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2022 NATIONAL HEALTHCARE SAFETY NETWORK ANTIMICROBIAL RESISTANCE (AR) OPTION REPORT

Division of Healthcare Quality Promotion

National Center for Emerging and Zoonotic Infectious Diseases

Centers for Disease Control and Prevention

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NATIONAL HEALTHCARE SAFETY NETWORK
ANTIMICROBIAL RESISTANCE OPTION

Executive Summary

Antimicrobial resistance (AR) is one of the most pressing threats to public health nationally and globally.[1,2] In 2019, an estimated 1.27 million deaths worldwide were directly linked to bacterial AR, and AR contributed to nearly 4.95 million fatalities.[2] To support efforts of addressing this threat, CDC's National Healthcare Safety Network (NHSN) collects antimicrobial susceptibility data from healthcare hospitals through its AR Option surveillance module.

This 2022 NHSN AR Option Report summarizes both the distribution of hospital-level standardized resistant infection ratios (SRIR) and pathogen-specific standardized infection ratios (pSIR) as well as the incidence of hospital-onset events and prevalence of community-onset events associated with specific organisms among hospitals reporting data for 2022. The SRIR and pSIR are NHSN's risk-adjusted measures of hospital-onset infections associated with specific organisms and drug-resistant phenotypes. For both measures, values above 1.0 indicate that more hospital-onset infections were observed than predicted, values equal to 1.0 indicate equivalence between observed and predicted infections, and values below 1.0 indicate that fewer hospital-onset infections were observed than predicted. These metrics are available to acute care hospitals participating in the NHSN AR Option. Hospitals can use this report to understand where their SRIR and pSIR values stand in the distribution among hospitals reporting to the AR Option in 2022.

This report also summarizes the percentages of clinical isolates with antimicrobial resistance or non-susceptibility among the isolates submitted with the relevant susceptibility testing results. We present these aggregated percentages of drug-resistant or non-susceptible phenotypes to promote awareness of AR at national level. These aggregated data are not intended to guide antimicrobial prescribing practices because the percentages of AR can vary across geographic regions, hospitals, and patient populations. To guide clinicians in the selection of empirical antimicrobial therapy, it is recommended that hospitals summarize their own cumulative antimicrobial susceptibility data.

Background

CDC's NHSN Antimicrobial Resistance (AR) Option is a module that has collected data on antimicrobial susceptibility from healthcare hospitals since 2014. The data are extracted directly from laboratory information systems (LIS) and from electronic health records linked to hospitals' LIS. These data are processed by either vendors or internally developed surveillance software, in accordance with the specifications outlined in the NHSN Antimicrobial Use and Resistance (AUR) Module Protocol. All NHSN inpatient hospitals enrolled for reporting to the Patient Safety Component are eligible to participate in the AR Option if they have electronic access to the data required for reporting. Eligible hospital types are:

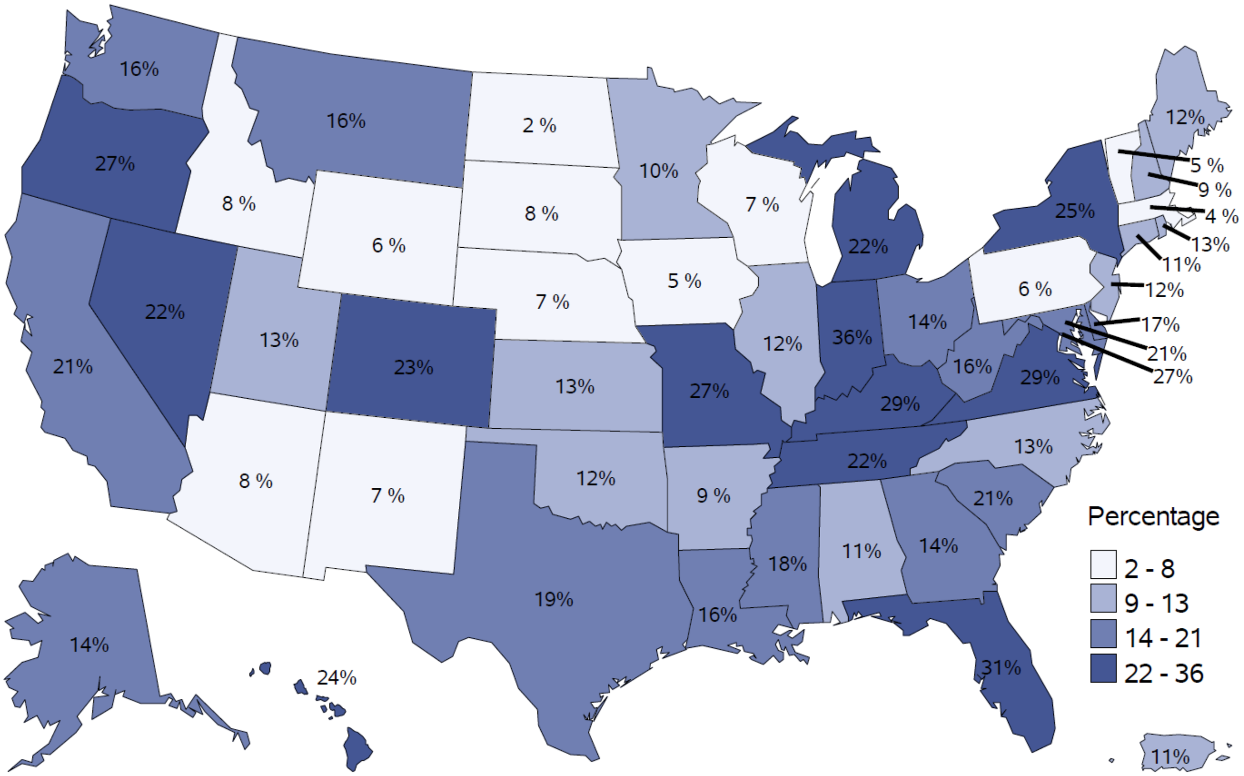
- General acute care and critical access hospitals
- Children’s hospitals
- Pediatric long term acute care hospitals
- Long-term acute care hospitals
- Military hospitals
- Veterans’ affair hospitals
- Specialty hospitals, including oncology, orthopedic, psychiatric, rehabilitation, surgical, women’s, and women’s-and-children’s hospitals
- Government and non-government hospitals designated for public health emergencies

For the purposes of the AR Option Data Report, all submitters will be referred to collectively as hospitals.

NHSN encourages reporting specimens at each hospital from all NHSN defined inpatient locations (including inpatient procedural areas like operating rooms) and three select outpatient locations: Emergency Department (ED), Pediatric ED, and any 24-hour Observation Area from which the numerator data can be accurately electronically captured. The AR Option does not accept specimens collected in other outpatient location types, such as outpatient clinics.

Beginning in 2017, submitting data to the AR Option became an option for fulfilling the measure of Public Health Registry Reporting under the Medicare Meaningful Use Program (now known as the Promoting Interoperability Program).[3] Participation in the AR Option has increased slowly over time. In August 2022, CMS published the 2023 Final Rule for the Medicare Promoting Interoperability Program for eligible hospitals and CAHs that required the AUR Surveillance measure under the Public Health and Clinical Data Exchange Objective beginning in 2023.[4] Although no federal AR reporting mandates were in effect during the period covered by this report, as of January 2023, 1,226 hospitals had submitted at least one month of data since the launch of the AR Option. **Figure 1** displays the proportion of eligible hospitals in each state or jurisdiction that submitted at least one month of data to the AR Option.

Figure 1. Percentage of hospitals that submitted data from 2022 to NHSN’s AR Option* among eligible hospitals** by state/jurisdiction



*Hospitals were considered to have submitted data from 2022 to NHSN's AR Option if they submitted at least one month of data from 2022 to NHSN by January 1, 2023.

** Eligible hospitals include critical access, children's, general acute care, long-term acute care, military, oncology, orthopedic, surgical, Veterans Affairs, women's, and women's and children's hospitals as well as psychiatric and inpatient rehabilitation facilities.

Abbreviations: Antimicrobial Resistance (AR), National Healthcare Safety Network (NHSN).

Methodology

Data Submission

Data for the NHSN AR Option are submitted electronically in accordance with the Health Level 7 (HL7) Clinical Data Architecture (CDA) Implementation Guide. Manual data entry is not supported for AR Option reporting. Each month, hospitals must submit two types of records: an event file for each eligible isolate and one or more summary files comprising a facility-wide inpatient (FacWideIN) denominator summary and separate summaries for each eligible outpatient location.

Each event record represents a single isolate identified as an eligible organism and recovered from an eligible specimen—blood, cerebrospinal fluid (CSF), urine, or lower respiratory tract (LRT). These events are submitted along with its antimicrobial susceptibility testing (AST) results for antimicrobials specified in the AUR Module Protocol. Each record also includes the NHSN facility identifier, isolate-related information (e.g., organism identification, specimen type, date of specimen collection, location of the patient at the time of specimen collection), and patient information, including a patient identifier, date of admission or encounter, and patient demographics (e.g., date of birth). Hospitals follow the guidance in the NHSN AR Option protocol to remove duplicated isolates before submission. The denominator records include total inpatient patient days and admissions (FacWideIN) or the total encounters (outpatient locations) for the month.

Data Preparation

First, we assessed data quality and eliminated duplicate and inconsistent records. To facilitate phenotype assignment and organism classification, organisms were grouped into designated surveillance categories, and specimens were categorized into four primary types: blood, CSF, LRT, and urine. Next, all reported susceptibility results were evaluated for consistency. Any invalid or non-standard entries were regarded as 'not tested.’

Hospital-level data from the 2022 NHSN Patient Safety Annual Hospital Survey were also merged into the dataset to provide descriptive information on hospital characteristics. The following fields from this survey were included in analysis: number of beds, intensive care unit (ICU) capacity, teaching status, and whether the hospital implemented up-to-date breakpoints for antimicrobial susceptibility interpretation recommended by the Clinical and Laboratory Standards Institution (CLSI).

Inclusion and Exclusion Criteria

Hospitals were included in the analysis if they submitted complete and valid AR Option data for at least nine months during the 2022 calendar year. This threshold was selected to ensure sufficient reporting for comparison and summary across hospitals.

Hospitals were excluded if no Patient Safety Annual Survey data were available for 2022, as this information was necessary to determine key characteristics required for analysis.

Additional exclusion criteria:

- Data from hospitals with >10% missing relevant AST results among all hospital-onset (HO) isolates for a phenotype and specimen type were excluded from the Standardized Resistant Infection Ratio (SRIR) calculation for that phenotype and specimen type.
- Data from hospitals with <0.3 events predicted for the year (minimum precision criteria for the number of predicted infections was not met) were excluded from the SRIR and the Pathogen-specific Standardized Infection Ratio (pSIR) distributions for that phenotype/pathogen and specimen type.
- Events from the hospitals that indicated in the NHSN 2022 Annual Hospital Survey that their laboratories had not implemented revised breakpoints recommended by CLSI for specific organisms were excluded from the calculation for percentages of isolates that tested resistant or non-susceptible or the associated phenotypes (See below).

Phenotypes for which events were excluded from SRIR and percent resistant or non-susceptible calculations when hospitals did not indicate use of revised CLSI breakpoints

For each measure and phenotype combinations listed below, events submitted from hospitals that did not implement the revised CLSI breakpoint(s) in 2022 were excluded from the calculations of corresponding measure(s).

Measures	Revised CLSI breakpoint required for inclusion
• SRIR: Extended-spectrum cephalosporin-resistant Enterobacterales (ESCEall_AR) • Percentage of resistance: Extended-spectrum cephalosporin-resistant Enterobacterales (ESCEall_AR)	2010 cephalosporin and monobactam breakpoints for Enterobacterales
• SRIR: Carbapenem-resistant Enterobacterales (CREall_AR) • Percentage of resistance: Carbapenem-resistant Enterobacterales (expanded) (CREexpanded_AR) • Percentage of resistance: Carbapenem-resistant Enterobacterales (CREall_AR)	2010 carbapenem breakpoints for Enterobacterales
• Percentage of resistance: Carbapenem-resistant Enterobacterales (expanded) (CREexpanded_AR) • Percentage of resistance: Carbapenem-resistant Enterobacterales (CREall_AR)	2012 ertapenem breakpoints for Enterobacterales
• Percentage of non-susceptibility: Carbapenem-non-susceptible *Pseudomonas aeruginosa* (carbNS_PA_AR) • Percentage of non-susceptibility: Multidrug-resistant *Pseudomonas aeruginosa* (MDR_PA_AR)	2012 carbapenem breakpoints for *Pseudomonas aeruginosa*

• Percentage of resistance: Fluoroquinolone-resistant *Pseudomonas aeruginosa* (FQPA_AR) • Percentage of non-susceptibility: Multidrug-resistant *Pseudomonas aeruginosa* (MDR_PA_AR)	2019 fluroquinolone breakpoints for *Pseudomonas aeruginosa*
• Percentage of resistance: Fluoroquinolone-resistant Enterobacterales (FQE_AR)	2019 fluroquinolone breakpoints for Enterobacterales

Abbreviations: Clinical and Laboratory Standards Institute (CLSI), Standardized Resistant Infection Ratio (SRIR).

Example: If a facility reported that it did not adopt the 2019 fluoroquinolone CLSI breakpoints for Enterobacterales, all Enterobacterales events from that facility were excluded from the calculation of fluoroquinolone resistance among Enterobacterales.

Frequencies of Organisms associated with AR Option events

This report summarizes the organisms associated with AR Option events for the hospitals included. The summary includes the following measures:

1. The frequencies of organisms associated with AR events by onset and specimen type (CSF, blood, LRT, and urine).
2. The median, 25th, and 75th percentiles of hospital-level prevalence of community-onset (CO) events by organism. The prevalence of CO events per 10,000 admissions was calculated as follows:

$$CO\ prevalence = \frac{\#CO\ AR\ Events}{\#\ admissions} \times 10{,}000$$

3. The median, 25th, and 75th percentiles of hospital-level incidence of hospital-onset (HO) events by organism. The incidence of HO events per 10,000 patient days was calculated as follows:

$$HO\ incidence = \frac{\#HO\ AR\ Events}{\#\ patient\ days} \times 10{,}000$$

The designation of HO or CO was based on the specimen collection date and date of admission. The date of hospital admission is day 1. If the specimen was collected in an outpatient location or in an inpatient location on days 1, 2, or 3, the AR Event was classified as CO. If the specimen was collected in an inpatient location on Day 4 or after, the AR Event was classified as HO.

Standardized Resistant Infection Ratio (SRIR) and Pathogen-specific Standardized Infection Ratio (pSIR)

This report includes the SRIR, which was calculated using the overall observed and predicted numbers of resistant infections by specimen type (blood, LRT, and urine) based on the 2019 baseline SRIR predictive models (Please refer to Appendix A of NHSN's Guide to the SRIR and pSIR for details of the predictive models). The SRIR was calculated for the following phenotypes:

- Carbapenem-resistant Enterobacterales
- Extended-spectrum cephalosporin-resistant Enterobacterales
- Fluoroquinolone-resistant Enterobacterales
- Vancomycin-resistant *Enterococcus*
- Fluoroquinolone-resistant *Pseudomonas aeruginosa*
- Multidrug-resistant *Pseudomonas aeruginosa*
- Methicillin-resistant *Staphylococcus aureus*

The SRIR was calculated by dividing observed number of resistant infections by the predicted number of resistant infections:

$$SRIR = \frac{Observed\ Resistant\ Infections}{Predicted\ Resistant\ Infections}$$

- Observed resistant infections are the number of HO AR Option Events isolated from a specimen type that met the resistance definition for the specified AR Option phenotype and were reported to the AR Option.
- Predicted resistant infections are the number of HO AR Option Events predicted for that same specimen type and AR Option phenotype. NHSN calculated the predicted number of resistant HO infections using risk-adjusted SRIR predictive models.

This report also includes the pSIR, which was calculated using the overall observed and predicted numbers of infections by specimen type (blood, LRT, and urine) based on the 2019 baseline pSIR predictive models. (Please refer to Appendix B of NHSN's Guide to the SRIR and pSIR for details of the predictive models.) The pSIR was calculated for the following pathogens:

- Enterobacterales
- *Enterococcus*
- *Staphylococcus aureus*
- *Pseudomonas aeruginosa*

The pSIR was calculated by dividing observed infections of specific pathogens by predicted infections of specific pathogens:

$$pSIR = \frac{Observed\ Infections\ of\ Specific\ Pathogens}{Predicted\ Infections\ of\ Specific\ Pathogens}$$

- The observed infections are the number of HO AR Option Events of a specific pathogen or pathogen group isolated from the specified specimen type and were reported to the AR Option.
- The predicted infections are the number of HO AR Option Events predicted for that pathogen or pathogen group and same specimen type. NHSN calculated predicted HO infections using risk-adjusted pSIR predictive models.

The 95% confidence limits (CL) around the SRIRs and pSIRs were determined using the mid-P exact method, which provides a robust estimation by adjusting for small sample sizes and ensuring accurate coverage probabilities. Though not included in the AR Report Excel data tables, the numbers and percentages of hospitals with an SRIR or pSIR significantly higher than one are described in this report. Statistical significance was assessed by examining each hospital's 95% confidence limits; if the lower limit was greater than one, the SRIR or pSIR was considered statistically significantly higher than one.

Percentages of isolates testing resistant or non-susceptible

This report includes calculations of the percentages of isolates that tested resistant or non-susceptible (%R or %NS) for each phenotype by onset type (CO vs. HO), specimen type (CSF, blood, LRT, and urine), and patient care location type (adult, pediatric, and neonatal). %R and %NS were calculated by dividing the number of isolates testing resistant or non-susceptible (specifically, intermediate [I] or resistant [R]) by the number of isolates tested for the relevant antimicrobial(s):

$$\%R = \frac{\#\ \text{isolates tested resistant}}{\#\ \text{isolates tested for phenotype-specific antimicrobial(s)}} \times 100$$

$$\%NS = \frac{\#\ \text{isolates tested non-susceptible}}{\#\ \text{isolates tested for phenotype-specific antimicrobial(s)}} \times 100$$

To provide information of the completeness of susceptibility results submitted for each phenotype, we also calculated the percentage tested (%Tested) for each phenotype by dividing the total number of isolates with valid AST results for phenotype-specific antimicrobial(s) by the total number of isolates. Valid AST results are phenotype-dependent and may include susceptible (S), susceptible dose-dependent (S-DD), intermediate (I), and resistant (R). Please refer to phenotype definitions in Appendix A. To calculate the %Tested for multidrug resistant organisms, isolates must be tested—based on the phenotype definition—for at least one drug from the minimum number of required categories to determine resistance. Criteria for multidrug resistant phenotypes are included in Appendix A.

$$\%\,\text{Tested} = \frac{\#\ \text{Isolates with valid phenotype-specific susceptibility testing results}}{\text{Total}\ \#\ \text{of isolates}} \times 100$$

These measures were calculated for the following organisms and phenotypes. The final interpretation(s) of susceptibility test results of pertinent antimicrobial(s) were used to determine whether an isolate met non-susceptibility or resistant phenotype definitions. Detailed phenotype definitions are included in Appendix A.

- *Acinetobacter* spp.
    - Carbapenem-non-susceptible *Acinetobacter* spp.
    - Multidrug-resistant *Acinetobacter* spp.
- Enterobacterales (Please note: For each phenotype below, a different set of organisms is included. All phenotypes include *Escherichia coli*, *Klebsiella*, and *Enterobacter*. Carbapenem-resistant Enterobacterales expanded includes eight additional species [*Citrobacter amalonaticus, C. freundii, C. koseri, Morganella morganii, Proteus mirabilis, Proteus penneri, Proteus vulgaris*, and *Serratia marcescens*].)
    - Carbapenem-resistant Enterobacterales (expanded)
    - Extended-spectrum cephalosporin-resistant Enterobacterales
    - Carbapenem-resistant Enterobacterales
    - Fluoroquinolone-resistant Enterobacterales
- *Pseudomonas aeruginosa*
    - Carbapenem-non-susceptible *Pseudomonas aeruginosa*
    - Fluoroquinolone-resistant *Pseudomonas aeruginosa*
    - Multidrug-resistant *Pseudomonas aeruginosa*
- Enterococci
    - *Enterococcus* spp. (all enterococci, including *E. faecalis* and *E. faecium*)
    - *Enterococcus faecalis*
    - *Enterococcus faecium*
- *Streptococcus agalactiae* (Group B *Streptococcus*)
    - Clindamycin-non-susceptible *Streptococcus agalactiae*
- *Staphylococcus aureus*
    - Methicillin-resistant *Staphylococcus aureus*
- *Streptococcus pneumoniae*
    - Drug-resistant *Streptococcus pneumoniae*

The data tables for each phenotype include the number of hospitals (No. Hospitals) that submitted at least one isolate for the respective organism, the total number of isolates (No. Isolates), the number and percentage of isolates that were tested for the antimicrobial(s) (% Tested), and the number and percentage of isolates that tested resistant (%R) or non-susceptible (%NS). Percent tested and percent resistant or non-susceptible values for phenotypes were not presented if fewer than 30 isolates are reported for the respective organism, as this sample size was considered insufficient for reliable data interpretation. Percentages of isolates testing resistant or non-susceptible were stratified and presented by onset (HO, CO), specimen type (CSF, blood, LRT, and urine), and patient population using patient care location type (Adult intensive care units [ICU], adult oncology locations [including oncology wards and ICUs], adult non-oncology wards, adult Emergency Department [ED] or 24-hour observation units, pediatric ICUs, pediatric wards, pediatric ED or 24-hour observation units, and neonatal locations). Isolates from neonatal locations are tested for resistance against an additional set of antimicrobials that are used to treat neonatal sepsis or meningitis; these results are shown in a separate table (2022 AR Report Excel Data Table 11).

Results

This section provides a summary of the measures included. Please refer to the 2022 AR Report Excel data tables for more detailed information.

Characteristics of Hospitals

A total of 842 hospitals were included in the analysis, with the majority being general acute care facilities (84.9%), followed by critical access hospitals (8.1%) and children's hospitals (2.9%). Most hospitals reported a medical school affiliation (75.7%). Hospitals included in the analysis reported a median of 12 months of data. Reporting hospitals had a median number of 166 hospital beds and 20 ICU beds (AR Report Excel Data Table 1).

A total of 93.7% of hospitals adopted the CLSI revised 2010 carbapenem breakpoints for Enterobacterales, 92.3% adopted the revised 2010 third-generation cephalosporin and monobactam breakpoints for Enterobacterales, 89.9% adopted the revised 2012 carbapenem breakpoints for *Pseudomonas aeruginosa*, and 88.7% adopted the revised 2012 ertapenem breakpoints for Enterobacterales. Less than 80% of the reporting hospitals adopted revised 2019 fluoroquinolone breakpoints for *P. aeruginosa* (78.2%) and for Enterobacterales (73.9%) (AR Report Excel Data Table 1).

Organisms associated with AR Option events

Among 43,252,539 patient days and 10,358,794 admissions in the 842 hospitals included in this report, a total of 676,370 CO and 125,303 HO events were submitted to the AR Option for 2022. The numbers of events for each organism by onset type and specimen type are shown in the AR Report Excel Data Table 2.

The most frequently identified organisms associated with CO events among different specimen types were *Escherichia coli* (31.8%) and *Staphylococcus aureus* (26.3%) in blood, *S. aureus* (26.0%) and *Streptococcus pneumoniae* (23.0%) in CSF, *S. aureus* (31.6%) and *Pseudomonas aeruginosa* (25.7%) in LRT, and *E. coli* (54.9%) and *Klebsiella pneumoniae* (12.3%) in urine (AR Report Excel Data Table 2).

The most frequently identified organisms associated with HO events among different specimen types, similarly, were *S. aureus* (26.4%) and *E. coli* (14.7%) in blood, *S. aureus* (25.1%) and *P. aeruginosa* (20.9%) in LRT, and *E. coli* (33.9%) and *K. pneumoniae* (12.9%) in urine. Among HO isolates from CSF, *Enterobacter* (13.7%) and *P. aeruginosa* (12.9%) were the top organisms reported with very few events overall.

Pathogen-specific Standardized Infection Ratios (pSIRs) and Standardized Resistant Infection Ratios (SRIRs) by pathogen

Enterobacterales (*Escherichia coli*, *Klebsiella aerogenes*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Enterobacter* spp.)

Among three drug-resistant phenotypes for Enterobacterales that were available for the SRIR, carbapenem resistance was the least frequently observed and predicted phenotype. Among the hospitals that met the minimum precision criteria (predicted number of events ≥0.3) for each specimen type (blood, LRT, and urine), the distributions of hospital-level SRIR for these three phenotypes in 2022 are shown in AR Report Excel Data Table 3a. Among these same hospitals, the numbers and percentages of hospitals with an SRIR significantly higher than one (lower bound of 95% confidence limit >1) are shown in the table below.

	Number and percentage of hospitals with an SRIR significantly higher than 1 among hospitals with ≥0.3 predicted events		
Phenotype	**Blood**	**Lower Respiratory Tract**	**Urine**
Carbapenem resistance	9 (4.9%)	23 (6.9%)	21 (9.4%)
Extended-spectrum cephalosporin resistance	41 (6.5%)	65 (9.9%)	84 (12.3%)
Fluoroquinolone resistance	39 (6.2%)	62 (9.9%)	42 (6.0%)

Abbreviations: Standardized Resistant Infection Ratio (SRIR).

The pooled mean pSIRs for HO Enterobacterales isolated from blood, LRT, and urine were 0.875 (95% CL: 0.853, 0.897), 0.995 (95% CL: 0.980, 1.011), and 0.791 (95% CL: 0.782, 0.801), respectively. The distributions of hospital-level pSIR for Enterobacterales in 2022 are shown in AR Report Excel Data Table 3b. Among hospitals that met the minimum precision criteria, the numbers and percentages of hospitals that had a pSIR significantly higher than one (lower bound of 95% confidence limit >1) for blood, LRT, and urine were 62 (7.8%), 151 (19.2%), and 99 (11.8%), respectively.

Enterococci

The pooled mean SRIRs for HO vancomycin-resistant *Enterococcus* isolated from blood, LRT, and urine were 1.091 (95% CL: 1.025, 1.160), 0.853 (95% CL: 0.728, 0.994), and 1.204 (95% CL: 1.158, 1.252), respectively. Among the hospitals that met the minimum precision criteria for each specimen type, the distributions of hospital-level SRIR for these three phenotypes are shown in AR Report Excel Data Table 3c. Among these same hospitals, the numbers and percentages of hospitals that had an SRIR significantly higher than one for blood, LRT, and urine were 47 (9.2%), 14 (6.3%), and 94 (14.5%), respectively.

The pooled mean pSIRs for HO Enterococci isolated from blood, LRT, and urine were 1.057 (95% CL: 1.020, 1.094), 0.985 (95% CL: 0.917, 1.056), and 0.835 (95% CL: 0.819, 0.850), respectively. The distributions of hospital-level pSIR for Enterococci in 2022 are shown in AR Report Excel Data Table 3d. Among hospitals that met the minimum precision criteria, the numbers and percentages of hospitals that had a pSIR significantly higher than one for blood, LRT, and urine were 83 (11.9%), 39 (7.1%), and 94 (11.2%), respectively.

Pseudomonas aeruginosa

Among the hospitals that met the minimum precision criteria for each specimen type (blood, LRT, and urine), the distributions of hospital-level SRIR for these two phenotypes in 2022 are shown in AR Report Excel Data Table 3e. Among these same hospitals, the numbers and percentages of hospitals that had SRIRs significantly higher than one are shown in the table below.

	Number and percentage of hospitals with an SRIR significantly higher than 1 among hospitals with ≥0.3 predicted events		
Phenotype	**Blood**	**Lower Respiratory Tract**	**Urine**
Fluoroquinolone resistance	7 (2.1%)	41 (6.9%)	16 (2.9%)
Multidrug resistance	7 (2.7%)	54 (7.7%)	18 (5.0%)

Abbreviations: Standardized Resistant Infection Ratio (SRIR).

The pooled mean pSIRs for HO *P. aeruginosa* isolated from blood, LRT, and urine were 0.884 (95% CL: 0.838, 0.932), 0.936 (95% CL: 0.919, 0.953), and 0.797 (95% CL: 0.776, 0.819), respectively. The distributions of hospital-level pSIR for *P. aeruginosa* in 2022 are shown in AR Report Excel Data Table 3f. In 2022, among hospitals that met the minimum precision criteria, the numbers and percentages of hospitals that had a pSIR significantly higher than one for blood, LRT, and urine were 36 (6.1%), 124 (15.1%), and 57 (7.0%), respectively.

Staphylococcus aureus

Overall, the pooled mean SRIRs for HO methicillin-resistant *Staphylococcus aureus* (MRSA) isolated from blood, LRT, and urine were 0.945 (95% CL: 0.902, 0.991), 0.952 (95% CL: 0.928, 0.977), and 0.620 (95% CL: 0.563, 0.681), respectively. Among the hospitals that met the minimum precision criteria, the distributions of hospital-level SRIR for these three phenotypes are shown in AR Report Excel Data Table 3g. Among these same hospitals, the numbers and percentages of hospitals that had an SRIR significantly higher than one for blood, LRT, and urine were 43 (6.4%), 72 (10.2%), and 10 (1.8%), respectively.

The pooled mean pSIRs for HO *S. aureus* isolated from blood, LRT, and urine were 0.977 (95% CL: 0.950, 1.006), 0.868 (95% CL: 0.853, 0.883), and 0.835 (95% CL: 0.785, 0.887), respectively. The distributions of hospital-level pSIR for *S. aureus* are shown in AR Report Excel Data Table 3h. Among hospitals that met the minimum precision criteria, the numbers and percentages of hospitals that had a pSIR significantly higher than one for blood, LRT, and urine were 83 (10.7%), 111 (14.5%), and 18 (2.8%), respectively.

Percentage of isolates testing resistant or non-susceptible

Key results of %R and %NS by onset, specimen type, and patient care location type (adult, pediatric, and neonatal care locations) for each organism are highlighted below.

Acinetobacter spp.

Compared to CO events of *Acinetobacter* spp., specimens collected for HO events had a higher percentage of isolates that were non-susceptible to carbapenems (38.3% vs. 29.7%) and multidrug resistant (39.6% vs. 30.1%). Compared to isolates from blood specimens, isolates from non-invasive specimens (urine and LRT) exhibited higher percentages of carbapenem non-susceptibility (urine: 29.9% and LRT: 42.7% vs. blood: 16.1%). A similar pattern was observed for multidrug-resistant *Acinetobacter* (urine: 30.1% and LRT: 44.6% vs. blood: 15.3%) (AR Report Excel Data Tables 4a, 4b).

Among isolates obtained in adult locations, the percentages of carbapenem non-susceptibility were highest in adult ward, non-oncology units (44.5%) and adult ICUs (43.5%), followed by adult oncology units (23.4%), and ED or 24-hour observation units (21.1%). Similarly, multidrug resistance was most common in adult ward non-oncology units (45.4%) and adult ICUs (44.4%), followed by oncology units (30.0%) and ED or 24-hour observation units (21.3%). Among 291 *Acinetobacter* spp. isolates reported from pediatric locations, the percentage of carbapenem non-susceptibility ranged from 4.3% (pediatric ED or 24-hour observation units) to 7.1% (pediatric wards), and multidrug resistance ranged from 5.2% (pediatric ED or 24-hour observation units) to 13.7% (pediatric wards). Among 105 *Acinetobacter* spp. isolates reported from neonatal locations, all were susceptible to carbapenems and 1.9% were multidrug resistant (AR Report Excel Data Tables 4c, 4d, 4e).

Enterobacterales

Greater proportions of HO Enterobacterales isolates were resistant to carbapenems (Enterobacterales_all: 2.6%, Enterobacterales_expanded: 2.3%) and extended-spectrum cephalosporins (ESC) (25.6%) compared to CO events (0.6% carbapenem resistance, 14.3% ESC resistance). Fluoroquinolone resistance was observed in approximately 22% of all *Escherichia coli*, *Klebsiella,* and *Enterobacter* isolates with no noteworthy difference between HO and CO events (AR Report Excel Data Table 5a).

Carbapenem resistance was highest among LRT specimens (~ 3%) compared to isolates from CSF, blood, or urine specimens (~1% in CSF and blood, 0.6% in urine). ESC resistance was also higher among isolates from LRT (25.7%) than among isolates from blood (18.3%) or urine (14.4%) specimens. However, fluoroquinolone resistance was less prevalent among LRT isolates (18%) than it was among blood and urine isolates (~22%). Only 20.6% of all CSF isolates were tested for fluroquinolone resistance (AR Report Excel Data Table 5b).

Among adult locations, adult ICUs had the highest carbapenem resistance (2.4%–2.7%), followed by adult oncology locations (~2%), adult non-oncology wards (~1.2%), and then adult ED and 24-hour observation units (0.4%). Percentages of ESC resistance were similar in adult ICU and adult oncology locations (~25%), followed by adult non-oncology wards (20%) and adult ED and 24-hour observation units (13.4%). Adult oncology locations had the highest percentage of isolates with fluoroquinolone resistance (31.7%) compared to other adult locations (21%–24%) (AR Report Excel Data Table 5c).

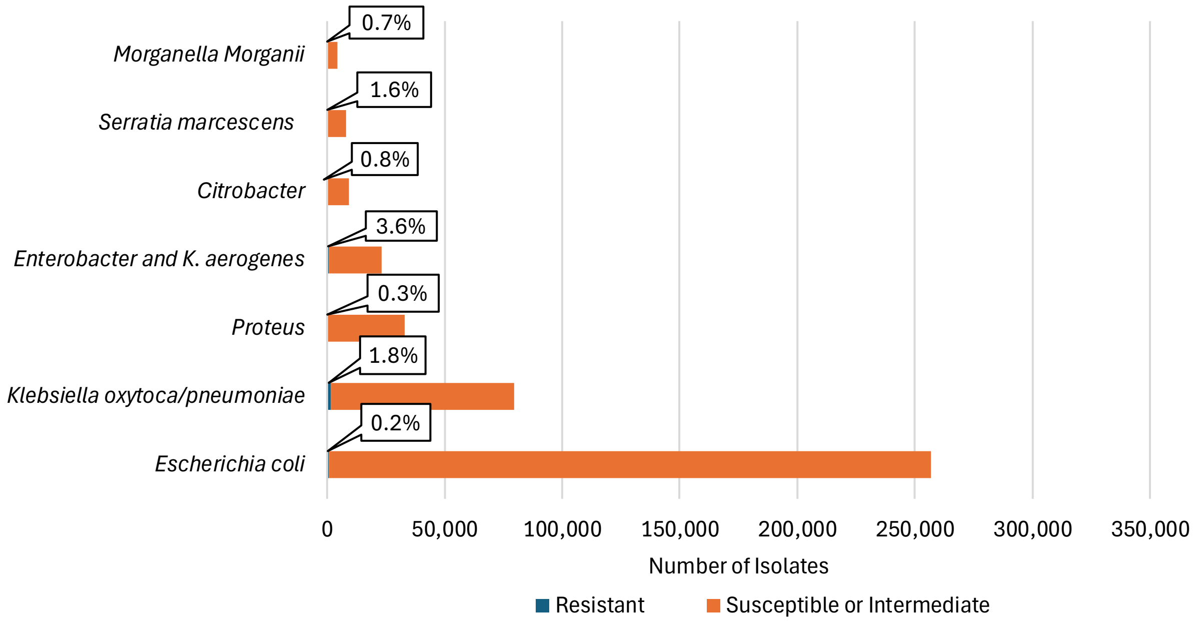
Compared to isolates from adult locations, isolates from pediatric locations exhibited lower percentages of carbapenem, ESC, and fluoroquinolone resistance. Carbapenem resistance was present in 0.9% of isolates from pediatric ICU and wards, 0.2% of isolates from pediatric ED or 24-hour observation units, and ~0.4% of isolates from neonatal locations. ESC resistance was highest in pediatric ICU (21.2%), followed by pediatric wards (16.4%), and lowest in pediatric ED or 24-hour observation units (7.7%). Fluoroquinolone resistance was present in approximately 12% isolates from pediatric ICU and ED or 24-hour observation units, and 16.6% of isolates from pediatric wards (AR Report Excel Data Tables 5d).

Among Enterobacterales isolates in neonatal settings, approximately 0.3% to 0.4% were resistant to carbapenems, while 10% exhibited resistance to extended-spectrum cephalosporins (AR Report Excel Data Tables 5e). Ad hoc analyses were performed to characterize neonatal isolates, revealing that the majority (2,137 out of 2,580, or 83%) were obtained after the third day of hospital admission. Half of the isolates originated from level III units, 31% from level II/III units, and 16% from level IV units, with only 3% coming from level I or II units. A total of 43% of the isolates were collected from urine, followed by LRT (35%) and blood (22%).

Slightly different susceptibility profiles were observed among groups of Enterobacterales species **(Figure 2)**. Isolates of *Enterobacter spp.* and *Klebsiella aerogenes* demonstrated higher rates of resistance to carbapenems (3.6%) and extended-spectrum cephalosporins (28.3%) compared to other organisms within their respective phenotypes (Figures 2A, 2B). Resistance to fluoroquinolones was notably more prevalent among *E. coli* isolates (25.7%) compared to other species (Figure 2C).

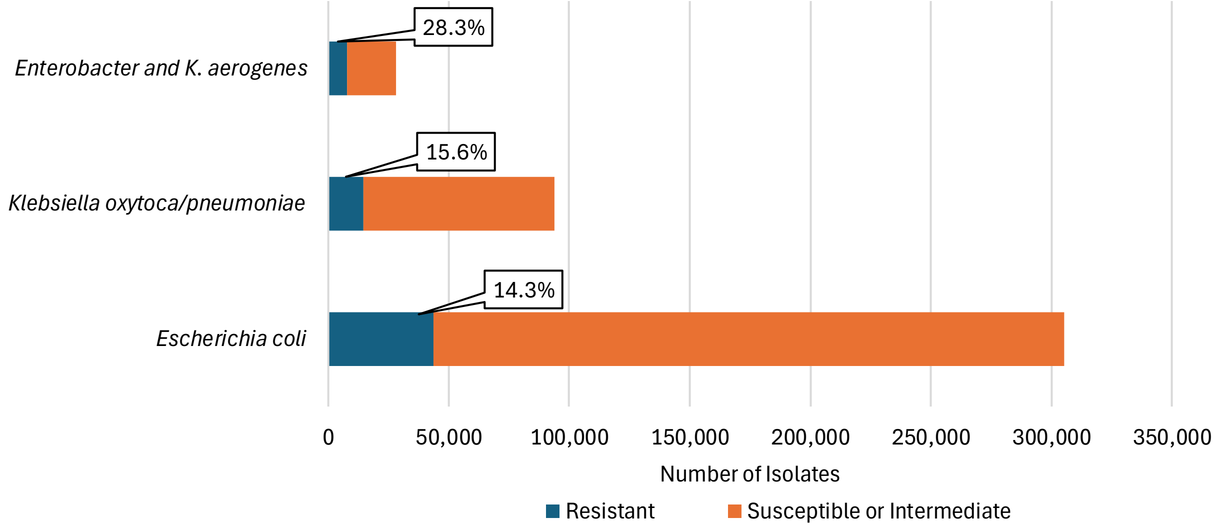
Figure 2. Number of Enterobacterales isolates tested for respective phenotypes and the percentages of isolates with carbapenem resistance (panel A), extended-spectrum cephalosporin resistance (panel B), and fluoroquinolone resistance (panel C) among tested isolates by organism categories

A. Carbapenem resistance* among Enterobacterales isolates by organism category

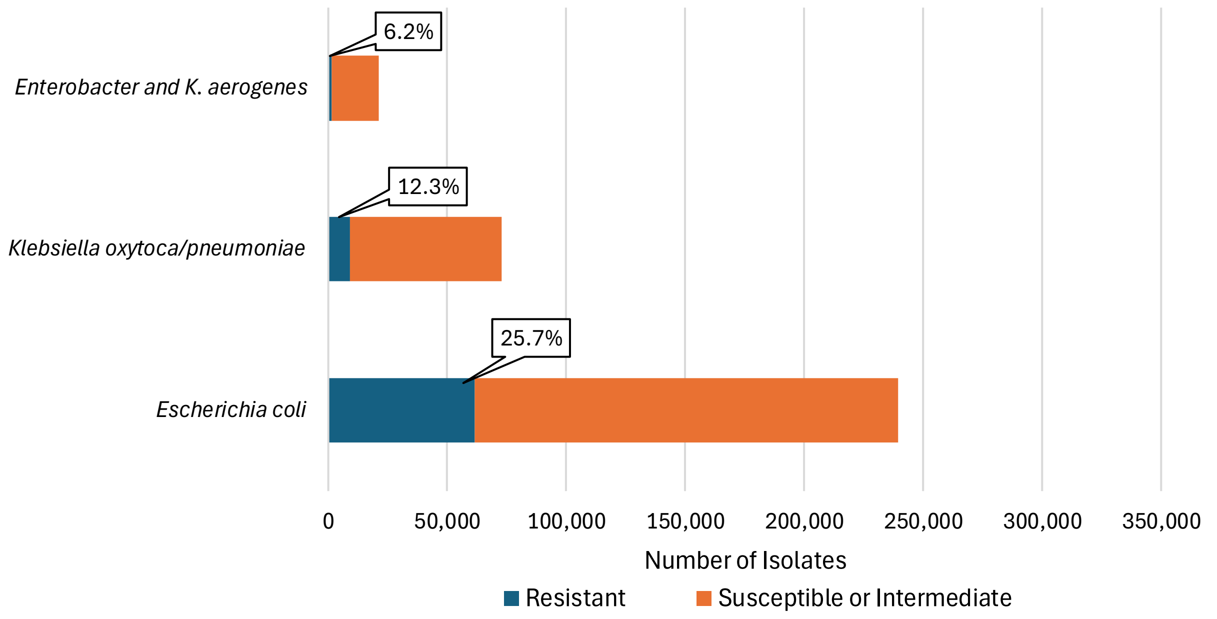


*Imipenem was not used to determine carbapenem resistance for *Proteus* or *Morganella morganii* isolates.

B. Extended-spectrum cephalosporin resistance among Enterobacterales isolates by organism category



C. Fluoroquinolone resistance among Enterobacterales isolates by organism category



Pseudomonas aeruginosa

Compared to CO isolates, higher proportions of HO *Pseudomonas aeruginosa* isolates exhibited carbapenem non-susceptibility (19.7% vs. 12.8%) and multidrug resistance (13.1% vs. 8.2%). Fluoroquinolone resistance was more frequent among CO *P. aeruginosa* isolates than among HO events (17.2% vs. 15.5%) (AR Report Excel Data Table 6a).

Specimens collected from the LRT showed a higher percentage of non-susceptibility to carbapenems, compared to CSF, blood, and urine specimens (20.7% vs. 10%–11.5%). Isolates from non-invasive specimens showed higher percentages of fluoroquinolone resistance (16.9%–18.0% vs 9.6%–13.3%) than isolates obtained through invasive methods (blood and CSF). Isolates from LRT specimens had the highest proportion of multidrug resistance (14.1%) (AR Report Excel Data Table 6b).

Among isolates from adult locations, the percentage of carbapenem non-susceptibility ranged from 10.5% in adult ED or 24-hour observation units to 21.0% in adult ICUs. Approximately 16.5%–18.5% of isolates were resistant to fluoroquinolones. The percentage of isolates with multidrug resistance ranged from 10.3% to 13.7% in adult inpatient locations and was 6.7% in adult ED or 24-hour observation units (AR Report Excel Data Table 6c).

Compared to isolates from adult locations, lower percentages of pediatric isolates had carbapenem non-susceptibility (8.2% in pediatric ED or 24-hour observation units, 12.8%–13.3% in pediatric inpatient locations), fluoroquinolone resistance (10.2%–13.9%), and multidrug resistance (4.8% in pediatric ED or 24-hour observation units, ~10% in pediatric wards and ICUs) (AR Report Excel Data Table 6d).

In neonatal locations, 9.4% of isolates were non-susceptible to carbapenems, and 3.1% of isolates were multidrug resistant (AR Report Excel Data 6e). Ad hoc analyses were conducted to understand the characteristics of neonatal *P. aeruginosa* isolates. The results showed that 92% of neonatal *P. aeruginosa* were isolated from specimens collected on or after the fourth day of hospital admission. The majority (70%) were from the LRT. The percentages of carbapenem non-susceptibility among unit levels II/III, III, and IV were 2.4%, 9.3%, and 18.9%, respectively. Only three isolates were submitted from level II units, and none were submitted from level I units.

Enterococcus spp.

The majority (90.2%) of enterococcal isolates were identified as *Enterococcus faecalis* or *Enterococcus faecium*. *E. faecium* represented approximately 18.9% of enterococcal isolates and exhibited significantly higher percentages of vancomycin resistance across HO (71.6%) and CO (57.1%) events when compared to *E. faecalis* (HO: 3.2%, CO: 2.7%) and all enterococci (HO: 27.0%, CO: 11.9%) (AR Report Excel Data Table 7a). Most enterococcal isolates were from urine (83%), followed by blood (16%) specimens (AR Report Excel Data Table 7b).

In adult locations, *E. faecium* isolates from adult ICUs were more often resistant to vancomycin (74.1%) than isolates from adult oncology (65.3%) and non-oncology wards (66.0%). A total of 53.1% of isolates from adult ED or 24-hour observation units were resistant to vancomycin (AR Report Excel Data Table 7c).

Compared to adult locations, pediatric and neonatal locations had much lower percentages of isolates resistant to vancomycin (<1% for *E. faecalis*, 27%–28.6% for *E. faecium*, and up to 6% enterococci as a whole) (AR Report Excel Data Tables 7d, 7e).

Staphylococcus aureus

Among *Staphylococcus aureus* isolates included in analysis, 74% were CO. A slightly higher percentage of specimens from HO *S. aureus* events were resistant to oxacillin/cefoxitin (methicillin-resistant *S. aureus*, MRSA) (43.4%) compared to specimens from CO events (41.9%) (AR Report Excel Data Table 8a).

Isolates from blood and LRT constituted approximately 82% of all *S. aureus* isolates with approximately 40%–44% MRSA (AR Report Excel Data Table 8b).

Percentages of MRSA varied across adult locations, with the highest observed in adult non-oncology wards at 46.8% and the lowest in adult ICUs and adult ED or 24-hour observation units at 41.8%. Compared to adult locations, pediatric and neonatal locations exhibited lower percentage of MRSA, with 29.2% in pediatric wards, 25.0% in pediatric ED or 24-hour observation units, 24.8% in pediatric ICUs, and 24.2% in neonatal locations (AR Report Excel Data Tables 8c, 8d, 8e).

Streptococcus agalactiae (Group B *Streptococcus*, GBS)

Over 95% of *Streptococcus agalactiae* isolates were from CO events. Both HO and CO events showed similar percentages of clindamycin non-susceptibility (~60%) (AR Report Excel Data Table 9a). Most *S. agalactiae* isolates were from urine (59.3%) and blood (36.7%) specimens, with 51.3% and 78.0% of the isolates tested for clindamycin, respectively. Seventy-nine percent of *S. agalactiae* isolates were collected from adult ED or 24-hour observation units (AR Report Excel Data Table 9c). Depending on patient care locations, approximately 54%–72% of all *S. agalactiae* isolates were non-susceptible to clindamycin (AR Report Excel Data Tables 9a–9e).

Streptococcus pneumoniae

Eighty-nine percent of *Streptococcus pneumoniae* isolates were from CO events; 41.8% were non-susceptible to at least one drug on the panel (Drug-Resistant *Streptococcus pneumoniae*, DRSP) (AR Report Excel Data Table 10a). Most *S. pneumoniae* isolates were from LRT (51.8%) and blood (45.4%) specimens. *S. pneumoniae* isolates from LRT had the highest percentage of DRSP (52.1%) compared to those from CSF, blood, or urine (32.3%–34.6%) (AR Report Excel Data Table 10b).

In adult locations, between 50% and 58% of *S. pneumoniae* isolates across ICUs, oncology locations, and non-oncology wards exhibited DRSP. Prevalence of DRSP was lower in adult ED or 24-hour observation units, with 35.6% of isolates exhibiting DRSP. DRSP percentages were similar across all pediatric location types, ranging from 45% to 46% (AR Report Excel Data Table 10b-10e).

Antimicrobial Resistance to Antimicrobials Frequently Used in Neonatal Locations

Enterobacterales

- **Aminoglycosides:** Gentamicin was the most frequently tested antimicrobial for Enterobacterales isolates obtained from neonatal locations (>96% tested); 5.8%–6.4% of specimens were resistant. *E. coli* exhibited higher percentage of resistance to gentamicin (13.6%) compared to *Klebsiella oxytoca/pneumoniae* (2.5%) or *Enterobacter* spp. (1.2%). Overall, 4.7% of *E. coli* and 2.6% of *K. oxytoca/pneumoniae* specimens were resistant to tobramycin, and 0.4% of *E. coli* and 0.2% of *K. oxytoca/pneumoniae* isolates were resistant to amikacin (AR Report Excel Data Table 11a).
- **Ampicillin:** Approximately 74%–94% of all neonatal Enterobacterales isolates were tested for ampicillin resistance, with a higher proportion of *E. coli* (94.3%) isolates tested. Overall, 62.9% of *E. coli* isolates and approximately 82% of all Enterobacterales isolates tested were resistant to ampicillin(AR Report Excel Data Table 11a).
- **Ampicillin/sulbactam:** Depending on organisms included, approximately 62%–65% of isolates were tested for ampicillin/sulbactam, with higher testing rates observed for *E. coli* (73.5%) and *K. oxytoca/pneumoniae* (71.6%). Resistance to ampicillin/sulbactam was identified in 26% and 31% of isolates among Enterobacterales_all and Enterobacterales_expanded when combining species. For individual species, 26.5% of *E. coli* specimens and 6.9% of *K. oxytoca/pneumoniae* specimens were resistant to ampicillin/sulbactam (AR Report Excel Data Table 11a).
- **Piperacillin/tazobactam:** Less than 4% of overall Enterobacterales isolates were resistant to piperacillin/tazobactam with exceptions for *Enterobacter* spp. and *Klebsiella aerogenes,* which had 9.2% of isolates resistant to piperacillin/tazobactam (AR Report Excel Data Table 11a).

Pseudomonas aeruginosa

Among neonatal *P. aeruginosa* isolates tested, 5.5% were resistant to cefepime or ceftazidime, 2.4% were resistant to amikacin, and 1.4% were resistant to tobramycin (AR Report Excel Data Table 11b).

Discussion

This report provides the first summary of data submitted voluntarily by hospitals to the NHSN AR Option. It includes risk-adjusted AR benchmarks and resistance/non-susceptibility metrics for frequently observed drug-resistant organisms of concern to healthcare hospitals. Among data from 842 hospitals submitted for 2022, *S. aureus*, Enterobacterales, and *P. aeruginosa* were the most common organisms in NHSN AR Option. Fluoroquinolone resistance was found in >20% of the Enterobacterales and >15% of the *P. aeruginosa* isolates in adult locations, even among community-onset isolates. Although carbapenem resistance was identified in fewer than 3% of the Enterobacterales isolates, non-susceptibility among *P. aeruginosa* was notably higher—over 10% in community-onset and nearly 20% in hospital-onset isolates. Furthermore, multidrug resistance was also common in *Acinetobacter* and *P. aeruginosa*, particularly in lower respiratory tract specimens. MRSA and VRE continued to be commonly reported AR phenotypes, with MRSA accounting for more than 40% of *S. aureus* and VRE accounting for 12% (CO) to 27% (HO) Enterococcus isolates, respectively. Approximately 60% *S. agalactiae* (GBS) were resistant to clindamycin. Approximately 40% of *S. pneumoniae* isolates were non-susceptible to at least one of the tested antimicrobials. In neonatal settings, over 80% of Enterobacterales were resistant to ampicillin and around 6% were resistant to gentamicin.

Although this report compiled a large amount of antimicrobial susceptibility data, there are several caveats to consider to ensure careful interpretation of these results:

1. Many hospitals were unable to generate specific SRIRs and/or pSIRs for 2022 because their data did not meet the minimum precision criterion, which requires a hospital's predicted number of events to be ≥0.3. This limitation may apply to hospitals with low patient days or characteristics associated with fewer events. However, this criterion does not necessarily indicate that a hospital's observed number of events was low. For instance, due to the minimum precision criterion, 358 hospitals could not generate a CRE SRIR for LRT infections. Among these hospitals, 344 reported no CRE events; however, one hospital recorded six CRE events. For that hospital with six CRE events, a data review and further investigation may be warranted, despite the absence of an SRIR.
2. The pooled mean SRIR and pSIR in this report aggregate data from hospitals that submitted data and met the inclusion criteria for 2022. These hospitals are not necessarily the same hospitals as the ones that contributed data to the 2019 SRIR/pSIR baseline. Therefore, while the pooled mean SRIR and/or pSIR for some HO phenotypes or organisms are significantly lower based on 2019 baseline predictive models, they do not necessarily indicate a temporal change within a cohort or reflect a national-level change.
3. For some organisms and phenotypes, the percentages of isolates with sufficient susceptibility results required to determine the phenotype were relatively low. Two possible reasons may have contributed to this issue: 1) the antimicrobial(s) for these phenotypes were not routinely tested in the microbiology laboratories of reporting hospitals, and 2) the use of selective and cascade reporting of susceptibility results for antimicrobial stewardship purposes. Selective and/or cascade reporting is an antimicrobial stewardship strategy in which antimicrobial susceptibility results for certain patients and/or antimicrobials are only made available to prescribers under specific conditions.[5] For NHSN AR Option reporting extracting data from a

source proximal to the application of selective reporting rules is recommended; however, this may not have been possible for some hospitals. Nonetheless, because most hospitals were able to submit complete susceptibility data, the percentage of tested isolates remained quite high for most of the organism-antimicrobial combinations in this report. This suggests that the bias caused by selective and cascade reporting to the results in this report may be minimal. On the other hand, among the organism-antimicrobial combinations for which <80% of isolates were tested, we recommend interpreting those percentage of resistance/non-susceptibility data with caution, since those percentages might have been impacted by selection biases.[6]

4. Although individual hospitals' cumulative antibiograms that typically include only the first isolate per patient annually within a hospital,[7] this report summarizes data collected following the NHSN AUR Module protocol, which allows an additional isolate from the same patient to be added after 14 days for invasive specimens (CSF or blood) and after the end of the calendar month for non-invasive specimen types (LRT and urine). In this report, 10% of isolates were from patients who contributed two or more isolates. Therefore, the percentage of non-susceptibility in this report might be slightly higher than it would be if only first isolate per patient was included in the calculation because the AR Option is more likely to include isolates of patients under antibiotic treatment.[8]
5. This report does not summarize antimicrobial susceptibility results for *Candida* species because many hospitals were unable to extract complete antimicrobial susceptibility data due to interoperability barriers. Moreover, many hospitals noted that *Candida* or yeast organisms were not routinely speciated in their hospitals and antimicrobial susceptibility tests, if performed, were usually conducted by an outside laboratory with reports returned via fax or Portable Document Format (PDF).

In conclusion, this report provides an overall picture of antimicrobial resistance among hospitals submitting data to the NHSN AR Option in 2022. To maximize the utility of the NHSN AR Option and this report, the following actions could be considered:

1. For individual hospitals, generating SRIR and pSIR annually using the NHSN application. Information on interpreting results is available in "Using the SRIR and pSIR for Action" section in the SRIR and pSIR Guide. The distribution of SRIR and pSIR of hospitals submitting data in 2022 presented in this report enables hospitals to see where their SRIR/pSIR values are located among all hospitals that submitted AR Option data in 2022.
2. For hospitals that did not have SRIR and/or pSIR values generated for 2022 due to small numbers of predicted events, if multiple (>2) events of certain organism(s) or phenotype(s) are found in your data, the number of observed events exceeded the number of expected events. Consider investigating the possible causes by following the steps recommended for those with high SRIR or pSIR (Figure 2 of SRIR and pSIR Guide). You may include a longer time period (for example, two years) to receive an SRIR or pSIR from within the NHSN application.
3. For individual hospitals, consider generating antibiogram reports containing percent susceptible and percent tested for your hospital using the NHSN application to better understand antimicrobial resistance within your hospital and how your hospital's data compare to the national aggregated data. The aggregated percentages of drug-resistant phenotypes provided in this report were provided to raise national awareness of AR. These data are not intended to

guide antimicrobial prescribing, as AR rates can differ by region, hospital, and patient population. For guiding empirical antimicrobial therapy decisions, hospitals could use their own cumulative antibiograms following CLSI M39.

4. During the calendar year 2022, many hospitals were excluded for not using up-to-date antimicrobial susceptibility interpretation breakpoints. This is necessary for NHSN to ensure that consistent interpretive criteria are applied across the data included in this report. We recommend individual hospitals and hospital systems understand which breakpoints are currently in use in their laboratories and identify any that are outdated (e.g., no longer recognized by CLSI or FDA).[9] Additionally, ensuring that the responses in your NHSN Annual Hospital Survey reflect the breakpoints used during the respective calendar year helps maintain data quality.
5. State and local health departments and hospital systems can generate SRIR and pSIR for the hospitals in your jurisdictions or network to better understand the impact of antibiotic resistance in their facilities or jurisdiction. Information on identifying hospitals with significantly higher SRIR or pSIR. Information on evaluating possible causes are available in "Using the SRIR and pSIR for Action" section in the SRIR and pSIR Guide.
6. For state and local health departments and hospital systems interested in generating antibiogram reports containing percent susceptible and percent tested for the hospitals in your jurisdiction or network, consider reaching out to the hospitals with low testing percentages of organism-antimicrobial combinations that are often routinely tested in clinical laboratories to understand the reasons and technical difficulties those hospitals might have extracting complete antimicrobial susceptibility data for surveillance. Organism-antimicrobial combinations that are often routinely tested in clinical laboratories may include Tier 1 and 2 drugs in CLSI M100 tables 1A–1J.[7] Examples include but are not limited to:
    a) Enterobacterales — ceftriaxone, cefepime, ciprofloxacin/levofloxacin, piperacillin/tazobactam
    b) *Pseudomonas aeruginosa* — cefepime, piperacillin/tazobactam, ciprofloxacin/levofloxacin, imipenem/meropenem
    c) *Acinetobacter* spp. — ampicillin/sulbactam, cefepime
    d) *Staphylococcus aureus* — oxacillin/cefoxitin
    e) *Enterococcus* — ampicillin
    f) *Streptococcus pneumoniae* — penicillin, cefotaxime/ceftriaxone

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References

1. Centers for Disease Control and Prevention. *Antibiotic Resistance Threats in the United States, 2019.* Atlanta, GA: U.S. Department of Health and Human Services; 2019.
2. World Health Organization. Antimicrobial resistance. Accessed June 26, 2025. https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance.
3. Centers for Medicare & Medicaid Services. *Medicare and Medicaid Programs; Electronic Health Record Incentive Program—Stage 3 and Modifications to Meaningful Use in 2015 Through 2017.* 80 Fed Reg 62762-62955. October 16, 2015. Published 2015. Accessed January 9, 2026. https://www.govinfo.gov/content/pkg/FR-2015-10-16/pdf/2015-25595.pdf
4. Centers for Medicare & Medicaid Services. FY 2023 Hospital Inpatient Prospective Payment System (IPPS) and Long-Term Care Hospital Prospective Payment System. Accessed July 2, 2025. https://www.cms.gov/newsroom/fact-sheets/fy-2023-hospital-inpatient-prospective-payment-system-ipps-and-long-term-care-hospital-prospective
5. Barlam TF, et al. Executive summary: Implementing an antibiotic stewardship program: guidelines by the Infectious Diseases Society of America and the Society for Healthcare Epidemiology of America. *Clin Infect Dis.* 2016;62(10):1197–1202.
6. Wu H, et al. Selective and cascade reporting of antimicrobial susceptibility testing results and its impact on antimicrobial resistance surveillance—National Healthcare Safety Network, April 2020 to March 2021. *Microbiol Spectr.* 2023;11(2):e0164622.
7. Clinical and Laboratory Standards Institute. *Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data.* 5th ed. 2022.
8. Viloria Winnett A, et al. The path of more resistance: a comparison of National Healthcare Safety Network and Clinical Laboratory Standards Institute criteria in developing cumulative antimicrobial susceptibility test reports and institutional antibiograms. *J Clin Microbiol.* 2022;60(2):e0136621.
9. Clinical and Laboratory Standards Institute. 2023 breakpoint implementation toolkit. Accessed April 28, 2025. https://clsi.org/resources/breakpoint-implementation-toolkit/.

Appendix A - NHSN AR Option Phenotype Definitions

Phenotype Name	Phenotype Code	Phenotype Definition
Methicillin-resistant *Staphylococcus aureus*[a]	MRSA_AR	*Staphylococcus aureus* that has tested resistant (R) to at least one of the following: oxacillin or cefoxitin
Carbapenem-resistant Enterobacterales (expanded)	CREexpanded_AR	Any *Citrobacter amalonaticus*, *Citrobacter freundii*, *Citrobacter koseri*, *Enterobacter* spp., *E. coli*, *Klebsiella aerogenes, Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Serratia marcescens* that has tested Resistant (R) to at least one of the following: imipenem, meropenem, doripenem, ertapenem, meropenem/vaborbactam, or imipenem/relebactam OR Any *Proteus mirabilis*, *Proteus penneri*, *Proteus vulgaris,* and *Morganella morganii* that has tested resistant (R) to at least one of the following: meropenem, doripenem, ertapenem, or meropenem/vaborbactam
Carbapenem-resistant Enterobacterales[a] (*E. coli, Klebsiella,* or *Enterobacter*)	CREall_AR	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to at least one of the following: imipenem, meropenem, doripenem, ertapenem, meropenem/vaborbactam, or imipenem/relebactam
Carbapenem-non-susceptible *Pseudomonas aeruginosa*	carbNS_PA_AR	*Pseudomonas aeruginosa* that has tested either intermediate (I) or resistant (R) to at least one of the following: imipenem, meropenem, doripenem or imipenem/relebactam
Extended-spectrum cephalosporin-resistant Enterobacterales[a]	ESCEall_AR	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to at least one of the following: cefepime[d], ceftriaxone, cefotaxime, ceftazidime, ceftazidime/avibactam, or ceftolozane/tazobactam

Phenotype Name	Phenotype Code	Phenotype Definition
Multidrug-resistant *Pseudomonas aeruginosa*[a]	MDR_PA_AR	*Pseudomonas aeruginosa* that has tested either intermediate (I) or resistant (R) to at least one drug in at least three of the following six categories[b]: 1. Extended-spectrum cephalosporin (cefepime, ceftazidime, ceftazidime/avibactam, ceftolozane/tazobactam) 2. Fluoroquinolones (ciprofloxacin, levofloxacin)[c] 3. Aminoglycosides (amikacin, gentamicin, tobramycin) 4. Carbapenems (imipenem, meropenem, doripenem, imipenem/relebactam)[c] 5. Piperacillin/tazobactam 6. Cefiderocol
Carbapenem-non-susceptible *Acinetobacter* spp.	carbNS_Acine_AR	Any *Acinetobacter* spp. that has tested either intermediate (I) or resistant (R) to at least one of the following: imipenem, meropenem, or doripenem
Multidrug-resistant *Acinetobacter* spp.	MDR_Acine_AR	Any *Acinetobacter* spp. that has tested either intermediate (I) or resistant (R) to at least one drug in at least three of the following seven categories[b]: 1. Extended-spectrum cephalosporin (cefepime, ceftazidime, ceftriaxone, cefotaxime) 2. Fluoroquinolones (ciprofloxacin, levofloxacin) 3. Aminoglycosides (amikacin, gentamicin, tobramycin) 4. Carbapenems (imipenem, meropenem, doripenem) 5. Piperacillin/tazobactam 6. Ampicillin/sulbactam 7. Cefiderocol
Vancomycin-resistant *Enterococcus*[a]	VREgeneral_AR	Any *Enterococcus* spp. that has tested resistant (R) to vancomycin
Vancomycin-resistant *Enterococcus faecalis*	VREfaecalis_AR	*Enterococcus faecalis* that has tested resistant (R) to vancomycin
Vancomycin-resistant *Enterococcus faecium*	VREfaecium_AR	*Enterococcus faecium* that has tested resistant (R) to vancomycin

Phenotype Name	Phenotype Code	Phenotype Definition
Fluoroquinolone-resistant Enterobacterales[a]	FQE_AR	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to at least one of the following: ciprofloxacin, levofloxacin, or moxifloxacin
Fluoroquinolone-resistant *Pseudomonas aeruginosa*[a]	FQPA_AR	*Pseudomonas aeruginosa* that has tested resistant (R) to at least one of the following: ciprofloxacin or levofloxacin
Drug-resistant *Streptococcus pneumoniae*	DR_SP_AR	*Streptococcus pneumoniae* that has tested either intermediate (I) or resistant (R) to at least one of the antimicrobials listed in the NHSN AR Option defined drug panel
Clindamycin-non-susceptible *Streptococcus agalactiae* (GBS)	CLIND_GBS_AR	*Streptococcus agalactiae* (GBS) that has tested either intermediate (I) or resistant (R) to clindamycin
Phenotypes only calculated for neonatal locations		
Ampicillin-resistant Enterobacterales (expanded)	N/A	Any *Citrobacter amalonaticus*, *Citrobacter freundii*, *Citrobacter koseri*, *Enterobacter* spp., *E. coli*, *Klebsiella aerogenes, Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Serratia marcescens* that has tested Resistant (R) to ampicillin OR Any *Proteus mirabilis*, *Proteus penneri*, *Proteus vulgaris,* and *Morganella morganii* that has tested resistant (R) to ampicillin
Ampicillin/sulbactam-resistant Enterobacterales (expanded)	N/A	Any *Citrobacter amalonaticus*, *Citrobacter freundii*, *Citrobacter koseri*, *Enterobacter* spp., *E. coli*, *Klebsiella aerogenes, Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Serratia marcescens* that has tested resistant (R) to ampicillin/sulbactam OR Any *Proteus mirabilis*, *Proteus penneri*, *Proteus vulgaris,* and *Morganella morganii* that has tested resistant (R) to ampicillin/sulbactam

Phenotype Name	Phenotype Code	Phenotype Definition
Gentamicin-resistant Enterobacterales (expanded)	N/A	Any *Citrobacter amalonaticus*, *Citrobacter freundii*, *Citrobacter koseri*, *Enterobacter* spp., *E. coli*, *Klebsiella aerogenes, Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Serratia marcescens* that has tested resistant (R) to gentamicin OR Any *Proteus mirabilis*, *Proteus penneri*, *Proteus vulgaris,* and *Morganella morganii* that has tested resistant (R) to gentamicin
Piperacillin/tazobactam-resistant Enterobacterales (expanded)	N/A	Any *Citrobacter amalonaticus*, *Citrobacter freundii*, *Citrobacter koseri*, *Enterobacter* spp., *E. coli*, *Klebsiella aerogenes, Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Serratia marcescens* that has tested resistant (R) to piperacillin/tazobactam[d] OR Any *Proteus mirabilis*, *Proteus penneri*, *Proteus vulgaris,* and *Morganella morganii* that has tested resistant (R) to piperacillin/tazobactam[d]
Amikacin-resistant Enterobacterales (expanded)	N/A	Any *Citrobacter amalonaticus*, *Citrobacter freundii*, *Citrobacter koseri*, *Enterobacter* spp., *E. coli*, *Klebsiella aerogenes, Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Serratia marcescens* that has tested resistant (R) to amikacin OR Any *Proteus mirabilis*, *Proteus penneri*, *Proteus vulgaris,* and *Morganella morganii* that has tested resistant (R) to amikacin
Tobramycin-resistant Enterobacterales (expanded)	N/A	Any *Citrobacter amalonaticus*, *Citrobacter freundii*, *Citrobacter koseri*, *Enterobacter* spp., *E. coli*, *Klebsiella aerogenes, Klebsiella oxytoca*, *Klebsiella pneumoniae*, and *Serratia marcescens* that has tested resistant (R) to tobramycin OR Any *Proteus mirabilis*, *Proteus penneri*, *Proteus vulgaris,* and *Morganella morganii* that has tested resistant (R) to tobramycin
Ampicillin-resistant Enterobacterales	N/A	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to ampicillin
Ampicillin/sulbactam-resistant Enterobacterales	N/A	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to ampicillin/sulbactam

Phenotype Name	Phenotype Code	Phenotype Definition
Gentamicin-resistant Enterobacterales	N/A	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to gentamicin
Piperacillin/tazobactam-resistant Enterobacterales	N/A	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to piperacillin/tazobactam[d]
Amikacin-resistant Enterobacterales	N/A	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to amikacin
Tobramycin-resistant Enterobacterales	N/A	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to tobramycin
Ampicillin-resistant *Escherichia coli*	N/A	Any *Escherichia coli* that has tested resistant (R) to ampicillin
Ampicillin/sulbactam-resistant *Escherichia coli*	N/A	Any *Escherichia coli* that has tested resistant (R) to ampicillin/sulbactam
Gentamicin-resistant *Escherichia coli*	N/A	Any *Escherichia coli* that has tested resistant (R) to gentamicin
Amikacin-resistant *Escherichia coli*	N/A	Any *Escherichia coli* that has tested resistant (R) to amikacin
Tobramycin-resistant *Escherichia coli*	N/A	Any *Escherichia coli* that has tested resistant (R) to tobramycin
Ampicillin-sulbactam-resistant *Klebsiella pneumoniae/oxytoca*	N/A	Any *Klebsiella oxytoca* or *Klebsiella pneumoniae* that has tested resistant (R) to ampicillin/sulbactam
Gentamicin-resistant *Klebsiella pneumoniae/oxytoca*	N/A	Any *Klebsiella oxytoca* or *Klebsiella pneumoniae* that has tested resistant (R) to gentamicin
Piperacillin-tazobactam-resistant *Klebsiella pneumoniae/oxytoca*	N/A	Any *Klebsiella oxytoca* or *Klebsiella pneumoniae* that has tested resistant (R) to piperacillin/tazobactam[d]
Amikacin-resistant *Klebsiella pneumoniae/oxytoca*	N/A	Any *Klebsiella oxytoca* or *Klebsiella pneumoniae* that has tested resistant (R) to amikacin

Phenotype Name	Phenotype Code	Phenotype Definition
Tobramycin-resistant *Klebsiella pneumoniae/oxytoca*	N/A	Any *Klebsiella oxytoca* or *Klebsiella pneumoniae* that has tested resistant (R) to tobramycin
Gentamicin-resistant *Enterobacter* spp. and *Klebsiella aerogenes*	N/A	Any *Enterobacter* spp. or *Klebsiella aerogenes* that has tested resistant (R) to gentamicin
Piperacillin-tazobactam-resistant *Enterobacter* spp. and *Klebsiella aerogenes*	N/A	Any *Enterobacter* spp. or *Klebsiella aerogenes* that has tested resistant (R) to piperacillin/tazobactam[d]
Amikacin-resistant *Enterobacter* spp. and *Klebsiella aerogenes*	N/A	Any *Enterobacter* spp. or *Klebsiella aerogenes* that has tested resistant (R) to amikacin
Tobramycin-resistant *Enterobacter* spp. and *Klebsiella aerogenes*	N/A	Any *Enterobacter* spp. or *Klebsiella aerogenes* that has tested resistant (R) to tobramycin
Ceftazidime/Cefepime-resistant *Pseudomonas aeruginosa*	N/A	*Pseudomonas aeruginosa* that has tested resistant (R) to ceftazidime/cefepime
Amikacin-resistant *Pseudomonas aeruginosa*	N/A	*Pseudomonas aeruginosa* that has tested resistant (R) to amikacin
Tobramycin-resistant *Pseudomonas aeruginosa*	N/A	*Pseudomonas aeruginosa* that has tested resistant (R) to tobramycin

[a] An SRIR is available for these phenotypes.

[b] The category names are for grouping purposes and are not inclusive of all drugs in that drug class.

[c] For fluoroquinolone and carbapenem categories, if a facility did not adopt the breakpoints revised by the CLSI in 2019 (fluoroquinolones) and 2012 (carbapenems), results for drugs in those categories were classified as not tested.

[d] Susceptible-dose dependent (S-DD) is considered a valid susceptibility result for specific drug-phenotype combinations in addition to susceptible (S), intermediate (I), and resistant (R).