	3	96

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
(non-typhoidal)	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	0.0, 2.7
Serratia marcescens	n	95	52	36	7	4	8	0	10	212
	%R	0.0, 0.0	0.0, 1.9	0.0, 0.0	n/a	n/a	n/a	n/a	0.0, 0.0	0.0, 0.9
Ticarcillin–clavulanic acid										
Acinetobacter baumannii complex	n	5	4	21	2	4	1	8	1	46
	%R	n/a	n/a	4.8, –[§]	n/a	n/a	n/a	n/a	n/a	4.3, –[§]
Enterobacter cloacae complex	n	113	98	80	18	51	19	9	18	406
	%R	33.6, 38.1	23.5, 28.6	20.0, 21.3	44.4, 55.6	5.9, 9.8	26.3, 31.6	n/a	5.6, 16.7	23.9, 28.6
Escherichia coli	n	1,219	1,053	652	174	695	231	170	190	4,384
	%R	7.1, 14.3	4.3, 10.0	3.7, 10.9	4.6, 13.8	6.9, 12.8	5.6, 8.2	5.9, 14.1	4.2, 10.0	5.5, 12.0
Klebsiella aerogenes	n	30	29	15	9	18	7	3	5	116
	%R	16.7, 33.3	20.7, 34.5	6.7, 13.3	n/a	11.1, 16.7	n/a	n/a	n/a	20.7, 32.8
Klebsiella oxytoca	n	58	78	27	13	43	16	5	10	250
	%R	6.9, 10.3	7.7, 11.5	0.0, 3.7	7.7, 7.7	7.0, 7.0	18.8, 18.8	n/a	10.0, 10.0	7.2, 10.0
Klebsiella pneumoniae complex	n	298	282	210	34	212	50	52	42	1,180
	%R	4.7, 9.1	4.3, 6.4	2.9, 4.3	2.9, 5.9	2.4, 4.7	0.0, 4.0	3.8, 15.4	7.1, 9.5	3.6, 6.8
Proteus mirabilis	n	70	69	42	14	48	9	4	6	262
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 0.0
Pseudomonas aeruginosa	n	184	146	133	26	113	35	13	30	680
	%R	15.2, 40.2	23.3, 51.4	12.0, 37.6	26.9, 46.2	9.7, 37.2	14.3, 62.9	15.4, 30.8	3.3, 33.3	15.3, 42.5
Salmonella species (non-typhoidal)	n	13	16	15	0	18	12	10	3	87
	%R	0.0, 0.0	0.0, 6.3	0.0, 0.0	n/a	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 1.1
Salmonella species (typhoidal)	n	5	15	2	1	5	1	1	3	33
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	3.0, 15.2
Serratia marcescens	n	55	32	34	1	35	8	4	10	179
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 2.9	n/a	n/a	0.0, 0.0	0.0, 1.1
Tobramycin										
Acinetobacter baumannii complex	n	8	18	21	3	4	3	8	1	66
	%R	n/a	0.0, 0.0	4.8, 4.8	n/a	n/a	n/a	n/a	n/a	3.0, 3.0
Enterobacter cloacae complex	n	160	98	88	22	51	19	9	18	465
	%R	4.4, 9.4	3.1, 5.1	2.3, 5.7	4.5, 4.5	0.0, 2.0	15.8, 15.8	n/a	0.0, 0.0	3.7, 6.7
Escherichia coli	n	1,744	1,054	710	439	695	231	170	190	5,233
	%R	2.4, 8.9	1.9, 6.5	2.3, 7.3	4.1, 12.1	2.4, 8.5	0.4, 3.5	4.7, 22.9	2.6, 7.4	2.4, 8.6

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	0.0, 2.3
Klebsiella oxytoca	n	86	78	30	28	43	16	5	10	296
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a	0.0, 10.0	0.0, 1.0
Klebsiella pneumoniae complex	n	436	282	227	83	211	50	52	42	1,383
	%R	2.3, 4.8	1.8, 3.5	1.3, 2.2	0.0, 2.4	0.5, 2.8	0.0, 2.0	1.9, 13.5	0.0, 11.9	1.4, 4.1
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%R	2.7, 4.4	2.9, 2.9	0.0, 2.3	0.0, 6.5	2.1, 4.2	n/a	n/a	n/a	1.9, 3.7
Pseudomonas aeruginosa	n	260	146	154	76	113	35	13	30	827
	%R	0.4, 0.8	0.0, 0.0	0.0, 1.3	0.0, 0.0	1.8, 1.8	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.4, 0.7
Serratia marcescens	n	103	52	36	7	35	8	4	10	255
	%R	1.0, 35.0	0.0, 36.5	0.0, 19.4	n/a	0.0, 34.3	n/a	n/a	20.0, 20.0	1.2, 31.4
Trimethoprim										
Enterobacter cloacae complex	n	170	98	80	22	51	19	9	18	467
	%R	23.5, 23.5	15.3, 15.3	21.3, 22.5	9.1, 9.1	13.7, 13.7	15.8, 15.8	n/a	16.7, 16.7	19.1, 19.3
Escherichia coli	n	1,771	1,054	653	439	694	231	170	190	5,202
	%R	30.3, 30.5	27.5, 27.6	30.3, 30.6	31.0, 31.0	35.0, 35.0	16.9, 16.9	55.9, 55.9	21.1, 21.1	30.3, 30.4
Klebsiella aerogenes	n	39	29	15	13	18	7	3	4	128
	%R	0.0, 0.0	3.4, 3.4	13.3, 13.3	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	3.1, 3.1
Klebsiella oxytoca	n	86	78	27	28	43	16	5	10	293
	%R	8.1, 9.3	3.8, 3.8	11.1, 11.1	3.6, 3.6	4.7, 4.7	6.3, 6.3	n/a	0.0, 0.0	6.8, 7.2
Klebsiella pneumoniae complex	n	444	282	210	83	212	50	52	42	1,375
	%R	16.9, 17.8	13.5, 14.5	15.2, 16.2	13.3, 14.5	11.3, 11.3	10.0, 10.0	28.8, 28.8	14.3, 14.3	15.0, 15.7
Proteus mirabilis	n	113	69	42	31	48	9	4	6	322
	%R	19.5, 20.4	21.7, 21.7	14.3, 14.3	22.6, 22.6	12.5, 12.5	n/a	n/a	n/a	18.6, 18.9
Salmonella species (non-typhoidal)	n	21	16	15	0	18	12	10	3	95
	%R	4.8, 4.8	6.3, 6.3	0.0, 0.0	n/a	5.6, 5.6	0.0, 0.0	0.0, 0.0	n/a	3.2, 3.2
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	18.9, 18.9
Serratia marcescens	n	105	52	34	7	35	8	4	10	255
	%R	2.9, 2.9	0.0, 0.0	0.0, 0.0	n/a	2.9, 2.9	n/a	n/a	0.0, 0.0	1.6, 1.6
Trimethoprim–sulfamethoxazole										
Acinetobacter baumannii complex	n	9	18	21	3	4	3	8	1	67
	%R	n/a	0.0, 0.0	4.8, 4.8	n/a	n/a	n/a	n/a	n/a	4.5, 4.5
Enterobacter cloacae complex	n	170	97	88	22	51	19	9	16	472
	%R	21.8,	14.4,	21.6,	9.1,	7.8,	10.5,	n/a	18.8,	17.6,

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		21.8	14.4	22.7	9.1	7.8	10.5		18.8	17.8
Escherichia coli	n	1,771	1,053	711	437	695	231	170	190	5,258
	%R	28.1, 28.0	25.4, 25.1	27.8, 27.8	27.5, 27.0	32.5, 32.5	14.3, 14.3	55.3, 55.3	19.5, 19.5	28.0, 27.9
Klebsiella aerogenes	n	39	29	15	13	18	7	3	5	129
	%R	0.0, 0.0	3.4, 3.4	13.3, 13.3	0.0, 0.0	0.0, 0.0	n/a	n/a	n/a	3.1, 3.1
Klebsiella oxytoca	n	87	78	30	28	43	16	5	10	297
	%R	8.0, 8.0	3.8, 3.8	6.7, 6.7	3.6, 3.6	4.7, 4.7	6.3, 6.3	n/a	0.0, 0.0	6.4, 6.4
Klebsiella pneumoniae complex	n	444	282	227	83	212	50	52	42	1,392
	%R	15.8, 15.5	10.3, 10.3	15.4, 15.4	9.6, 9.6	8.5, 8.5	10.0, 10.0	25.0, 25.0	7.1, 7.1	13.0, 12.9
Proteus mirabilis	n	113	69	43	31	48	9	4	6	323
	%R	13.3, 13.3	15.9, 15.9	9.3, 9.3	16.1, 16.1	10.4, 10.4	n/a	n/a	n/a	13.6, 13.6
Salmonella species (non-typhoidal)	n	21	16	16	0	18	12	10	3	96
	%R	4.8, 4.8	6.3, 6.3	0.0, 0.0	n/a	5.6, 5.6	0.0, 0.0	0.0, 0.0	n/a	3.1, 3.1
Salmonella species (typhoidal)	n	9	15	2	1	5	1	1	3	37
	%R	n/a	0.0, 0.0	n/a	n/a	n/a	n/a	n/a	n/a	16.2, 16.2
Serratia marcescens	n	105	52	36	7	35	8	4	10	257
	%R	2.9, 1.9	0.0, 0.0	0.0, 0.0	n/a	0.0, 0.0	n/a	n/a	0.0, 0.0	1.2, 0.8

CLSI = Clinical and Laboratory Standards Institute; ECOFF = epidemiological cut-off value; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate (CLSI) or susceptible, increased exposure (EUCAST); n/a = insufficient numbers (<10) to calculate; NS = intermediate plus resistant; R = resistant; SDD = sensitive dose dependent (CLSI)

* Category analysed for each organism. If different for CLSI and EUCAST, they are separated by a comma.

† For susceptibility testing purposes, CLSI uses a 2:1 ratio. EUCAST fixes the concentration of clavulanic acid at 2 mg/L; this formulation is only available specific cards

§ No breakpoints defined for indicated species

\# No category defined

** The ciprofloxacin concentration range available on the Vitek® card used restricts the ability to accurately identify susceptible (CLSI/EUCAST) and intermediate (CLSI) categories for *Salmonella* species. Results of MIC strips or a perflocaxin 1 ug disc were applied if available

Appendix D. Multiple acquired resistance by species and state or territory

The most problematic pathogens are those with multiple acquired resistances. Although there is no agreed benchmark for the definition of multidrug resistance, acquired resistance to one or more agent in three or more antimicrobial categories has been chosen to define multi-drug resistance in this survey.[5] For each species, antimicrobials were excluded from the count if they are affected by natural resistance mechanisms, and/or neither CLSI nor EUCAST breakpoints were available. For this analysis, resistance included intermediate susceptibility, if applicable.

Tables D1–D10 show multiple acquired resistances for different species. Only isolates for which the full range of antimicrobial agents was tested were included for determination of multi-drug resistance. The agents included for each species are listed in the notes after each table. EUCAST breakpoints were used throughout the analysis.

Table D1: Multiple acquired resistance in *Acinetobacter baumannii* complex, by state and territory, AGAR, 2022

State or territory		Number of categories (non-multidrug resistant)				Number of categories (multidrug resistant)		
	Total	0	1	2	%	3	4	%
NSW	9	9	0	0	–*	0	0	–*
Vic	18	17	1	0	–*	0	0	–*
Qld	19	17	1	0	–*	1	0	–*
SA	3	3	0	0	–*	0	0	–*
WA	4	3	1	0	–*	0	0	–*
Tas	3	3	0	0	–*	0	0	–*
NT	8	7	0	0	–*	0	1	–*
ACT	1	1	0	0	–*	0	0	–*
Total	**65**	**60**	**3**	**0**	**96.9**	**1**	**1**	**3.1**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Notes:
1. Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), carbapenems (meropenem), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim-sulfamethoxazole).
2. *Acinetobacter baumannii* complex includes *A. nosocomialis* (*n* = 6) and *A. pittii* (*n* = 5).

Table D2: Multiple acquired resistance in *Citrobacter koseri,* by state and territory, AGAR, 2022

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	26	22	3	1	–*	0	0	0	0	0	–*
Vic	12	11	0	0	–*	1	0	0	0	0	–*
Qld	9	8	0	1	–*	0	0	0	0	0	–*
SA	8	8	0	0	–*	0	0	0	0	0	–*
WA	14	13	1	0	–*	0	0	0	0	0	–*
Tas	4	4	0	0	–*	0	0	0	0	0	–*
NT	4	4	0	0	–*	0	0	0	0	0	–*
ACT	3	3	0	0	–*	0	0	0	0	0	–*
Total	**80**	**73**	**4**	**2**	**98.8**	**1**	**0**	**0**	**0**	**0**	**1.3**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D3: Multiple acquired resistance in *Citrobacter freundii* complex, by state and territory, AGAR, 2022

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	31	14	2	3	61.3	0	0	0	0	0.0
Vic	19	6	1	0	–*	0	0	0	0	–*
Qld	7	0	3	2	–*	0	0	0	0	–*
SA	6	16	2	2	–*	0	1	0	0	–*
WA	20	3	0	1	–*	0	0	0	0	–*
Tas	4	0	0	0	–*	0	0	0	0	–*
NT	0	3	1	1	n/a	0	0	0	0	n/a
ACT	5	71	10	10	–*	0	0	0	0	–*
Total	**92**	**71**	**10**	**10**	**98.9**	**0**	**1**	**0**	**0**	**1.1**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable (no isolates)

* Not applicable, insufficient numbers (<30) to calculate

Notes:
1. Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).
2. *Citrobacter freundii* complex includes *C. braakii* (*n* = 7), *C. youngae* (*n* = 2).

Table D4: Multiple acquired resistance in *Klebsiella aerogenes*, by state and territory, AGAR, 2022

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	39	23	3	11	94.9	2	0	0	0	5.1
Vic	29	17	1	11	–*	0	0	0	0	–*
Qld	15	11	1	3	–*	0	0	0	0	–*
SA	13	6	1	5	–*	1	0	0	0	–*
WA	18	14	2	2	–*	0	0	0	0	–*
Tas	7	3	1	2	–*	0	1	0	0	–*
NT	3	1	0	1	–*	0	1	0	0	–*
ACT	5	1	0	4	–*	0	0	0	0	–*
Total	**129**	**76**	**9**	**39**	**96.1**	**3**	**2**	**0**	**0**	**3.9**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D5: Multiple acquired resistance in *Klebsiella oxytoca*, by state and territory, AGAR, 2022

State or territory		Number of categories (non- multidrug resistant)				Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	85	70	6	7	97.6	1	1	0	0	0	2.4
Vic	78	63	11	4	100.0	0	0	0	0	0	0.0
Qld	30	27	3	0	100.0	0	0	0	0	0	0.0
SA	28	25	2	1	–*	0	0	0	0	0	–*
WA	43	36	5	2	100.0	0	0	0	0	0	0.0
Tas	16	11	2	3	–*	0	0	0	0	0	–*
NT	5	2	0	3	–*	0	0	0	0	0	–*
ACT	10	8	1	1	–*	0	0	0	0	0	–*
Total	**295**	**242**	**30**	**21**	**99.3**	**1**	**1**	**0**	**0**	**0**	**0.7**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D6: Multiple acquired resistance in *Morganella morganii*, by state and territory, AGAR, 2022

State or territory	Number of categories (non- multidrug resistant)					Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	47	25	17	2	93.6	1	2	0	0	0	6.4
Vic	19	12	6	1	–*	0	0	0	0	0	–*
Qld	11	6	4	1	–*	0	0	0	0	0	–*
SA	11	5	4	1	–*	1	0	0	0	0	–*
WA	9	4	4	1	–*	0	0	0	0	0	–*
Tas	7	3	3	0	–*	1	0	0	0	0	–*
NT	1	0	1	0	–*	0	0	0	0	0	–*
ACT	1	0	1	0	–*	0	0	0	0	0	–*
Total	**106**	**55**	**40**	**6**	**95.3**	**3**	**2**	**0**	**0**	**0**	**4.7**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), and folate pathway inhibitors (trimethoprim–sulfamethoxazole).

Table D7: Multiple acquired resistance in *Proteus mirabilis*, by state and territory, AGAR, 2022

State or territory		Number of categories (non- multidrug resistant)				Number of categories (multidrug resistant)						
	Total	0	1	2	%	3	4	5	6	7	8	Total
NSW	113	84	12	10	93.8	3	2	2	0	0	0	6.2
Vic	69	53	10	4	97.1	1	1	0	0	0	0	2.9
Qld	42	36	4	1	97.6	1	0	0	0	0	0	2.4
SA	31	23	3	4	96.8	0	1	0	0	0	0	3.2
WA	48	37	4	6	97.9	0	1	0	0	0	0	2.1
Tas	9	5	1	3	–*	0	0	0	0	0	0	–*
NT	4	4	0	0	–*	0	0	0	0	0	0	–*
ACT	6	5	1	0	–*	0	0	0	0	0	0	–*
Total	**322**	**247**	**35**	**28**	**96.3**	**5**	**5**	**2**	**0**	**0**	**0**	**3.7**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable, insufficient numbers (<30) to calculate

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins (ampicillin).

Table D8: Multiple acquired resistance in *Salmonella* species (non-typhoidal), by state and territory, AGAR, 2022

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	21	16	3	1	–*	1	0	0	0	–*
Vic	16	11	3	1	–*	0	1	0	0	–*
Qld	16	16	0	0	–*	0	0	0	0	–*
SA	0	0	0	0	n/a	0	0	0	0	n/a
WA	18	16	1	0	–*	0	1	0	0	–*
Tas	12	12	0	0	–*	0	0	0	0	–*
NT	10	9	1	0	–*	0	0	0	0	–*
ACT	3	2	1	0	–*	0	0	0	0	–*
Total	**96**	**82**	**9**	**2**	**96.9**	**1**	**2**	**0**	**0**	**3.1**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable (no isolates)

* Not applicable (insufficient numbers)

Note: Antimicrobial categories (agents) are antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins (ampicillin)

Table D9: Multiple acquired resistance in *Salmonella* species (typhoidal), by state and territory, AGAR, 2022

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)				
	Total	0	1	2	%	3	4	5	6	%
NSW	9	1	4	0	–*	3	0	1	0	–*
Vic	15	3	12	0	–*	0	0	0	0	–*
Qld	2	1	0	0	–*	1	0	0	0	–*
SA	1	0	1	0	–*	0	0	0	0	–*
WA	5	0	4	0	–*	1	0	0	0	–*
Tas	1	0	1	0	–*	0	0	0	0	–*
NT	1	0	1	0	–*	0	0	0	0	–*
ACT	3	0	2	0	–*	0	1	0	0	–*
Total	**37**	**5**	**25**	**0**	**81.1**	**5**	**1**	**1**	**0**	**18.9**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories

* Not applicable (insufficient numbers)

Note: Antimicrobial categories (agents) are antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), and penicillins (ampicillin).

Table D10: Multiple acquired resistance in *Serratia marcescens*, by state and territory, AGAR, 2022

State or territory	Number of categories (non-multidrug resistant)					Number of categories (multidrug resistant)					
	Total	0	1	2	%	3	4	5	6	7	%
NSW	95	22	53	15	94.7	3	2	0	0	0	5.3
Vic	52	21	20	7	92.3	2	2	0	0	0	7.7
Qld	36	11	23	2	100.0	0	0	0	0	0	0.0
SA	7	1	6	0	–*	0	0	0	0	0	–*
WA	4	2	1	1	–*	0	0	0	0	0	–*
Tas	8	2	5	0	–*	0	1	0	0	0	–*
NT	0	0	0	0	n/a	0	0	0	0	0	n/a
ACT	10	5	5	0	–*	0	0	0	0	0	–*
Total	**212**	**64**	**113**	**25**	**95.3**	**5**	**5**	**0**	**0**	**0**	**4.7**

Multi-drug resistant = resistant to one or more agent in three or more antimicrobial categories; n/a = not applicable (no isolates)

* Not applicable (insufficient numbers)

Note: Antimicrobial categories (agents) are aminoglycosides (gentamicin or tobramycin), antipseudomonal penicillins + β-lactamase inhibitor (piperacillin–tazobactam), carbapenems (meropenem), extended-spectrum cephalosporins (ceftriaxone or ceftazidime), cephamycins (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole).