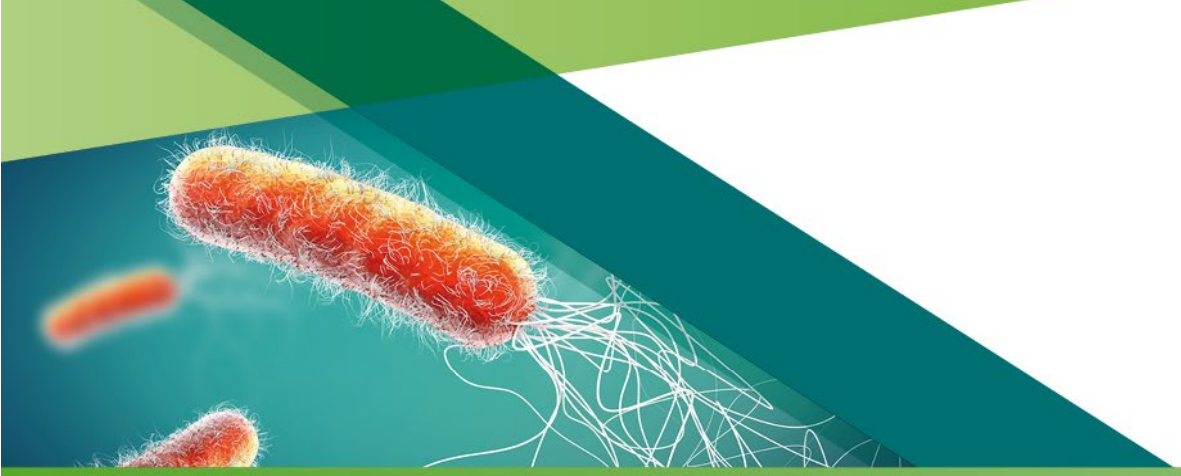


SURVEILLANCE REPORT

Antimicrobial resistance in the EU/EEA (EARS-Net)

Annual Epidemiological Report for 2025

Key findings

- In 2026, all European Union/European Economic Area (EU/EEA) countries reported data for 2025 to the European Antimicrobial Resistance Surveillance Network (EARS-Net).

Progress towards EU targets on antimicrobial resistance

- In 2025, the estimated total EU incidence of meticillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections was 4.56 per 100 000 population (EU country range 0.58–12.07). This was 19% lower than in 2019 (baseline year) and 0.23 per 100 000 population lower than the 2030 target of 4.79 per 100 000 population. For the EU overall, a statistically significant decreasing trend was detected between 2019 (baseline year) and 2025, although in the last two years the estimated incidence has been increasing.
- The estimated total EU incidence of third-generation cephalosporin-resistant *Escherichia coli* bloodstream infections in 2025 was 12.13 per 100 000 population (EU country range 3.40–24.61). This was 16.4% higher than in 2019 (baseline year) and 2.75 per 100 000 population higher than the 2030 target of 9.38 per 100 000 population. For the EU overall, no statistically significant trend was detected between 2019 (baseline year) and 2025, although in the last two years the estimated incidence has been higher than in 2019.
- The estimated total EU incidence of carbapenem-resistant *Klebsiella pneumoniae* bloodstream infections in 2025 was 3.75 per 100 000 population (EU country range 0.00–21.29). This was 72% higher than in 2019 (baseline year) and 1.68 per 100 000 population higher than the 2030 target of 2.07 per 100 000 population. For the EU overall, a statistically significant increasing trend was detected between 2019 (baseline year) and 2025.
- In summary, while the EU target for the incidence of MRSA bloodstream infections had been reached by 2025, the results for the other two EU targets were not on track. The estimated EU incidence of third-generation cephalosporin-resistant *E. coli* bloodstream infections with a 10% reduction target had increased by more than 15% compared to 2019 (baseline year). Moreover, the estimated EU incidence of carbapenem-resistant *K. pneumoniae* bloodstream infections increased by over 70% compared to 2019, which differs substantially from the target of a 5% reduction by 2030.

Overall antimicrobial resistance situation in the EU/EEA

- Data from EARS-Net show that, as in previous years, AMR levels remained high in the EU/EEA in 2025.
- Increases in the estimated EU/EEA incidences of bloodstream infections with resistant bacteria were observed not only for the three AMR-pathogen combinations with an EU target, but also for many other bacteria and antimicrobial groups under surveillance during the period 2021–2025, such as

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carbapenem-resistant *E. coli*, all estimated resistance incidences for *Streptococcus pneumoniae*, and vancomycin-resistant *Enterococcus faecium*. Some of these increases occurred in parallel with increases in the corresponding EU/EEA population-weighted AMR percentages, such as carbapenem-resistant *K. pneumoniae* and several of the combinations for *E. coli*.

- AMR levels varied widely among EU/EEA countries, depending on the bacterial species, antimicrobial group and geographical region. Higher AMR levels generally continued to be reported by countries in southern, central and eastern Europe.
- For each bacterial species, country-specific information about the estimated incidence of antimicrobial-resistant bloodstream infections (including the recommended EU targets on AMR), the percentage of invasive isolates with AMR, data availability and the percentage of intensive care unit patients is available in the country summaries. Results by age group and sex are available in the ECDC Surveillance Atlas of Infectious Diseases (https://atlas.ecdc.europa.eu).

Public health conclusions

- Estimates based on EARS-Net data from 2020 indicate that over 35 000 people die in the EU/EEA annually as a direct consequence of antimicrobial-resistant infections.
- The poor progress towards the EU targets on AMR overall and the many increases in the estimated EU/EEA incidences of bloodstream infections with resistant bacteria in the EU/EEA highlight the urgent need for intensified public health action against AMR.
- The Council of the European Union Recommendation on stepping up EU actions to combat AMR in a One Health approach (2023/C 220/01) not only encourages Member States to develop and implement national action plans to tackle AMR, but also highlights the need for countries to allocate appropriate human and financial resources for the effective implementation of these plans. In addition, ECDC has been conducting Public Health Emergency Preparedness Assessments, which have included an assessment of the national activities and structures to address AMR. These assessments have resulted in recommendations specifically tailored for the respective countries.
- In the absence of stronger and swifter public health action, it is unlikely that the EU will reach all its AMR targets by 2030. AMR will instead continue to increasingly jeopardise public health in the EU/EEA through an increased number of difficult-to-treat infections with antimicrobial-resistant bacteria, greater challenges for patient safety, and a rise in AMR-related deaths.

Methods

The results presented in this report are based on antimicrobial resistance (AMR) data from invasive isolates (retrieved from blood or cerebrospinal fluid samples) reported to the European Antimicrobial Resistance Surveillance Network (EARS-Net) by all (n=30) European Union (EU) and European Economic Area (EEA) countries in 2026 (data referring to 2025). France did not report isolate-level 2023 data for some of the bacterial species-antimicrobial group combinations and therefore 2023 data for France have been imputed for the EU and EU/EEA results in this report. The latest country-specific data, based on the isolate level data reported to ECDC, can be retrieved from the ECDC Surveillance Atlas of Infectious Diseases [1].

EARS-Net

EARS-Net is coordinated by ECDC with the aim of collecting, analysing and reporting data on AMR through a network of national surveillance systems across EU/EEA countries and, as defined in the EARS-Net reporting protocol [2], facilitating action to address AMR.

EARS-Net is based on a network of representatives nominated by EU/EEA countries (i.e. national focal points for AMR, and operational contact points for epidemiology, microbiology and The European Surveillance System (TESSy) and EpiPulse Cases for diseases caused by antimicrobial-resistant microorganisms). These representatives collect routine clinical antimicrobial susceptibility testing (AST) data through national AMR surveillance networks. Participating institutions are listed in Annex 1. Scientific guidance and support are provided by the EARS-Net Disease Network Coordination Committee, which is composed of experts elected from the nominated national focal points and operational contact points, complemented by observers from organisations involved in AMR surveillance. EARS-Net activities are coordinated in close collaboration with three other ECDC surveillance networks: the European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net), the European Surveillance of Antimicrobial Consumption Network (ESAC-Net) and the Healthcare-Associated Infections Surveillance Network (HAI-Net). EARS-Net also collaborates with the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) and with the European Committee on Antimicrobial Susceptibility Testing (EUCAST), which is supported by ECDC and ESCMID. Data from EARS-Net are also provided to the World Health Organization (WHO) Regional Office for Europe and made available via the WHO Regional Office for Europe AMR dashboard, together with AMR data from the WHO European Region collected via Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) [3]. A summary for the WHO European Region is published jointly with the WHO Regional Office for Europe [4]. ECDC also provides EARS-Net data via the WHO Regional Office for Europe to the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) [5].

In 2025, all EU Member States and three EEA countries participated in EARS-Net. Since the initiation of the network, there has been a large increase in the number of participating laboratories, which suggests that national AMR surveillance systems in the EU/EEA are being strengthened. The laboratories that participate in the annual EARS-Net external quality assessment (EQA) exercise contribute to improved data quality and the increasing ability of EU/EEA countries to report comparable AMR data [6]. However, not all the laboratories providing EARS-Net data for 2025 participated in the 2025 EARS-Net EQA exercise. Moreover, not all the laboratories invited to the EARS-Net EQA exercise participated. This fact is reflected in the country summaries. The results from the EARS-Net EQA exercise for 2025, including details of the participation rate by country, are published in a separate report [6].

It is possible for reporting countries to correct and reupload historical data. The latest published report therefore supersedes previous reports and reflects the most recent available data. This report is based on data reported to EARS-Net for the period 2019–2025 and retrieved from EpiPulse Cases on 17 August 2026.

Antimicrobial susceptibility data

Each year, countries report routine AST results, collected from one or more clinical microbiology laboratories, to ECDC. When it is not possible to include data from all the relevant laboratories, countries can report data from sentinel laboratories. Either way, the data reflect the laboratory AST data that are collected in the surveillance system of each country. The AMR surveillance focuses on invasive (blood and cerebrospinal fluid) isolates of eight key bacterial species (*Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter* species, *Streptococcus pneumoniae*, *Staphylococcus aureus, Enterococcus faecalis* and *Enterococcus faecium*). Other notifiable diseases caused by microorganisms with AMR, such as *Campylobacter* spp., *Mycobacterium tuberculosis, Neisseria gonorrhoeae*, and *Salmonella* spp., are also monitored by ECDC [7] but are not included in EARS-Net.

EARS-Net collects AMR data from EU/EEA countries through EpiPulse, a web-based platform for data submission and storage hosted by ECDC [8]. The data were previously collected through TESSy. Since 28 April 2025, the EARS-Net AMR data have been collected through EpiPulse Cases on the EpiPulse platform. For detailed information on data collection, refer to the EARS-Net reporting protocol [2].

Only data from invasive (blood and cerebrospinal fluid) isolates are included in EARS-Net. This restriction aims to reduce the impact of different sampling frames, case definitions, diagnostic and treatment guidelines as well as healthcare utilisation in the countries. These differences would otherwise hamper data interpretation.

Starting with the data collected for 2019, EARS-Net only accepts data generated using EUCAST clinical breakpoints [9]. Before this, the use of EUCAST breakpoints was encouraged, but results based on other interpretive criteria used by reporting countries were also accepted for analysis.

Coverage and representativeness of population, hospitals and patients included in EARS-Net

Data sources

Since 2018, data on population coverage, number of blood culture sets, and country representativeness have been collected via TESSy/EpiPulse [8]. Data for previous years combined TESSy data with data collected through questionnaires distributed to the national focal points for AMR.

Indicators of coverage and representativeness

Population coverage

Population coverage is expressed as the estimated percentage of the country population covered by the laboratories reporting data to EARS-Net. This value is a crude estimate, due to overlapping hospital catchment areas and patients seeking care in areas other than their area of residence. The population coverage is calculated as the mean of the coverage for the following bacterial species: *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *S. aureus*, *E. faecalis* and *E. faecium*. Due to outliers in some countries, *S. pneumoniae* and *Acinetobacter* spp. are not included in the calculation.

Geographical representativeness

Geographical representativeness is a qualitative indicator referring to geographical coverage. The categories for 2025 are listed and described in Table 1. The definition was adjusted as of the data collection in 2022 [2]. For data reported for 2019–2020, the definition of geographical representativeness can be found in the report 'Antimicrobial resistance surveillance in Europe 2022 – 2020 data' [10].

Hospital representativeness

Hospital representativeness is a qualitative indicator referring to representativeness of hospitals served by the EARS-Net-participating laboratories, compared to the country distribution of the various types of hospitals. The categories are listed and described in Table 1.

Isolate representativeness

Isolate representativeness is a qualitative indicator referring to representativeness of data reported by EARS-Net laboratories in relation to the microorganisms causing invasive infections in the included hospitals. The categories are listed and described in Table 1. The collection of data on isolate representativeness was modified in the 2022 data collection [2]. With data reported for 2019–2020, isolate representativeness refers to patient and isolate representativeness, defined in the report 'Antimicrobial resistance surveillance in Europe 2022 – 2020 data' [10].

Blood culture rate

The blood culture rate refers to the number of blood culture sets taken per 1 000 patient-days in hospitals served by EARS-Net laboratories and sent to these laboratories. The definition of a 'blood culture set' and a 'patient-day' may differ between and within countries, and this may influence the estimate. Blood culture rates were calculated as the mean of the number of blood culture sets divided by the mean total number of patient-days for hospitals served by laboratories that provided the number of blood culture sets performed, as reported for the following bacterial species: *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *S. aureus*, *E. faecalis* and *E. faecium* and multiplied by 1 000. Due to outliers in some countries, data reported for *S. pneumoniae* and *Acinetobacter* spp. are not included in the calculation of the mean blood culture rate.

Isolates from intensive care units

The percentage of isolates reported from intensive care units (ICUs) are calculated for each bacterial species. Isolates with missing information on hospital department are excluded from the calculation, and the results are only presented if there are ≥20 isolates, with 70% having data on hospital department.

Data analysis

Before being analysed, data are de-duplicated to include only the first isolate per patient, year, and bacterial species. Moreover, EU and EU/EEA analyses do not include countries that have reported data for less than three years to EARS-Net during the relevant time-period.

Estimated EU/EEA incidence of invasive isolates

For each bacterial species, the total number of invasive isolates in the EU/EEA was estimated by dividing the number of isolates for the bacterial species reported by a country to EARS-Net by the reported population coverage of the country, and then adding the resulting numbers. This sum was then divided by the EU/EEA population to estimate the EU/EEA incidence of invasive isolates for each species.

For each year (Y), the most recently reported coverage available for that year is used, based on data submitted to TESSy/EpiPulse Cases for 2018–2025. If coverage for year Y is unavailable, coverage from the nearest available year is used, giving priority to the preceding year (Y–1) and then the following year (Y+1). If coverage remains unavailable, the search is extended one year at a time in the same order, first backwards and then forwards, until an available value is identified or all data for 2018–2025 have been considered.

The calculation of the estimated incidence does not consider the blood culture rate reported by the countries.

Susceptibility test categories

For the analysis, the qualitative susceptibility categories – 'susceptible, standard dosing regimen' (S), 'susceptible, increased exposure' (I) and 'resistant' (R) – are used, as reported by the laboratory, since quantitative susceptibility information is missing for a large part of the data. An isolate is considered resistant to an antimicrobial agent when tested and interpreted as R, in accordance with the clinical breakpoint criteria used by the local laboratory.

For *P. aeruginosa*, *E. coli*, *K. pneumoniae*, and *Acinetobacter* spp. and some antimicrobial agent combinations presented in this report, EUCAST breakpoints are available, as of 2021, for isolates from meningitis versus other isolates ('non-meningitis'). When possible, and starting with 2021 data, it is recommended that EU/EEA countries that generate the susceptibility categorisation of isolates at national level use 'non-meningitis' breakpoints for all interpretations, although EARS-Net does accept data as they are. As clinical patient data are not collected in EARS-Net, no information is available on which breakpoint was used to categorise susceptibility. However, it is assumed that only a very small number of infections reported to EARS-Net are meningitis cases and that the large majority are bloodstream infections. Moreover, as it is recommended that countries report the susceptibility categories according to 'non-meningitis' breakpoints even for cases of meningitis, the impact on the overall results is expected to be minor.

The term 'penicillin non-wild-type' is used in this report for *S. pneumoniae*, referring to *S. pneumoniae* isolates reported by local laboratories as I or R to penicillin, assuming minimum inhibitory concentrations (MICs) to benzylpenicillin above those of wild-type isolates (>0.06 mg/L). This cut-off is also the EUCAST S-breakpoint for all indications (the R-breakpoint is variable depending on type of infection).

The bacterial species–antimicrobial agent combinations presented in this report for 2025 are shown in Table 2. When combining results for antimicrobial agents representing an antimicrobial group, the outcome is based on the most resistant result. For example, if the AST result is I for imipenem and R for meropenem, then the AST result for the group carbapenems is set as R. Combined AMR is defined as R to at least one antimicrobial agent in each of the antimicrobial groups (except for *S. pneumoniae*, for which combined AMR is calculated as combined penicillin non-wild-type and R to macrolides). Isolates with missing data for one or more of the required antimicrobial groups are excluded from the analysis of combined AMR.

Estimated incidence and estimated number of cases of bloodstream infections with resistant bacteria

The estimated incidence of invasive isolates is considered to reflect the incidence of bloodstream infections with the respective resistant bacteria since, in the de-duplicated EARS-Net data, the number of isolates from blood samples far outweighs that from cerebrospinal fluid samples. As an example, during the period 2019–2025, each year the full de-duplicated dataset consisted of more than 99% isolates from blood samples and less than 1% isolates from cerebrospinal fluid samples.

For each bacterial species–antimicrobial agent/group combination (or for *S. pneumoniae* and penicillin, non-wild-type), the national estimated incidence of bloodstream infections with resistant bacteria was calculated by dividing the number of cases reported as R by the national population, as reported to Eurostat [11], multiplied by the estimated population coverage, as reported to EARS-Net. The estimated national number of cases was calculated by dividing the number of resistant cases reported by the estimated population coverage applying the formula included in the EARS-Net reporting protocol [2]. The national results are included in the respective country summary.

For the EU and the EU/EEA respectively, first the number of cases in each country was divided by the respective national coverage. Next, the results for all countries were totalled, resulting in the estimated number of cases in the EU or EU/EEA, which was then divided by the respective total EU or EU/EEA population to estimate the EU or EU/EEA incidence of bloodstream infections with resistant bacteria.

The coverage data were applied as described in the section 'Estimated EU/EEA incidence of invasive isolates'.

It should be noted that the reported incidence rates per population are estimates which are based on the estimated national population coverage of the AMR data, as reported by each country. The estimated incidence of bloodstream infections with resistant bacteria should therefore be interpreted with caution if the national population coverage is estimated as less than 100%. In addition, when national representativeness is considered by a country to be less than 'High', further caution must be exercised when interpreting the results. In tables with results for one country or where countries are specified, the estimated incidences of bloodstream infections with resistant bacteria are marked with a footnote if one or more of the three representativeness indicators (geographical, hospital and/or isolate representativeness) were not reported as 'High', or when the antimicrobial group/agent was tested for <90% of isolates.

For the EU, EU/EEA and each individual country, the statistical significance of temporal trends in the estimated incidence for 2019–2025 and the last five years (2021–2025) was assessed by negative binomial regression, and trends with a p-value of <0.05 were considered significant.

National percentages

AMR (or for *S. pneumoniae* and penicillin, non-wild-type) percentages are presented for a single antimicrobial agent and/or group of antimicrobial agents. If fewer than 20 isolates are reported for a specific bacterial species–antimicrobial group combination in a country, percentages are not displayed.

The AMR percentages for novel antimicrobials with activity versus gram-negative bacilli are reported only for carbapenem-resistant isolates from laboratories with at least 70% of carbapenem-resistant isolates tested for the novel antimicrobial. The number of carbapenem-resistant isolates with AST results for the respective novel antimicrobials and bacterial species reported by these laboratories is used as the denominator for calculating the AMR percentage. The limited number of laboratories included in the analysis should be considered when interpreting the results and if comparing across countries. It is possible that these laboratories are highly specialised and only receive a select number of isolates, which could lead to an inflated resistance percentage.

The statistical significance of temporal trends in AMR percentages by country is calculated based on data for the last five years (2021–2025). EU/EEA countries that did not report data for all years within the period under consideration or that reported fewer than 20 isolates for the specific bacterial species–antimicrobial agent/group combination in any year within the period are not included in the analysis. The statistical significance of trends was assessed by a chi-square test for trend, and trends with a p-value of <0.05 were considered significant. An additional sensitivity analysis was performed when assessing the significance of the trends, by including only laboratories that reported data for the full five-year period without interruption. This minimises bias due to changes in reporting laboratories over time (due to expansion of the surveillance network, for instance). In some cases, this restriction results in a considerably lower number of isolates when compared with the analysis that includes all laboratories. This analysis relies on countries consistently using the same code for the respective reporting laboratory.

Population-weighted EU/EEA mean percentage

A population-weighted EU/EEA mean percentage is calculated for each bacterial species–antimicrobial agent/group combination by multiplying the AMR percentage for each country with the population weight (i.e. the proportion of the total EU/EEA population represented by each country) and summing the results. Weights are rescaled if AMR percentages are not available for one or more countries. Annual population data are retrieved from the Eurostat online database [11].

The statistical significance of temporal trends in AMR percentages for the population-weighted EU/EEA mean is calculated based on data for the last five years (2021–2025). EU/EEA countries that did not report data for all years within the period under consideration, or for which synthetic case-based data were not available for one year of missing data, or that reported fewer than 20 isolates for the specific bacterial species–antimicrobial agent/group combination in any year within the period are not included in the analysis. The assessment of the statistical significance of trends and the additional sensitivity analysis including only laboratories that continuously reported data for the full five-year period were applied as described in the section 'National percentages'.

Combined resistance

The analysis of combined resistance excludes isolates with incomplete AST information for the antimicrobial groups covered. This analysis can also highlight bacterial species for which AMR results in EARS-Net may be biased, due to selective testing or reporting. For example, a high proportion of isolates with missing AST information on the antimicrobials included for one of the species under EARS-Net surveillance may indicate selective testing.

Definitions of geographical areas

Definitions of geographical areas are based on the definitions by the Publications Office of the EU [12]. The definitions are adjusted to only include EU/EEA countries and avoid countries being included in more than one geographical area.

- **Central and Eastern Europe:** Bulgaria, Croatia, Czechia, Estonia, Hungary, Latvia, Lithuania, Poland, Romania, Slovakia, Slovenia.
- **Northern Europe:** Denmark, Finland, Iceland, Norway, Sweden.
- **Southern Europe:** Cyprus, Greece, Italy, Malta, Portugal, Spain.
- **Western Europe:** France, Germany, Ireland, Liechtenstein, Luxembourg, the Netherlands, Austria, Belgium.

Imputed national data applied for EU and EU/EEA estimates

Before pooling the respective EU and EU/EEA isolate data, for countries with one year of missing data but with data available for the years before and after that year (France 2023 data, except for *S. pneumoniae*), a dataset was created by linear interpolation, with the number of reported resistant and susceptible isolates for the relevant bacterial species-antimicrobial group/agent combination, using the observed data from the preceding and following year. These counts were expanded into a synthetic case-based dataset for the relevant year and country so that the marginal distribution of each binary variable matched the interpolated counts. These data were added to the reported national data for all EU and EU/EEA estimates, but not to the respective national estimates.

Before using national coverage data for EU and EU/EEA estimations, the coverage for countries with one year of missing data, but with data for the years before and after that year (France 2023 data, except for *S. pneumoniae*) was estimated as the mean coverage, based on the data reported for the preceding and following year.

Novel antimicrobials

In 2024, EARS-Net pilot-tested the collection of AST data on novel antimicrobials that have potential use for treatment of infections with carbapenem-resistant gram-negative bacteria. Novel antimicrobials included in the 'Reserve' group of the 2023 WHO Access Watch Reserve (AWaRe) classification [13] were selected. These remained unchanged for 2025 data based on the 2025 AWaRe classification [14]. In 2024, countries could report available AST data for cefiderocol, ceftazidime-avibactam, ceftolozane-tazobactam, imipenem-relebactam, and meropenem-vaborbactam for *E. coli, K. pneumoniae, P. aeruginosa* and *Acinetobacter* spp. Starting in 2025, EARS-Net updated this list, with countries asked to report AST data for aztreonam-avibactam, cefiderocol, ceftazidime-avibactam, imipenem-relebactam, and meropenem-vaborbactam for *E. coli* and *K. pneumoniae*, and cefiderocol, ceftazidime-avibactam, ceftolozane-tazobactam, imipenem-relebactam, and meropenem-vaborbactam for *P. aeruginosa,* and cefiderocol for *Acinetobacter* spp.

The national 2024 and 2025 results on novel antimicrobials are presented in the respective country summaries and in line with the analysis described in the section 'National percentages'. In addition, we report the number of EU/EEA countries that fulfilled the analysis inclusion criteria by bacterial species and novel antimicrobial combination and year for the available years (2024-2025).

An ECDC survey regarding AST of six 'Reserve' antimicrobials (ceftazidime-avibactam, cefiderocol, ceftolozane-tazobactam, imipenem-relebactam, meropenem-vaborbactam and aztreonam-avibactam) was contacted at local/regional and national clinical laboratories in the EU/EEA that participated in the 2024 EARS-Net EQA. In summary the survey indicated that the selection criteria applied in most laboratories in the EU/EEA permit analysis of the antimicrobial results for the novel antimicrobials for carbapenem-resistant gram-negative bacteria at EU/EEA level [15]. However, given the number of countries with missing data on the novel antimicrobials in 2026 (Table 3), EU/EEA-level analysis is not included in this report. National-level results are presented in each respective country summary.

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Table 1. Population and hospitals contributing data: coverage, representativeness and blood culture rate, EU/EEA, 2025

Country	Estimated population coverage[a] (%)	Geographical representativeness[b]	Hospital representativeness[c]	Isolate representativeness[d]	Blood culture rate (blood culture sets/ 1 000 patient-days)[e]
Austria	90	High	High	High	ND
Belgium	40[f]	Medium	Medium	High	ND
Bulgaria	45	Medium	Medium	Medium	12.7
Croatia	90	High	High	High	32.3
Cyprus	86	High	High	High	70.9
Czechia	75	High	High	High	23.4
Denmark	99	High	High	High	269.1
Estonia	100	High	High	High	42.8
Finland	84	High	High	High	167.6
France	70[f]	High	High	High	62.4
Germany	54	High	High	High	ND
Greece	63	High	High	High	ND
Hungary	90	High	High	High	21.3
Iceland	100	High	High	High	73.5
Ireland	76	High	High	High	65.6
Italy	70	High	High	High	66.8
Latvia	100	High	High	High	20.1
Liechtenstein	40	Medium	Medium	Medium	2.1
Lithuania	100	High	High	High	20.1
Luxembourg	99	High	High	High	54.0
Malta	95	High	High	High	33.2
Netherlands	82	High	High	High	ND
Norway	94	High	High	High	92.8
Poland	20	Medium	Medium	High	67.2
Portugal	98	High	High	High	254.6
Romania	17	Low	Low	Low	44.9
Slovakia	51	High	High	High	33.0
Slovenia	99	High	High	High	47.4
Spain	29	Medium	High	High	524.1
Sweden	89	High	High	High	165.3

ND: no data available.

[a] *As estimated by the national focal points for AMR and/or operational contact points for AMR. Estimated national population coverage: mean population coverage (%) of laboratories reporting* Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis *and* Enterococcus faecium *to EARS-Net. Due to outliers in some countries,* Streptococcus pneumoniae *and* Acinetobacter *spp. are not included in the calculation.*

[b] *Geographical representativeness. High: all main geographical regions of the country are covered. Medium: most geographical regions of the country are covered. Low: only a few geographical areas of the country are covered.*

[c] *Hospital representativeness. High: the hospital selection is representative of the acute care hospital distribution in the country. Medium: the hospital selection is partly representative of the acute care hospital distribution in the country. Low: the hospital selection is insufficiently representative of the acute care hospital distribution in the country.*

[d] *Isolate representativeness. High: the isolate selection is representative of microorganisms causing invasive infections in the included hospitals. Medium: the isolate selection is partly representative of microorganisms causing invasive infections in the included hospitals. Low: the isolate selection is insufficiently representative of microorganisms causing invasive infections in the included hospitals.*

[e] *Blood culture rate (blood culture sets/1 000 patient-days): refers to the mean number of blood culture sets divided by the mean total of patient-days of hospitals served by laboratories that provided the blood culture sets performed, as reported for the following bacterial species:* Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis *and* Enterococcus faecium*, and multiplied by 1 000. The definition of a 'blood culture set' and a 'patient-day' might differ between countries and influence the estimate.*

[f] *Not including the country's* S. pneumoniae *network.*

Table 2. Bacterial species-antimicrobial group/agent combinations presented in this report for 2025

Bacterial species	Assessed antimicrobial group/agent resistance or specific resistance mechanism	Indicative antimicrobial agent(s)
Escherichia coli	Aminopenicillins	Ampicillin or amoxicillin
	Third-generation cephalosporins	Cefotaxime, ceftriaxone or ceftazidime
	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin, levofloxacin or ofloxacin
	Aminoglycosides	Gentamicin or tobramycin
	Novel antibiotics and combinations[a]	Aztreonam-avibactam, cefiderocol, ceftazidime-avibactam, imipenem-relebactam, or meropenem-vaborbactam
Klebsiella pneumoniae	Third-generation cephalosporins	Cefotaxime, ceftriaxone or ceftazidime
	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin, levofloxacin or ofloxacin
	Aminoglycosides	Gentamicin or tobramycin
	Novel antibiotics and combinations[a]	Aztreonam-avibactam, cefiderocol, ceftazidime-avibactam, imipenem-relebactam, or meropenem-vaborbactam
Pseudomonas aeruginosa	Piperacillin-tazobactam	Piperacillin-tazobactam
	Ceftazidime	Ceftazidime
	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin or levofloxacin
	Aminoglycosides	Tobramycin
	Novel antibiotics and combinations[a]	Cefiderocol, ceftazidime-avibactam, ceftolozane-tazobactam, imipenem-relebactam, or meropenem-vaborbactam
Acinetobacter species	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin or levofloxacin
	Aminoglycosides	Gentamicin or tobramycin
	Novel antibiotics and combinations[a]	Cefiderocol
Staphylococcus aureus	MRSA	Cefoxitin or oxacillin[b]
	Fluoroquinolones	Ciprofloxacin, levofloxacin or norfloxacin[c]
	Rifampicin	Rifampicin
Streptococcus pneumoniae	Penicillins	Penicillin or oxacillin[d]
	Third-generation cephalosporins	Cefotaxime or ceftriaxone
	Fluoroquinolones	Levofloxacin, norfloxacin or moxifloxacin[e]
	Macrolides	Azithromycin, clarithromycin or erythromycin
Enterococcus faecalis	High-level aminoglycoside resistance	Gentamicin
Enterococcus faecium	Aminopenicillins	Ampicillin or amoxicillin
	High-level aminoglycoside resistance	Gentamicin
	Vancomycin	Vancomycin

MRSA: meticillin-resistant Staphylococcus aureus.

[a] *Analysed for carbapenem-resistant gram-negative bacteria.*

[b] *MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene by PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

[c] *AST results for norfloxacin are accepted if neither ciprofloxacin nor levofloxacin results are available.*

[d] *Penicillin results are based on penicillin or, if not available, oxacillin.*

[e] *AST results for norfloxacin are accepted if neither levofloxacin nor moxifloxacin results are available.*

Table 3. Number of EU/EEA countries that fulfilled the novel antibiotics analysis inclusion criteria by bacterial species/antimicrobial combination and year, 2024–2025

Bacterial species	Antimicrobial agent	Number of countries	
		2024	2025
		(n)	(n)
Escherichia coli	aztreonam-avibactam	0	0
	cefiderocol	0	0
	ceftazidime-avibactam	1	3
	imipenem-relebactam	1	1
	meropenem-vaborbactam	1	1
Klebsiella pneumoniae	aztreonam-avibactam	0	3
	cefiderocol	4	5
	ceftazidime-avibactam	10	9
	imipenem-relebactam	6	5
	meropenem-vaborbactam	5	4
Pseudomonas aeruginosa	cefiderocol	1	2
	ceftazidime-avibactam	8	10
	ceftolozane-tazobactam	7	8
	imipenem-relebactam	3	3
	meropenem-vaborbactam	2	1
Acinetobacter spp.	cefiderocol	2	2

Overview

EU/EEA country participation in EARS-Net

In 2026, all EU Member States and EEA countries reported data for 2025 to EARS-Net. Twenty-one of these 30 countries (70%) reported that their participating laboratories had a population coverage of over two thirds of the national population, including 13 countries that reported having a coverage of 90% or more. However, six countries reported data with a coverage of less than half of the population (Table 1).

Twenty-four of the 30 participating countries (80%) indicated that their reported data had a high national representativeness based on three metrics: geographical areas covered; acute care hospitals included; and microorganisms that caused invasive infections in these hospitals. A further country reported that the representativeness was 'high' for two of the three metrics, and one country reported representativeness as 'low' for all three metrics (Table 1).

The blood culture rate in hospitals served by the laboratories that reported data to EARS-Net for 2025 was reported by 25 countries. The blood culture rates, measured as blood culture sets per 1 000 patient-days, varied widely among the countries. However, these estimates should be interpreted with caution since the definitions of a 'blood culture set' and a 'patient-day' can differ between and within countries.

In 2025, all but one country reported isolate data for all eight bacterial species under surveillance by EARS-Net (*E. coli*, *K. pneumoniae*, *P. aeruginosa*, *Acinetobacter* spp., *S. pneumoniae*, *S. aureus*, *E. faecalis* and *E. faecium*). Liechtenstein reported isolate data for *E. coli*, *K. pneumoniae*, *P. aeruginosa, S. pneumoniae*, *S. aureus* and *E. faecalis*.

Based on the laboratory identifiers provided by the countries, the number of laboratories participating in EARS-Net has increased since 2021, indicating that national AMR surveillance systems may have been strengthened in the EU/EEA. For 2025, data were reported from 2 191 laboratories. Moreover, 807 laboratories were identified as having reported data for each year during the period 2021–2025.

As part of the reporting of AST data for novel antimicrobials, at most 10 of the 29 countries (34.5%) (Table 3) that reported carbapenem-resistant gram-negative bacteria for 2025 reported data on susceptibility to a specific novel antimicrobial that could be included in an analysis. Due to the amount of missing data, these data were analysed at country level, but not at EU/EEA level.

Epidemiology of bacterial species under surveillance in EARS-Net in the EU/EEA

Progress towards the EU targets on antimicrobial resistance

In 2023, the Council of the European Union recommendation on stepping up EU actions on antimicrobial resistance in a One Health approach established EU targets on AMR to reduce the total EU incidence of meticillin-resistant *S. aureus* (MRSA), third-generation cephalosporin-resistant *E. coli*, and carbapenem-resistant *K. pneumoniae* bloodstream infections by 15%, 10% and 5% by 2030 against the baseline year 2019, respectively [1].

In the data for 2025, the estimated total EU incidence of MRSA bloodstream infections was 4.56 per 100 000 population (EU country range 0.58–12.07) (Table 5). This was 19% lower than in 2019 (baseline year) and 0.23 per 100 000 population lower than the 2030 target of 4.79 per 100 000 population. For the EU overall, a statistically significant decreasing trend was detected between 2019 (baseline year) and 2025, although in the last two years the estimated incidence has been increasing. At country level, 14 countries (Austria, Bulgaria, Czechia, Denmark, France, Germany, Ireland, Italy, Latvia, Luxembourg, Malta, Portugal, Romania, and Slovakia)[1] had reached their respective target in 2025. However, seven EU countries had seen a statistically significant increasing trend in the estimated incidence since 2019.

The estimated total EU incidence of third-generation cephalosporin-resistant *E. coli* bloodstream infections was 12.13 per 100 000 population (EU country range 3.40–24.61) in 2025 (Table 4). This was 16.4% higher than in 2019 (baseline year) and 2.75 per 100 000 population higher than the 2030 target of 9.38 per 100 000 population. For the EU overall, no statistically significant trend was detected between 2019 (baseline year) and 2025, although in the last two years the estimated incidence has been higher than in 2019. At country level, three countries (Bulgaria, Finland and France)[2] had reached their respective targets in 2025. Meanwhile, there was a statistically significant increasing trend in the estimated incidence in 14 EU countries since 2019.

[1] The results for Bulgaria, Denmark and France should be interpreted with caution.

[2] The results for Bulgaria and France should be interpreted with caution.

The estimated total EU incidence of carbapenem-resistant *K. pneumoniae* bloodstream infections was 3.75 per 100 000 population (EU country range 0.00–21.29) in 2025 (Table 6). This was 72% higher than in 2019 (baseline year) and 1.68 per 100 000 population higher than the 2030 target of 2.07 per 100 000 population. For the EU overall, a statistically significant increasing trend was detected between 2019 (baseline year) and 2025. At country level, five countries had reached their respective target (Austria, France, Ireland, Luxembourg and Malta)[3]. However, since 2019 a statistically significant increasing trend in the estimated incidence has been noted in 18 EU countries.

Epidemiological summary

Compared to 2021, the total number of reported invasive isolates for the EU/EEA increased from 370 544 to 517 966 in 2025. For bacteria, the highest estimated EU/EEA incidence of invasive isolates from all reporting laboratories in 2025 was *E. coli* (76.4 per 100 000 population), followed by *S. aureus* (39.3 per 100 000 population), *K. pneumoniae* (26.1 per 100 000 population), *E. faecalis* (14.7 per 100 000 population), *P. aeruginosa* (11.2 per 100 000 population), *E. faecium* (11.1 per 100 000 population), *S. pneumoniae* (9 per 100 000 population) and *Acinetobacter* spp. (4.1 per 100 000 population) (Table 7). This ranking did not differ from the ranking for 2024 (Table 7). Compared to 2021, all the estimated incidences of invasive isolates under EARS-Net surveillance in the EU/EEA had increased, except for *Acinetobacter* spp. which decreased with 25.5% (Table 7). The largest increase in estimated incidence occurred for *S. pneumoniae* (+150%; from 3.6 to 9) followed by *K. pneumoniae* (+35.2%; from 19.3 to 26.1). Since 2021, *S. pneumoniae* has increased on an annual basis. Annual increases for *E. coli, K. pneumoniae*, *P. aeruginosa* and *S. aureus* have also been observed since 2021 (Table 7).

For AMR, the situation reported by EU/EEA countries to EARS-Net for 2025 varied widely, depending on the bacterial species, antimicrobial group and geographical region, as demonstrated by varying AMR percentages and often also the estimated incidence of bloodstream infections with AMR (Tables 8a and 8b, Figures 1–10 and 'Country summaries').

Overall, in 2025 more than 85% (23/27) of the estimated EU/EEA incidences of bloodstream infections with AMR under EARS-Net surveillance exceeded one per 100 000 population. Moreover, the results showed increases from 2021 to 2025 for two thirds of the combinations (66.7%), ranging from +1.2% to +141.5% (Table 8a). In particular, there was a statistically significant increasing trend in all AMR combinations for *E. coli, K. pneumoniae* and *S. pneumoniae*.

Overall, in 2025, the population-weighted EU/EEA mean AMR percentages exceeded 10% in (23/27) 85% of the combinations under regular surveillance. From 2021 to 2025, the results showed increases for one third of the combinations (33.3%), ranging from +0.1% to +3% (Table 8b). The AMR percentage for most of the bacterial species–antimicrobial combinations showed either a significantly decreasing or no significant trend. However, there were seven combinations for which a significantly increasing trend was observed: aminopenicillin resistance, third-generation cephalosporin resistance, carbapenem resistance, aminoglycoside resistance and combined resistance in *E. coli*, carbapenem resistance in *K. pneumoniae*, and combined penicillin non-wild-type and macrolide resistance in *S. pneumoniae* (Table 8b).

For some of the pathogens, the trend between 2021 and 2025 in the population-weighted EU/EEA mean AMR percentages differed from the corresponding trend in the estimated EU/EEA incidence of bloodstream infections with AMR. The differences can mainly be seen in *K. pneumoniae* and *S. aureus*. The estimated AMR incidence and AMR percentage may move in different directions, as the AMR percentage also depends on the incidence of infections by susceptible bacteria.

In 2025, the bacterial species with the highest estimated EU/EEA incidence of invasive infections (Table 7) and the highest estimated EU/EEA incidences of bloodstream infections with AMR was *E. coli* (Table 8a). Resistance to carbapenems was rare in *E. coli* (Table 8a), but all the estimated EU/EEA incidences of *E. coli* bloodstream infections with AMR under EARS-Net surveillance (aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) increased compared to 2021, with significantly increasing trends for all combinations under surveillance (Table 8a). The trend pattern was similar for the respective EU/EEA population-weighted mean percentages, with one exception: no significant trend in the EU/EEA population-weighted mean percentage for fluoroquinolone resistance (Table 8b). Resistance to multiple antimicrobial groups was common (Table 9). During the period 2021–2025, the estimated EU/EEA incidence of bloodstream infections with combined AMR showed a statistically significant increasing trend (Table 8a), as did the equivalent EU/EEA population-weighted mean (Table 8b). Except for carbapenem resistance, which remained low in almost all countries, with Cyprus showing the highest estimated incidence and resistance proportion ('Country summaries' and Figure 3), larger inter-country variations were noted for all the other antimicrobial groups under surveillance (Tables 8a and 8b, Figures 1 and 2). Overall, the highest estimated national incidences of bloodstream infections with AMR *E. coli* were noted in countries in southern Europe. Otherwise, the geographical pattern was quite mixed. The national AMR percentages for aminoglycoside, fluoroquinolone, third-generation cephalosporin resistance and combined resistance were highest in southern, central and eastern Europe but otherwise the geographical pattern was mixed.

[3] The result for France should be interpreted with caution.

During the period 2021–2025, all the estimated EU/EEA incidences of *K. pneumoniae* bloodstream infections with AMR under EARS-Net surveillance (fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) increased and showed significantly increasing trends (Table 8a). With the EU/EEA population-weighted mean percentage, this trend was only seen for carbapenem resistance (Table 8b). For the other antimicrobial groups, the EU/EEA population-weighted mean percentage showed statistically significant decreasing trends. Resistance to multiple antimicrobial groups was common (Table 10). The estimated EU/EEA incidence of combined resistance to fluoroquinolones, third-generation cephalosporins and aminoglycosides in *K. pneumoniae* bloodstream infections showed a statistically significant increasing trend during the period 2021–2025 (Table 8a), whereas the equivalent EU/EEA population-weighted mean percentage showed a statistically significant decreasing trend during the same period (Table 8b). Large inter-country variations were noted for all the antimicrobial groups under surveillance (Tables 8a and 8b, Figures 4 and 5). Overall, the higher estimated national incidences of bloodstream infections with AMR *K. pneumoniae* were noted in countries in southern, central and eastern Europe. The same pattern was noted for the national AMR percentages.

Between 2021 and 2025, the estimated EU/EEA incidence of *P. aeruginosa* bloodstream infections with resistance to piperacillin-tazobactam, ceftazidime, and carbapenem increased, whereas resistance to fluoroquinolones and aminoglycosides decreased (Table 8a). Only fluoroquinolone resistance showed a significant decreasing trend (Table 8a). For aminoglycosides and combined resistance, these results should be interpreted with caution due to limited AST in many of the EU/EEA countries (see 'Country summaries'). For 2021–2025, the EU/EEA population-weighted mean AMR percentage decreased for all combinations and showed significantly decreasing trends for all the percentages (Table 8b). In 2025, all countries except one (Greece) showed estimated incidences of *P. aeruginosa* bloodstream infections with resistance to carbapenem of less than two per 100 000 population (see 'Country summaries'), and 19 countries reported more than 10% carbapenem resistance, seven of which reported more than 20% carbapenem resistance ('Country summaries'). Resistance to two or more antimicrobial groups was frequent (Table 11). During the period 2021–2025, the estimated EU/EEA incidence of combined resistance, defined as resistance to at least three of the antimicrobial groups under surveillance, showed no statistically significant trend in *P. aeruginosa* bloodstream infections, whereas the equivalent EU/EEA population-weighted mean percentage showed a statistically significant decreasing trend (Table 8b). Large inter-country variations were noted in all antimicrobial groups for the AMR percentages (Table 8b and Figure 6), but less so for the estimated incidences of AMR bloodstream infections (Table 8a). Overall, the higher estimated national incidences of bloodstream infections with AMR *P. aeruginosa,* as well as the national AMR percentages, were noted in countries in southern, central and eastern Europe.

Between 2021 and 2025, all the estimated EU/EEA incidences of *Acinetobacter* spp. bloodstream infections with resistance under EARS-Net surveillance showed a statistically significant decreasing trend (Table 8a). Moreover, all the estimated EU/EEA resistance incidences had almost halved compared to the high incidences seen in 2021. The EU/EEA population-weighted mean AMR percentage also showed statistically significant decreasing trends for all the antimicrobial groups under surveillance in the EU/EEA between 2021 and 2025 (Table 8b). However, compared to 2024 there were increases or only a minor decrease in the EU/EEA population-weighted mean AMR percentages. Moreover, two countries showed estimated incidence of *Acinetobacter* spp. bloodstream infections with resistance to carbapenem above 10 per 100 000 (Greece and Romania) (see 'Country summaries'). Resistance to multiple antimicrobial groups was common (Table 12). However, the estimated EU/EEA incidence of combined resistance to carbapenems, fluoroquinolones and aminoglycosides in bloodstream infections decreased between 2021 and 2025 with a statistically significant decreasing trend. The EU/EEA population-weighted mean percentage of combined resistance showed a similar pattern. Large inter-country variations were noted for all antimicrobial groups (Tables 8a and 8b and Figure 7). Overall, the higher estimated national incidences of bloodstream infections with AMR *Acinetobacter* spp. were noted in countries in southern, central and eastern Europe. The national AMR percentages showed a similar geographical pattern.

The estimated EU/EEA incidence of MRSA bloodstream infections showed a statistically significant increasing trend for the period 2021–2025 (Table 8a), with three countries reporting national estimated incidences above 10 per 100 000 (Cyprus, Italy and Romania). On the other hand, the EU/EEA population-weighted mean MRSA percentage exhibited a significantly decreasing trend (Table 8b). Moreover, the MRSA percentage either showed a statistically significant decreasing trend or no statistically significant trend (i.e. neither decreasing nor increasing) in most EU/EEA countries. With MRSA, combined resistance to another antimicrobial group was quite common (Table 13). Large inter-country variations were noted for MRSA (Tables 8a and 8b and Figure 8). Overall, both the higher estimated national incidences of bloodstream infections with MRSA as well as the higher national MRSA percentages were noted in countries in southern, central and eastern Europe.

Compared to 2021, the 2025 estimated EU/EEA incidences of bloodstream infections with resistant *S. pneumoniae* more than doubled and there was a statistically significant increasing trend for the EU/EEA for all incidences between 2021 and 2025 (Table 8a). Increases were also seen in the equivalent EU/EEA population-weighted mean percentages (Table 8b), but with no statistically significant trend. Combined resistance to another antimicrobial group was quite common, although rarely for three or four antimicrobial groups (Table 14). The estimated EU/EEA incidence of combined AMR (i.e. macrolide resistance and penicillin non-wild-type) in *S. pneumoniae* bloodstream infections had also more than doubled compared to 2021 and showed a statistically significant increasing trend during the period 2021–2025. The EU/EEA population-weighted mean percentage for combined resistance also showed a significantly increasing trend (Table 8b). At country level, 18 EU/EEA countries showed this trend in the estimated incidence of penicillin non-wild-type *S. pneumoniae* bloodstream infections for 2021–2025, and 18 EU/EEA countries showed an

equivalent trend in the estimated incidence of macrolide-resistant *S. pneumoniae* bloodstream infections for 2021–2025 ('Country summaries'). Large inter-country variations in AMR percentages were noted for all antimicrobial groups (Table 8b and Figure 9), although there was less inter-country variation in the estimated incidences. Overall, there was a mixed geographical pattern of the estimated national incidences of bloodstream infections with AMR *S. pneumoniae,* as well as the national AMR percentages, across the EU/EEA.

During the period 2021–2025, the estimated EU/EEA incidence of high-level gentamicin-resistant *E. faecalis* bloodstream infections decreased from 2021 to 2024, before a slight increase in 2025, with a statistically significant decreasing trend (Table 8a). However, it should be noted that for each year more than one third of the countries reported that susceptibility to gentamicin was tested for less than 90% of isolates ('Country summaries'). The EU/EEA population-weighted mean percentage has been decreasing since 2021 (Table 8b) and showed a significantly decreasing trend for the period 2021–2025. However, at country level seven countries reported an estimated incidence of high-level gentamicin resistance above three per 100 000 population ('Country summaries'). Large inter-country variations in AMR percentages were noted (Table 8b) although there was less variation in the estimated incidence. Overall, higher estimated national incidences of bloodstream infections with high-level gentamicin resistance, as well as national AMR percentages, were noted in countries in southern, central and eastern Europe.

Although the estimated EU/EEA incidence of vancomycin-resistant *E. faecium* bloodstream infections decreased somewhat between 2021 and 2025, it increased in 2025 compared to 2024 and did not show a statistically significant trend (Table 8a). At country level eight countries showed a statistically significant increasing trend. The EU/EEA population-weighted mean percentage of vancomycin-resistant *E. faecium* was higher than that for 2021, but there was no statistically significant trend (Table 8b). AMR to two or more antimicrobial groups was common (Table 15). For the estimated incidence of vancomycin-resistant *E. faecium* bloodstream infections, 15 countries reported an incidence below 0.50 per 100 000 population ('Country summaries') and three countries reported an incidence above 5 per 100 000 population. Eight countries reported vancomycin-resistant *E. faecium* percentages below 5% (Figure 10) and 10 countries reported percentages above 25%, resulting in large inter-country variations in AMR percentages and less variation in the estimated incidence. Overall, the higher estimated national incidences of bloodstream infections with vancomycin resistant *E. faecium* were noted in countries in southern, central and eastern Europe. The pattern of the national AMR percentages was similar except for one country (Ireland).

In general, higher AMR percentages and estimated incidences of bloodstream infections with AMR were reported by countries in southern, central and eastern Europe.

For each bacterial species, country-specific information is available in the country summaries on: the estimated incidence of antimicrobial-resistant bloodstream infections (including the recommended EU targets on AMR); the percentage of invasive isolates with AMR; data availability, and the percentage of ICU patients. Results by age group and sex are available in ECDC's Surveillance Atlas of Infectious Diseases [2]. The country summaries also include information on susceptibility to novel antimicrobials among gram-negative carbapenem-resistant isolates.

Discussion

In 2026, all EU/EEA countries reported data for 2025 to EARS-Net. Representativeness, as reported by the countries, was high at 80%. This indicates that although all EU/EEA countries actively participate in EARS-Net, some countries can still improve surveillance representativeness.

The EARS-Net data showed an overall increase in the EU/EEA estimated incidences of invasive infections between 2021 and 2025, except for *Acinetobacter* spp., the incidence of which considerably decreased. The former could potentially reflect changes in the EU/EEA population, such as an increase in the number of people vulnerable to developing these severe infections over time, due to factors such as aging, invasive medical treatments and immunosuppression. The latter may reflect successful control efforts after a large increase was noted for 2020–2021 [3], which was a time of COVID-19 interventions and pandemic-associated pressures on healthcare. The effects of COVID-19 and the related interventions during this period should also be kept in mind when interpreting the other results in this report.

The results for the EU targets continued to show a combination of an achieved target for MRSA and concerning developments for the other two EU targets. The estimated EU incidence of third-generation cephalosporin-resistant *E. coli* bloodstream infections with a 10% reduction target increased by more than 15% compared to 2019 (baseline year). Meanwhile, the estimated EU incidence of carbapenem-resistant *K. pneumoniae* bloodstream infections increased by over 70% compared to 2019 (baseline year), which is in stark contrast to the target of a 5% reduction by 2030. This indicates the continued need to rapidly strengthen prevention and control, as well as antimicrobial stewardship, including accessibility to relevant antimicrobials in the EU, as highlighted in the Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach [1].

Overall, AMR levels remained high in the EU/EEA in 2025, as in previous years, with wide variability among EU/EEA countries, depending on the bacterial species, antimicrobial group and geographical region. In general, higher AMR percentages and estimated incidences of bloodstream infections with AMR continued to be reported by countries in southern, central and eastern Europe [4]. By providing an overview of the wide variability across EU/EEA countries in

2025, the report suggests that there are further opportunities for significant AMR reduction through interventions to improve IPC and antimicrobial stewardship practices. For example, for carbapenem-resistant *K. pneumoniae* and other carbapenem-resistant Enterobacterales (CRE), the updated ECDC rapid risk assessment on CRE noted that the spread could be reduced by consistently applied IPC and antimicrobial stewardship, including access to relevant antimicrobials, and the impact mitigated by measures such as timely laboratory detection and infection management [5].

At the EU/EEA level, increases in the estimated incidences of bloodstream infections with resistant bacteria were observed not only for two of the above-mentioned AMR-pathogen combinations with an EU target, but also for many other bacteria and antimicrobial groups under surveillance. These increases in the estimated incidences are a cause for concern.

Among the most worrying developments are:

- the increasing carbapenem resistance in *K. pneumoniae* together with ECDC's assessment that the probability of further spread in the EU/EEA can be considered high [5], especially in combination with the presence of genetic markers of increased virulence [6];
- the increasing estimated AMR incidences (including for carbapenems) and population-weighted mean AMR percentages for *E. coli*, indicating that the EU/EEA is not progressing in the right direction for *E. coli,* a bacterial species that is one of the most common causes of bloodstream infections in Europe. Moreover, already in 2016–2020, the largest EU/EEA AMR burden of disease was caused by infections with third-generation cephalosporin-resistant *E. coli*, both in terms of the number of cases and the number of attributable deaths [7];
- the more than doubled estimated AMR incidences for *S. pneumoniae* since 2021, with increasing trends in most EU/EEA countries, although there were smaller increases in the corresponding EU/EEA population-weighted mean percentages. The observed increases possibly reflect the lifting of non-pharmaceutical interventions (NPIs) for SARS-CoV-2, in parallel with factors that could influence AST, such as laboratories switching from gradient test, which underestimates resistance, and for macrolides also a change of the EUCAST breakpoint for R as of 2023 [8]. However, these aspects should not detract from the noted increases in AMR;
- the increasing estimated incidence of MRSA bloodstream infections, indicating that the one EU target that is currently met may be in jeopardy, while also considering that MRSA is one of the most common causes of bloodstream infections, with a high burden in terms of morbidity and mortality [7,9]. In addition, the decreasing trend in EU/EEA population-weighted mean MRSA percentage and the increasing estimated incidence of invasive *S. aureus* infections suggest that it occurs concomitant with an increase in meticillin-susceptible bloodstream infections in the EU/EEA;
- the increase in the estimated EU/EEA incidence of vancomycin-resistant *E. faecium* bloodstream infections compared to 2024, with statistically significant increasing trends observed for eight countries, together with an increase in the EU/EEA population-weighted mean percentage and an increase in the estimated incidence of invasive *E. faecium* infections. An ECDC study estimated that there were 117 866 *E. faecalis* and *E. faecium* infections in the EU/EEA in 2020, with 3 414 deaths [7]. A rise in the estimated EU/EEA incidence of vancomycin-resistant *E. faecium* bloodstream infections compared to 2020 would contribute to a further increase in the health burden of vancomycin-resistant enterococci infections. At the same time, enterococci have intrinsic resistance to several antimicrobial classes and are easily disseminated in healthcare settings.

Concerns raised regarding CRE, specifically carbapenem-resistant *K. pneumoniae* and carbapenem-resistant *E. coli,* led to the adoption of a Health Security Committee (HSC) opinion on this topic in 2025 [10]. The HSC opinion noted that the deteriorating situation may have been influenced by the COVID-19 pandemic, as well as war casualties and patients transferred from Ukraine since 2022 [11]. The HSC opinion also stated that CRE pose a threat to EU preparedness in future pandemics or significant mass casualty events and emphasised the importance of reducing the spread. To counteract the deteriorating situation for CRE, the HSC opinion proposed measures for the EU/EEA, including support that can be provided by the European Reference Laboratory on AMR (EURL-PH-AMR), the EU guidelines on IPC in human health developed by the European Commission in collaboration with ECDC [12], and the European Commission support of research and access to antimicrobials. At EU/EEA country level, the HSC opinion's proposed measures include CRE national management teams and management plans.

There are also encouraging developments at EU/EEA level. For example, the high levels of AMR among *Acinetobacter* spp. noted in 2021 have decreased substantially. Another example is the EU/EEA AMR percentages for *P. aeruginosa* for 2021−2025, which showed statistically significant decreasing trends. However, it should be noted that some of the corresponding estimated EU/EEA AMR incidences for *P. aeruginosa* increased and the *P. aeruginosa* results that include aminoglycosides should be interpreted with caution due to limited AST in many EU/EEA countries. Although there are a few signs that the AMR situation is improving at EU/EEA level for some of the EARS-Net pathogens, the situation at country level is still a cause for concern. For *Acinetobacter* spp., two countries showed estimated incidence of *Acinetobacter* spp. bloodstream infections with resistance to carbapenem above 10 per 100 000 population. In addition, *Acinetobacter* spp. continue to display high EU/EEA population-weighted mean AMR percentages. For *P. aeruginosa*, high AMR percentages were observed in several countries, and carbapenem resistance was frequent among the tested invasive isolates. As *P. aeruginosa* is intrinsically resistant to many antimicrobial agents, additional acquired resistance is further complicating the treatment of *P. aeruginosa* infections. Moreover, *P. aeruginosa* is one of the major causes of healthcare-associated infections in Europe [13-14].

When interpreting the EARS-Net data, it is important to be mindful of the structure of the surveillance system, including variations in national blood culture rates, as well as changes in the national surveillance systems and in EARS-Net over time. For example:

- The estimated incidence relies on the estimated national population coverage of the AMR data, as reported by each country. The estimated incidences should be interpreted with caution, especially when the national population coverage is estimated as less than 100%. The interpretation of AMR percentages can also be challenging, as they depend not only on the number of resistant isolates but also on the number of identified susceptible isolates included in the denominator. The AMR percentage could therefore for example decrease despite an unchanged number of resistant isolates if this coincides with an increase in the number of susceptible isolates. Both measures, estimated incidence and AMR percentage, should be considered for EARS-Net results and should be interpreted with some caution.
- Although ECDC published the report 'Operational public health considerations for the prevention and control of infectious diseases in the context of Russia's aggression towards Ukraine' [15], which specifically raises the issue of multidrug-resistant organisms, data reported to EARS-Net cannot assess the magnitude of the impact of this war in terms of AMR occurrence in the EU/EEA.
- EARS-Net currently only covers eight pathogens. However, other relevant pathogens may be covered at country level, and several of the pathogens are covered by other disease networks coordinated by ECDC; for example, EURGen-Net published an investigation into carbapenemase-producing *Providencia stuartii* [16].
- EARS-Net focuses on specimens from blood and cerebrospinal fluid, which allows some pooling of EU/EEA data and comparison, although limited, of results across EU/EEA countries. However, this should not prevent countries from collecting data from other sample types to better inform national and/or local treatment guidelines.
- There are also limitations for specific bacterial species. For example, it should be noted that the data reported on *K. pneumoniae* may have been affected by changes over time in the identification and nomenclature of *K. pneumoniae*. Species previously but no longer identified as *K. pneumoniae sensu stricto* are less often found to be resistant. As a result, the reported percentage of resistant *K. pneumoniae* in the EU/EEA may have increased over time. However, in many cases, laboratories will have difficulties in distinguishing species belonging to the *K. pneumoniae* complex (the main members being *K. pneumoniae sensu stricto*, *K. variicola*, and *K. quasipneumoniae*). The size of the impact, in terms of changes in identification and nomenclature, is unknown.

One previous limitation of EARS-Net was the lack of AST data on novel antimicrobials for treatment of carbapenem-resistant gram-negative bacteria. However, as of 2025 these data are collected and presented at country level, although currently EU/EEA level analysis is not undertaken due to the limited data reported to ECDC.

Another aspect that is important to consider when interpreting the results is the quality of the laboratory data that EARS-Net collects. To address this, EARS-Net conducts annual EQA exercises. Overall, the EARS-Net EQA results for 2025 were favourable. All 29 participating countries achieved either 'excellent' or 'very good' results [17]. The results also indicated that there was no systematic overestimation or underestimation of AMR in the EU/EEA. However, the results continued to show that AST for carbapenems for *E. coli* and *K. pneumoniae* (underestimation of resistance), for the macrolide azithromycin for *S. pneumoniae* (overestimation of resistance), and for the aminoglycoside gentamicin in *Acinetobacter* spp. (overestimation of resistance) pose a challenge to laboratories in EARS-Net [17]. In addition, more recently noted challenges include the novel antimicrobials (with e.g. both overestimation and underestimation of resistance to cefiderocol) and AST of the fluoroquinolone levofloxacin for *K. pneumoniae* (overestimation of resistance) [17]. Previous EARS-Net EQAs have also indicated that there may be an underestimation of ceftazidime resistance in *P. aeruginosa,* and overestimation of resistance to third-generation cephalosporins in *E. coli*, piperacillin-tazobactam in *P. aeruginosa*, and MRSA [18-19]. The overall very good 2025 EARS-Net EQA results, as well as the noted challenges, should be considered when interpreting the results in this report, as applicable.

To address the various challenges posed by AMR, ECDC surveillance and monitoring are not restricted to EARS-Net. To complement the phenotypic-based surveillance data available from EARS-Net, and to further investigate the sources and routes of transmission for carbapenemase-producing Enterobacterales (CPE) (including *E. coli* and *K. pneumoniae*) and *Acinetobacter* spp. periodic surveys are conducted within EURGen-Net [20-21]. The results from such a survey were recently published [22]. Moreover, ECDC is also able, to a limited extent, to provide Member States with access to whole-genome sequencing services, primarily for investigating potential multi-country outbreaks. The need for follow-up of antimicrobial consumption is met by the surveillance carried out by the European Surveillance of Antimicrobial Consumption Network (ESAC-Net) [23]. The ESAC-Net Annual Epidemiological Report (AER) has for example in 2026 shown that, despite some recent progress, the EU remains unlikely to achieve the antimicrobial consumption targets of a 20% reduction in total consumption of antibacterials for systemic use between 2019 and 2030 and ensuring that at least 65% of antimicrobial consumption comprises WHO AWaRe Access group antimicrobials by 2030 [24]. In addition, point prevalence surveys as well as indicator- and event-based surveillance of healthcare-associated infections are undertaken within the Healthcare-Associated Infections Surveillance Network (HAI-Net) [25]. Among the recent outputs from the network are the AER on healthcare-associated infections acquired in intensive care units [13] and on surgical site infections in healthcare-associated infections [26], and the results from the point prevalence survey of healthcare-associated infections and antimicrobial use in European long-term care

facilities 2023–2024 [27]. To address the One Health aspect of AMR, a joint annual report is produced by ECDC and the European Food Safety Authority (EFSA) [28], showing for example reduction in AMR in *E. coli* in food-producing animals, although with large variations across the participating countries, and occurrence of CPE, although at a low level [28]. A full One Health perspective is presented in a joint inter-agency report on the integrated analysis of consumption of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from humans and food-producing animals in the EU/EEA (JIACRA) which is produced by ECDC, EFSA, and the European Medicines Agency (EMA) approximately every three years [29].

Moreover, ECDC has produced rapid risk assessments with options for response and recommendations to address several of the challenges highlighted in this report such as CRE [5], emergence of hypervirulent *K. pneumoniae* sequence type 23 carrying carbapenemase genes [6], and carbapenem-resistant *Acinetobacter baumannii* in healthcare settings [30].

In recent years, ECDC has also conducted Public Health Emergency Preparedness Assessments (PHEPA) in EU/EEA countries. These assessments, which include the topic of AMR, result in country-specific recommendations [31] for which the countries should, as needed, produce an action plan.

In addition, data collected by ECDC contribute to providing a regional [32] and global [33] picture of AMR by being included in outputs produced by WHO. Moreover, ECDC and WHO Regional Office for Europe jointly produce a summary of AMR in Europe [34].

Furthermore, at EU level, the European Health Union was created in 2020 to better protect the health of EU citizens [35]. One of the main instruments for the European Health Union is a large budget available under the EU4Health programme (EUR 4.4 billion for the period 2021–2027), dedicated to wider policy areas, including action on AMR.

At a global level, the Political Declaration of the High-Level Meeting on AMR at the United Nations (UN) General Assembly (September 2024) highlighted the public health threat posed by AMR [36]. The Declaration called for the establishment of an independent panel to collect evidence for action against AMR. The European Commission declared that it will be providing funds for the establishment of such a panel [37] and the plan is for the Independent Panel on Evidence for Action against AMR (IPEA) to be established in 2026 [38]. WHO has also published a list of priority bacteria as a guide for AMR research, investments and public health action [39].

Public health implications

Estimates based on EARS-Net data from 2020 indicate that over 35 000 people die in the EU/EEA each year as a direct consequence of antimicrobial-resistant infections [7]. The overall poor progress towards the EU targets on AMR and the increases in the estimated EU/EEA incidences of bloodstream infections with resistant bacteria highlight the urgent need for intensified public health action against AMR.

The 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach' (2023/C 220/01) not only encourages Member States to develop and implement national action plans against AMR, but also highlights the need for the countries to allocate appropriate human and financial resources for the effective implementation of these plans [1]. In addition, the Public Health Emergency Preparedness Assessments reports provide recommendations, specifically tailored to the respective country, on addressing AMR and healthcare-associated infections [31].

Implementing public health interventions to tackle AMR would not only have a significant positive impact on population health but also future healthcare expenditure in the EU/EEA. A mixed intervention package has been estimated to potentially not only prevent nearly 613 000 resistant infections and avoid more than 10 000 deaths per year in the EU/EEA, but it would also lead to a reduction in health expenditure and gains in productivity, which together would be three times higher than the average cost of implementing the package [40].

However, in the absence of stronger and swifter public health action, it is unlikely that the EU AMR targets will be reached by 2030. AMR will instead continue to increasingly jeopardise public health in the EU/EEA, including its preparedness. This will lead to an increased number of infections with antimicrobial-resistant bacteria that will be more difficult to treat, as well as greater challenges for patient safety and a rise in AMR-related deaths.

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Table 4. Third-generation cephalosporin-resistant *Escherichia coli* bloodstream infections, EU/EEA countries, 2019 and 2025: estimated incidence, trend, change in proportion, estimated incidence and estimated total number of cases, and target as percentage reduction and estimated incidence in 2030

Country[a]	Estimated incidence[b] (n per 100 000 population)								Progress towards target			Target[c]	
	2019	2020	2021	2022	2023	2024	2025	Trend 2019–2025[d]	Change in estimated incidence (%) 2019–2025	Change in estimated incidence (n per 100 000 population) 2019–2025	Changes in estimated number of cases 2019–2025*	Recommended change (%) 2019–2030	Target 2030 (n per 100 000 population)
Liechtenstein	ND	ND	ND	6.36#	0.00#	0.00#	**0.00#**	NA	NA	NA	NA	NA	NA
Bulgaria	4.05#	3.24#	2.95#	2.92#	3.68#	3.75#	**3.40#**	-	-16	-0.65	-65	0	4.05
Netherlands	4.54	3.97	3.47	4.29	4.62	5.84	**5.08**	↑	+11.9	+0.54	+133	0	4.54
Norway	5.03	4.32	4.16	4.27	4.34	5.18	**5.46**	-	+8.5	+0.43	+37	NA	NA
Greece	2.58#	3.86#	3.52#	3.99	5.61	5.40	**6.57**	↑	+154.7	+3.99	+404	0	2.58
France[e]	8.60	5.52	4.20	4.01	ND	5.74	**6.61**	NA	-23.1	-1.99	-1 204	-10	7.74
Finland	8.02	7.26	7.21	5.78	6.46	6.70	**7.08**	-	-11.7	-0.94	-44	-10	7.22
Slovakia	6.39	6.45	4.91	5.98	5.12	6.64	**7.31**	-	+14.4	+0.92	+48	-5	6.07
Denmark	6.61	6.08^	5.72^	6.01^	5.61^	6.09^	**7.54^**	-	+14.1	+0.93	+68	-5	6.28
Austria	7.14	6.35	5.71	5.25	6.60	7.90	**7.73**	-	+8.3	+0.59	+79	-10	6.43
Croatia	5.31	4.22	3.34	4.93	7.56	5.90	**8.35**	↑	+57.3	+3.04	+107	0	5.31
Hungary	5.65	4.49	5.75	6.64	6.81	7.37	**8.79**	↑	+55.6	+3.14	+287	0	5.65
Ireland	8.28	7.07	6.01	6.18	6.70	7.54	**8.88**	-	+7.2	+0.60	+77	-10	7.45
Iceland	5.04	7.41	7.86	6.11	7.99	10.69	**9.24**	↑	+83.3	+4.20	+18	NA	NA
Estonia	7.93	6.09	5.64	8.86	9.08	8.07	**9.27**	-	+16.9	+1.34	+22	-10	7.14
Slovenia	7.67	8.24	7.47	7.43	6.78	7.37	**9.53**	-	+24.3	+1.86	+43	-10	6.90
Romania	6.32#	4.19#	4.40#	4.97#	7.63#	9.68#	**9.70#**	↑	+53.5	+3.38	+620	-5	6.00
Poland	7.44#	6.24#	5.87#	6.98#	7.77#	9.43#	**9.77#**	↑	+31.3	+2.33	+741	-10	6.70
Sweden	9.24	8.73	8.19	8.52	9.08	10.55	**10.47**	↑	+13.3	+1.23	+164	-10	8.32
Czechia	6.56	4.65	4.94	6.25	8.15	8.83	**10.78**	↑	+64.3	+4.22	+477	-5	6.23
Latvia	5.03#	5.30#	4.23#	5.75#	6.96#	10.98#	**11.13**	↑	+121.3	+6.10	+110	0	5.03

Country[a]	Estimated incidence[b] (n per 100 000 population)								Progress towards target			Target[c]	
	2019	2020	2021	2022	2023	2024	2025	Trend 2019 – 2025[d]	Change in estimated incidence (%) 2019–2025	Change in estimated incidence (n per 100 000 population) 2019–2025	Changes in estimated number of cases 2019–2025*	Recommended change (%) 2019–2030	Target 2030 (n per 100 000 population)
Luxembourg	10.20	7.91	6.30	7.67	8.17	10.22	**12.15**	-	+19.1	+1.95	+20	-12	8.98
Belgium	13.19#	10.29	7.84	8.07#	10.14#	13.39#	**13.25#**	-	+0.5	+0.06	+63	-12	11.61
Germany	12.02#	10.74#	9.07#	9.15#	9.93#	12.27	**13.51**	-	+12.4	+1.49	+1 315	-12	10.58
Portugal	10.32	8.38	7.36	7.76	10.73	13.08	**13.61**	↑	+31.9	+3.29	+402	-12	9.08
Lithuania	5.62	6.51	5.62	7.20	8.78	9.53	**13.73**	↑	+144.3	+8.11	+240	0	5.62
Spain	7.84#	6.40#	6.65#	10.02#	11.16#	12.45#	**13.81#**	↑	+76.1	+5.97	+3 105	-10	7.06
Malta	12.37	6.96	8.36	7.48	9.13	22.79	**19.25**	↑	+55.6	+6.88	+49	-12	10.89
Cyprus	6.20	5.11	9.37	10.76	15.23	19.56	**23.30**	↑	+275.8	+17.10	+175	-5	5.89
Italy	22.96	17.67	14.77	17.29	19.56	22.19	**24.61**	-	+7.2	+1.65	+650	-12	20.20
EU	**10.42**	**8.38**	**7.32**	**8.26**	**9.47**	**11.08**	**12.13**	**-**	**+16.4**	**+1.71**	**+8 088**	**-10**	**9.38**
EU/EEA	**10.35**	**8.33**	**7.28**	**8.21**	**9.41**	**11.01**	**12.04**	**-**	**+16.3**	**+1.69**	**+8 143**	**NA**	**NA**

ND, no data available; NA, not applicable.
^ The antimicrobial group/agent was tested for <90% of isolates. The results should be interpreted with caution.
 # One or more of the three representativeness indicators (geographical, hospital and/or isolate representativeness) were not reported as 'High'. The results should be interpreted with caution.
[a] Countries are ranked by increasing estimated incidence in 2025.
[b] Total number of cases and incidence were estimated for each country and the EU separately. Each de-duplicated isolate from a blood sample (>99% data) or cerebrospinal fluid sample (<1% data) was considered a proxy for bloodstream infection (for more information, see https://www.ecdc.europa.eu/en/publications-data/reporting-protocol-antimicrobial-resistance-amr)
[c] The 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health Approach' (2023/C220/01) includes 2030 EU targets, with 2019 as the baseline year: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=oj:JOC_2023_220_R_0001
[d] ↑ indicates a statistically significant increasing trend; ↓ indicates a statistically significant decreasing trend; - indicates absence of a statistically significant trend.
[e] Due to changes in the surveillance network in 2020 the progress toward the target should be interpreted with caution.
** Country level calculations differ from the EU and EU/EEA level calculation and are calculated as described in the EARS-Net reporting protocol.*

National reduction target reached (see 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach' (2023/C 220/01): https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=oj:JOC_2023_220_R_0001)

Table 5. Meticillin-resistant *Staphylococcus aureus* (MRSA)[a] bloodstream infections, EU/EEA countries, 2019 and 2025: estimated incidence, trend, change in proportion, estimated incidence and estimated total number of cases, and target as percentage reduction and estimated incidence in 2030

Country[b]	Estimated incidence[c] (n per 100 000 population)								Progress towards target			Target[d]	
	2019	2020	2021	2022	2023	2024	2025	Trend 2019–2025[e]	Change in estimated incidence (%) 2019–2025	Change in estimated incidence (n per 100 000 population) 2019–2025	Changes in estimated number of cases 2019–2025*	Recommended change (%) 2019–2030	Target 2030 (n per 100 000 population)
Liechtenstein	ND	ND	ND	6.36#	0.00#	6.25#	**0.00#**	NA	NA	NA	NA	NA	NA
Netherlands	0.40	0.39	0.39	0.52	0.49	0.59	**0.58**	↑	+45.0	+0.18	+36	-3	0.39
Norway	0.34	0.50	0.30	0.39	0.64	0.69	**0.67**	↑	+97.1	+0.33	+19	NA	NA
Denmark	0.83	0.70	0.79	0.61^	0.47^	0.55^	**0.77^**	-	-7.2	-0.06	-2	-3	0.81
Bulgaria	1.43#	0.78#	0.96#	0.85#	1.49#	1.13#	**0.97#**	-	-32.2	-0.46	-38	-3	1.39
Iceland	1.96	1.65	0.27	1.06	2.06	2.09	**1.03**	-	-47.4	-0.93	-3	NA	NA
Latvia	1.91#	1.92#	1.41#	2.19#	1.48#	1.96#	**1.29**	-	-32.5	-0.62	-13	-6	1.80
Luxembourg	2.14	0.97	1.73	1.72	1.66	1.50	**1.33**	-	-37.9	-0.81	-4	-6	2.01
Austria	2.17	1.56	1.22	1.51	1.81	2.21	**1.61**	-	-25.8	-0.56	-44	-6	2.04
Estonia	0.83	0.83	0.45	0.68	0.66	1.09	**1.68**	↑	+102.4	+0.85	+12	-3	0.81
Sweden	1.34	1.80	1.65	1.58	1.79	2.07	**1.83**	↑	+36.6	+0.49	+56	-3	1.30
Finland	1.06	1.07	1.19	1.14	1.28	1.85	**1.96**	↑	+84.9	+0.90	+52	-3	1.03
Czechia	3.06	2.28	2.51	2.15	2.92	2.79	**2.29**	-	-25.2	-0.77	-77	-6	2.88
Malta	3.84	3.68	4.28	4.45	3.11	2.99	**2.57**	-	-33.1	-1.27	-4	-10	3.46
Ireland	3.06	2.50	2.68	2.61	2.47	2.57	**2.73**	-	-10.8	-0.33	-1	-6	2.88
Germany	3.56#	2.91#	2.64#	2.15#	2.33#	2.51	**2.78**	-	-21.9	-0.78	-633	-10	3.20
Belgium	2.62#	2.43	1.33	1.27#	2.07#	2.96#	**2.92#**	-	+11.5	+0.30	+48	-6	2.46
France[f]	5.61	4.02	3.41	2.97	ND	3.06	**3.42**	NA	-39.0	-2.19	-1 401	-18	4.60
Slovenia	2.38	3.37	2.87	2.68	3.24	2.81	**3.60**	-	+51.3	+1.22	+27	-6	2.24
Slovakia	5.01	4.38	4.25	3.42	2.05	3.27	**3.69**	↓	-26.3	-1.32	-73	-10	4.51
Lithuania	2.18	2.47	2.40	2.78	2.45	3.22	**3.87**	↑	+77.5	+1.69	+51	-6	2.05
Poland	4.26#	3.08^#	3.74^#	3.91#	3.52#	3.43#	**4.25^#**	-	-0.2	-0.01	-68	-10	3.83
Spain	4.21#	3.13#	3.53^#	4.54^#	4.29^#	3.90^#	**4.44^#**	-	+5.5	+0.23	+208	-10	3.79
Croatia	2.73	3.82	5.18	5.44	6.35	5.03	**4.56**	↑	+67.0	+1.83	+65	-6	2.57
Hungary	4.15	3.61	5.20	4.97	4.85	4.42	**4.82**	-	+16.1	+0.67	+54	-10	3.73

Country[b]	Estimated incidence[c] (n per 100 000 population)								Progress towards target			Target[d]	
	2019	2020	2021	2022	2023	2024	2025	Trend 2019–2025[e]	Change in estimated incidence (%) 2019–2025	Change in estimated incidence (n per 100 000 population) 2019–2025	Changes in estimated number of cases 2019–2025*	Recommended change (%) 2019–2030	Target 2030 (n per 100 000 population)
Greece	4.59#	5.60#	5.44#	4.96	6.51	5.54	**5.48**	-	+19.4	+0.89	+76	-10	4.13
Portugal	11.39	9.80	7.23	8.81	7.39	8.22	**7.83**	↓	-31.3	-3.56	-328	-18	9.34
Italy	13.42	13.07	10.28	11.70	10.18	10.54	**10.27**	↓	-23.5	-3.15	-2047	-18	11.00
Romania	13.72#	9.03#	8.95#	9.37#	11.99#	13.15#	**10.78#**	-	-21.4	-2.94	-611	-18	11.25
Cyprus	6.85	7.81	11.31	14.59	15.50	13.63	**12.07**	↑	+76.2	+5.22	+59	-18	5.62
EU	**5.63**	**4.73**	**4.26**	**4.44**	**4.37**	**4.50**	**4.56**	↓	**-19.0**	**-1.07**	**-4 599**	**-15**	**4.79**
EU/EEA	**5.57**	**4.68**	**4.21**	**4.39**	**4.32**	**4.45**	**4.51**	↓	**-19.0**	**-1.06**	**-4 583**	**NA**	**NA**

ND, no data available; NA, not applicable.

^ The antimicrobial group/agent was tested for <90% of isolates. The results should be interpreted with caution.

 # One or more of the three representativeness indicators (geographical, hospital and/or isolate representativeness) were not reported as 'High'. The results should be interpreted with caution.

[a] MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of mecA *gene PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

[b] Countries are ranked by increasing estimated incidence in 2025.

[c] Total number of cases and incidence were estimated for each country and the EU separately. Each de-duplicated isolate from a blood sample (>99% data) or cerebrospinal fluid sample (<1% data) was considered a proxy for bloodstream infection (for more information, see https://www.ecdc.europa.eu/en/publications-data/reporting-protocol-antimicrobial-resistance-amr)

[d] The 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health Approach' (2023/C220/01) includes 2030 EU targets, with 2019 as the baseline year: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=oj:JOC_2023_220_R_0001

[e] ↑ indicates a statistically significant increasing trend; ↓ indicates a statistically significant decreasing trend; - indicates absence of a statistically significant trend.

[f] Due to changes in the surveillance network in 2020 the progress toward the target should be interpreted with caution.

** Country level calculations differ from the EU and EU/EEA level calculation and are calculated as described in the EARS-Net reporting protocol.*

National reduction target reached (see 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach' (2023/C 220/01): https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=oj:JOC_2023_220_R_0001)

Table 6. Carbapenem-resistant *Klebsiella pneumoniae* bloodstream infections, EU/EEA countries, 2019 and 2025: estimated incidence, trend, change in proportion, estimated incidence and estimated total number of cases, and the target as percentage reduction and estimated incidence in 2030

Country[a]	Estimated incidence[b] (n per 100 000 population)								Progress towards target			Target[c]	
	2019	2020	2021	2022	2023	2024	2025	Trend 2019–2025[d]	Change in estimated incidence (%) 2019–2025	Change in estimated incidence (n per 100 000 population) 2019–2025	Changes in estimated number of cases 2019–2025*	Recommended change (%) 2019–2030	Target 2030 (n per 100 000 population)
Iceland	ND	0.00	0.00	0.00	0.00	0.00	**0.00**	NA	NA	NA	NA	NA	NA
Liechtenstein	ND	ND	ND	ND	0.00#	0.00#	**0.00#**	NA	NA	NA	NA	NA	NA
Luxembourg	0.16	0.16	0.16	0.31	0.30	0.15	**0.00**	-	-100.0	-0.16	-1	-2	0.16
Ireland	0.11	0.04	0.06	0.06	0.04	0.02	**0.02**	-	-81.8	-0.09	-4	-2	0.11
Norway	0.04	0.02	0.04	0.04	0.08	0.13	**0.02**	-	-50.0	-0.02	-1	NA	NA
Finland	0.06	0.02	0.00	0.00	0.02	0.04	**0.06**	-	0.0	0.00	0	-2	0.06
Sweden	0.03	0.06	0.03	0.04	0.12	0.14	**0.08**	↑	+166.7	+0.05	+6	0	0.03
Denmark	0.07	0.19	0.10	0.10	0.08	0.10	**0.10**	-	+42.9	+0.03	+2	-2	0.07
Netherlands	0.02	0.01	0.02	0.05	0.04	0.09	**0.11**	↑	+450.0	+0.09	+15	0	0.02
Austria	0.20	0.12	0.15	0.14	0.29	0.29	**0.18**	-	-10.0	-0.02	-1	-2	0.20
France[e]	0.22	0.08	0.10	0.13	ND	0.19	**0.21**	NA	-4.5	-0.01	-9	-2	0.22
Germany	0.20#	0.11#	0.18#	0.23#	0.23#	0.32	**0.30**	↑	+50.0	+0.10	+85	-2	0.20
Czechia	0.09^	0.07^	0.16^	0.24^	0.26^	0.41^	**0.35^**	↑	+288.9	+0.26	+29	-2	0.09
Estonia	0.00^	0.00^	0.15	0.23^	0.44^	0.29^	**0.44^**	↑	NA	+0.44	+6	0	0.00
Belgium	0.27#	0.24	0.26	0.25#	0.47#	0.44#	**0.46#**	↑	+70.4	+0.19	+24	-2	0.26
Malta	2.13	2.05	1.84	1.21	0.97	0.93	**0.73**	↓	-65.7	-1.40	-6	-4	2.04
Slovenia	0.05	0.00	0.14	0.34	0.62	0.62	**0.76**	↑	+1 420.0	+0.71	+15	-2	0.05
Spain	0.76#	0.60#	0.72^#	1.08#	0.96#	1.20#	**1.27#**	↑	+67.1	+0.51	+268	-4	0.73
Hungary	0.09	0.06	0.11	0.57	0.76	0.97	**1.55**	↑	+1 622.2	+1.46	+139	-2	0.09
Latvia	0.00#	0.12#	0.23#	0.47#	0.89#	2.08#	**1.67**	↑	NA	+1.67	+31	0	0.00
Slovakia	0.52	1.05	1.96	1.87	1.33	1.74	**1.92**	↑	+269.2	+1.40	+75	-4	0.50
Lithuania	0.54	0.43	0.18	0.11	0.73	2.39	**2.08**	↑	+285.2	+1.54	+45	-4	0.52
Portugal	2.93	3.22	2.92	3.01	4.19	4.22	**6.06**	↑	+106.8	+3.13	+350	-5	2.78
Croatia	1.20	1.57	2.87	2.52	4.53	4.49	**6.11**	↑	+409.2	+4.91	+188	-4	1.15
Poland	1.38#	1.45#	3.69#	3.30#	3.69#	5.15#	**6.81#**	↑	+393.5	+5.43	+1 961	-4	1.32

Country[a]	Estimated incidence[b] (n per 100 000 population)								Progress towards target			Target[c]	
	2019	2020	2021	2022	2023	2024	2025	Trend 2019–2025[d]	Change in estimated incidence (%) 2019–2025	Change in estimated incidence (n per 100 000 population) 2019–2025	Changes in estimated number of cases 2019–2025*	Recommended change (%) 2019–2030	Target 2030 (n per 100 000 population)
Italy	8.43	8.73	6.99	7.77	9.29	9.29	**10.00**	-	+18.6	+1.57	+806	-5	8.01
Bulgaria	2.24#	2.19#	3.52#	3.91#	7.75#	10.62#	**10.23#**	↑	+356.7	+7.99	+502	-4	2.15
Greece	13.05#	14.96#	23.30#	18.02	21.44	14.89	**16.28**	-	+24.8	+3.23	+289	-5	12.40
Romania	7.12#	10.77#	13.87#	12.12#	20.02#	20.31#	**18.66#**	↑	+162.1	+11.54	+2 171	-5	6.76
Cyprus	2.61	2.55	5.51	9.87	9.80	19.81	**21.29**	↑	+715.7	+18.68	+186	-5	2.48
EU	**2.18**	**2.37**	**2.72**	**2.66**	**3.39**	**3.50**	**3.75**	↑	**+72.0**	**+1.57**	**+7 175**	**-5**	**2.07**
EU/EEA	**2.15**	**2.34**	**2.69**	**2.62**	**3.34**	**3.46**	**3.70**	↑	**+72.1**	**+1.55**	**+7 174**	**NA**	**NA**

ND, no data available; NA, not applicable.

^ The antimicrobial group/agent was tested for <90% of isolates. The results should be interpreted with caution.

 # One or more of the three representativeness indicators (geographical, hospital and/or isolate representativeness) were not reported as 'High'. The results should be interpreted with caution.

[a] Countries are ranked by increasing estimated incidence in 2025.

[b] Total number of cases and incidence were estimated for each country and the EU separately. Each de-duplicated isolate from a blood sample (>99% data) or cerebrospinal fluid sample (<1% data) was considered a proxy for bloodstream infection (for more information, see https://www.ecdc.europa.eu/en/publications-data/reporting-protocol-antimicrobial-resistance-amr)

[c] The 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health Approach' (2023/C220/01) includes 2030 EU targets, with 2019 as the baseline year: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=oj:JOC_2023_220_R_0001

[d] ↑ indicates a statistically significant increasing trend; ↓ indicates a statistically significant decreasing trend; - indicates absence of a statistically significant trend.

[e] Due to changes in the surveillance network in 2020 the progress toward the target should be interpreted with caution.

** Country level calculations differ from the EU and EU/EEA level calculation and are calculated as described in the EARS-Net reporting protocol.*

National reduction target reached (see 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach' (2023/C 220/01): https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=oj:JOC_2023_220_R_0001)

Table 7. Estimated incidence of invasive isolates (per 100 000 population) by bacterial species, EU/EEA 2021–2025

Bacterial species	Estimated incidence (per 100 000 population)					
	2021	2022	2023	2024	2025	Change 2021–2025 (%)
Escherichia coli	60.4	63.6	67.7	74.0	76.4	+26.5
Klebsiella pneumoniae	19.3	20.5	22.7	25.4	26.1	+35.2
Pseudomonas aeruginosa	9.6	9.9	10.3	11.1	11.2	+16.7
Acinetobacter **spp.**	5.5	4.3	4.3	4.5	4.1	-25.5
Staphylococcus aureus	34.0	35.5	35.6	38.0	39.3	+15.6
Streptococcus pneumoniae	3.6	5.6	7.1	8.0	9.0	+150.0
Enterococcus faecalis	14.3	13.7	13.6	14.6	14.7	+2.8
Enterococcus faecium	10.5	9.9	9.8	10.6	11.1	+5.7

Table 8a. Estimated total incidence of bloodstream infections with resistance phenotype (number per 100 000 population) and trend, 2025 EU/EEA country range in estimated incidence, 2021–2025, by bacterial species and antimicrobial group/agent, EU/EEA

Bacterial species	Antimicrobial group/agent	Estimated incidence[a] of isolates from bloodstream infections with resistance phenotype (number per 100 000 population)						
		2021	2022	2023	2024	2025	Trend 2021–2025[b]	EU/EEA country range 2025
Escherichia coli	Aminopenicillin (amoxicillin/ampicillin) resistance	24.09	25.62	27.73	31.77	33.69	↑	5.86-61.18
	Third-generation cephalosporin (cefotaxime/ceftriaxone/ceftazidime) resistance	7.28	8.21	9.41	11.01	12.04	↑	0.00-24.61
	Carbapenem (imipenem/meropenem) resistance	0.07	0.11	0.13	0.15	0.15	↑	0.00-1.30
	Fluoroquinolone (ciprofloxacin/levofloxacin/ofloxacin) resistance	11.78	12.73	14.18	15.69	15.94	↑	0.00-33.73
	Aminoglycoside (gentamicin/tobramycin) resistance	4.80	5.23	6.00	6.71	6.94	↑	1.88-16.86
	Combined resistance to third-generation cephalosporins, fluoroquinolones, and aminoglycosides	2.33	2.58	2.99	3.32	3.39	↑	0.00-12.46
Klebsiella pneumoniae	Third-generation cephalosporin (cefotaxime/ceftriaxone/ceftazidime) resistance	6.95	7.16	8.33	9.04	9.17	↑	0.00-30.28
	Carbapenem (imipenem/meropenem) resistance	2.69	2.62	3.34	3.46	3.70	↑	0.00-21.29
	Fluoroquinolone (ciprofloxacin/levofloxacin/ofloxacin) resistance	6.77	6.90	7.92	8.52	8.33	↑	0.00-28.98
	Aminoglycoside (gentamicin/tobramycin) resistance	4.53	4.60	5.33	5.58	5.61	↑	0.00-16.90
	Combined resistance to third-generation cephalosporins, fluoroquinolones, and aminoglycosides	4.03	4.05	4.67	4.83	4.82	↑	0.00-15.26
Pseudomonas aeruginosa	Piperacillin-tazobactam resistance	1.74	1.88	1.89	1.82	1.88	-	0.00-8.69
	Ceftazidime resistance	1.49	1.58	1.61	1.53	1.52	-	0.00-8.66
	Carbapenem (imipenem/meropenem) resistance	1.72	1.82	1.84	1.74	1.74	-	0.00-9.23
	Fluoroquinolone (ciprofloxacin/levofloxacin) resistance	1.75	1.81	1.81	1.65	1.67	↓	0.18-9.30
	Aminoglycoside (tobramycin) resistance	0.66	0.64	0.72	0.58	0.57	-	0.00-5.91
	Combined resistance to ≥3 antimicrobial groups (among piperacillin-tazobactam, ceftazidime, carbapenems, fluoroquinolones and aminoglycosides)	0.87	0.94	0.96	0.80	0.78	-	0.00-5.92

Bacterial species	Antimicrobial group/agent	Estimated incidence[a] of isolates from bloodstream infections with resistance phenotype (number per 100 000 population)						
		2021	2022	2023	2024	2025	Trend 2021–2025[b]	EU/EEA country range 2025
***Acinetobacter* species**	Carbapenem (imipenem/meropenem) resistance	3.99	2.71	2.50	2.49	2.22	↓	0.00-16.04
	Fluoroquinolone (ciprofloxacin/levofloxacin) resistance	4.14	2.81	2.55	2.50	2.24	↓	0.00-15.36
	Aminoglycoside (gentamicin/tobramycin) resistance	3.68	2.46	2.25	2.13	1.92	↓	0.00-14.58
	Combined resistance to carbapenems, fluoroquinolones and aminoglycosides	3.50	2.31	2.15	2.03	1.80	↓	0.00-14.17
Staphylococcus aureus	MRSA[c]	4.21	4.39	4.32	4.45	4.51	↑	0.00-12.07
Streptococcus pneumoniae	Penicillin non-wild-type[d]	0.51	0.63	0.75	0.98	1.10	↑	0.00-3.43
	Macrolide (azithromycin/clarithromycin/erythromycin) resistance	0.53	0.73	0.95	1.12	1.28	↑	0.00-3.72
	Combined penicillin non-wild-type and resistance to macrolides[d]	0.28	0.34	0.43	0.55	0.61	↑	0.00-2.12
Enterococcus faecalis	High-level gentamicin resistance	2.94	2.45	2.31	2.21	2.22	↓	0.00-6.45
Enterococcus faecium	Vancomycin resistance	2.15	2.06	1.94	1.96	2.10	-	0.00-9.61

[a] Incidence was estimated using the EARS-Net data reported to EpiPulse. Each de-duplicated isolate from a blood sample (>99% data) or cerebrospinal fluid sample (<1% data) was considered a proxy for a bloodstream infection.

[b] ↑ and ↓ indicate statistically significant increasing and decreasing trends, respectively.

[c] MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of mecA *gene PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

[d] Penicillin results are based on penicillin or, if unavailable, oxacillin. For S. pneumoniae*, the term 'penicillin non-wild-type' is used in this report, referring to* S. pneumoniae *isolates reported by local laboratories as susceptible, increased exposure (I) or resistant (R) to penicillin, assuming MIC to benzylpenicillin above those of wild-type isolates (>0.06 mg/L). This cut-off is also the EUCAST S-breakpoint for all indications (the R-breakpoint is variable depending on type of infection). The qualitative susceptibility categories (S/I/R) as reported by the laboratory are used, since quantitative susceptibility information is missing for a large part of the data.*

Table 8b. Total number of invasive isolates tested (n) and percentages of isolates with AMR phenotype, by bacterial species and antimicrobial group/agent, population-weighted EU/EEA mean and trend and 2025 EU/EEA country range, 2021–2025

Bacterial species	Antimicrobial group/agent	2021		2022		2023		2024		2025		Trend 2021 – 2025[a]	2025 EU/EEA country range[b]
		n	%	n	%	n	%	n	%	n	%		
Escherichia coli	Aminopenicillin (amoxicillin/ampicillin) resistance	109 168	53.2	118 681	53.4	128 670	54.5	155 353	54.7	166 535	55.5	↑*	35.9-70.3
	Third-generation cephalosporin (cefotaxime/ceftriaxone/ceftazidime) resistance	144 030	13.9	154 773	14.3	167 872	15.2	194 086	16.0	206 027	16.9	↑*	6.8-42.7
	Carbapenem (imipenem/meropenem) resistance	138 372	0.2	149 933	0.2	163 373	0.3	189 219	0.3	201 434	0.2	↑*	0.0-2.4
	Fluoroquinolone (ciprofloxacin/levofloxacin/ofloxacin) resistance	144 012	22.0	153 982	22.0	167 570	22.5	193 399	22.4	205 044	22.0	-	8.8-50.9
	Aminoglycoside (gentamicin/tobramycin) resistance	140 285	9.7	149 754	9.6	162 431	10.3	185 014	10.4	195 088	10.3	↑*	4.3-23.1
	Combined resistance to third-generation cephalosporins, fluoroquinolones, and aminoglycosides	138 516	5.1	147 057	5.1	159 473	5.5	181 644	5.5	191 624	5.4	↑*	1.3-17.1
Klebsiella pneumoniae	Third-generation cephalosporin (cefotaxime/ceftriaxone/ceftazidime) resistance	43 839	34.3	48 342	32.8	54 353	33.5	63 381	33.0	67 520	32.8	↓*	5.8-84.8
	Carbapenem (imipenem/meropenem) resistance	42 584	11.7	47 334	10.9	53 575	11.5	62 151	11.3	66 620	12.0	↑	0.0-69.7
	Fluoroquinolone (ciprofloxacin/levofloxacin/ofloxacin) resistance	43 651	33.6	48 066	32.1	54 174	32.2	63 068	31.3	67 135	30.1	↓*	6.9-82.8
	Aminoglycoside (gentamicin/tobramycin) resistance	42 759	23.8	47 147	22.5	53 080	22.5	60 812	21.4	64 791	21.1	↓*	2.4-77.0
	Combined resistance to third-generation cephalosporins, fluoroquinolones, and aminoglycosides	42 105	21.3	46 302	20.0	51 989	19.9	59 596	18.8	63 317	18.4	↓*	1.1-73.6
Pseudomonas aeruginosa	Piperacillin-tazobactam resistance	21 778	18.8	23 242	19.4	24 923	18.2	27 958	16.5	29 286	16.7	↓*	0.0-59.5
	Ceftazidime resistance	22 112	15.9	23 689	16.2	25 393	15.2	28 306	13.9	29 777	13.5	↓*	1.5-56.0
	Carbapenem (imipenem/meropenem) resistance	22 629	18.2	24 082	18.7	25 776	17.5	28 769	15.9	30 142	15.6	↓*	0.0-57.4
	Fluoroquinolone (ciprofloxacin/levofloxacin) resistance	22 489	18.8	23 874	18.6	25 651	17.2	28 536	15.4	30 157	14.9	↓*	2.2-57.7

Bacterial species	Antimicrobial group/agent	2021		2022		2023		2024		2025		Trend 2021 – 2025[a]	2025 EU/EEA country range[b]
		n	%	n	%	n	%	n	%	n	%		
	Aminoglycoside (tobramycin) resistance	14 573	8.9	18 359	8.9	20 266	8.7	22 253	7.1	23 440	6.9	↓*	0.0-50.0
	Combined resistance to ≥3 antimicrobial groups (among piperacillin-tazobactam, ceftazidime, carbapenems, fluoroquinolones and aminoglycosides)	13 720	12.6	17 377	13.4	19 233	12.2	21 085	10.0	22 129	10.0	↓*	0.0-53.8
***Acinetobacter* species**	Carbapenem (imipenem/meropenem) resistance	11 289	40.0	9 442	36.3	9 936	34.5	10 440	31.6	9 845	31.5	↓*	0.0-95.4
	Fluoroquinolone (ciprofloxacin/levofloxacin) resistance	11 183	43.2	9 384	38.8	9 786	36.9	10 196	33.2	9 693	33.9	↓*	0.0-96.5
	Aminoglycoside (gentamicin/tobramycin) resistance	10 955	39.8	9 212	34.2	9 585	31.9	9 763	29.0	9 165	30.0	↓*	0.0-92.3
	Combined resistance to carbapenems, fluoroquinolones and aminoglycosides	10 728	36.9	8 878	31.8	9 370	30.2	9 520	27.0	8 879	27.1	↓*	0.0-91.8
Staphylococcus aureus	MRSA[c]	79 551	16.2	85 625	15.2	87 696	14.9	98 312	14.2	104 483	14.1	↓*	1.8-39.5
Streptococcus pneumoniae	Penicillin non-wild-type[d]	8 490	16.2	13 370	16.3	16 785	15.2	20 068	17.2	23 093	16.4	-	5.1-30.2
	Macrolide (azithromycin/clarithromycin/ erythromycin) resistance	8 784	18.4	14 086	17.9	17 861	17.8	20 933	19.0	23 803	18.5	-	4.0-30.7
	Combined penicillin non-wild-type and resistance to macrolides[d]	8 166	9.8	12 832	9.7	16 147	9.3	19 339	11.0	22 157	10.1	↑*	1.0-18.9
Enterococcus faecalis	High-level gentamicin resistance	16 523	28.9	17 406	25.2	17 510	24.3	19 193	22.5	18 954	22.3	↓*	2.3-62.1
Enterococcus faecium	Vancomycin resistance	22 792	17.0	23 079	17.6	23 619	17.0	26 537	16.5	28 617	17.2	-	0.0-62.2

*[a] ↑ and ↓ indicate statistically significant increasing and decreasing trends, respectively, in the overall data; * indicates confirmation by a significant trend in the data that only includes laboratories reporting continuously for all five years; – indicates no statistically significant trend. NA: not applicable indicates that a significant change in data sources occurred during the period.*

[b] Lowest and highest national AMR percentage among reporting EU/EEA countries (n=30).

[c] MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of mecA *gene by PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

[d] Penicillin results are based on penicillin or, if unavailable, oxacillin. For S. pneumoniae*, the term penicillin non-wild-type is used in this report, referring to* S. pneumoniae *isolates reported by local laboratories as susceptible, increased exposure (I) or resistant (R) to penicillin, assuming MIC to benzylpenicillin above those of wild-type isolates (> 0.06 mg/L). This cut-off is also the EUCAST S-breakpoint for all indications (the R-breakpoint is variable depending on type of infection). The qualitative susceptibility categories (S/I/R) as reported by the laboratory are used, since quantitative susceptibility information is missing for a large part of the data.*

Table 9. ***Escherichia coli*****. Total number of invasive isolates tested (n =151 893)[a] and AMR percentage (%) per phenotype, EU/EEA, 2025**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**67 021**	**44.1**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**48 440**	**31.9**
Aminopenicillins	4 4487	29.3
Fluoroquinolones	3 363	2.2
Other antimicrobial groups	590	0.4
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**16 428**	**10.8**
Aminopenicillins + fluoroquinolones	7 683	5.1
Aminopenicillins + third-generation cephalosporins	5 514	3.6
Aminopenicillins + aminoglycosides	3 080	2.0
Other antimicrobial group combinations	151	0.1
Resistance to three antimicrobial groups		
Total (any three-group combinations)	**12 938**	**8.5**
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	9 452	6.2
Aminopenicillins + fluoroquinolones + aminoglycosides	2 323	1.5
Other antimicrobial group combinations	1 163	0.8
Resistance to four antimicrobial groups		
Total (any four-group combinations)	**6 961**	**4.6**
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	6 839	4.5
Other antimicrobial group combinations	122	0.1
Resistance to five antimicrobial groups		
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	**105**	**0.1**

[a] Only isolates with complete susceptibility information for aminopenicillins (amoxicillin or ampicillin), third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin) were included in the analysis. This represented 73% (151 893/207 898) of all reported E. coli *isolates. If the antimicrobial susceptibility testing (AST) result for third-generation cephalosporins is reported as resistant (R) then resistance to aminopenicillins is assumed even if the AST result is reported as S or I.*

[b] Only AMR combinations >1% of the total are specified.

[c] Not adjusted for population differences in the reporting countries.

[d] Aminopenicillins (amoxicillin or ampicillin), third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin).

Figure 1. ***Escherichia coli.*** **Percentage of invasive isolates resistant to fluoroquinolones (ciprofloxacin/levofloxacin/ofloxacin), by country, EU/EEA, 2025**

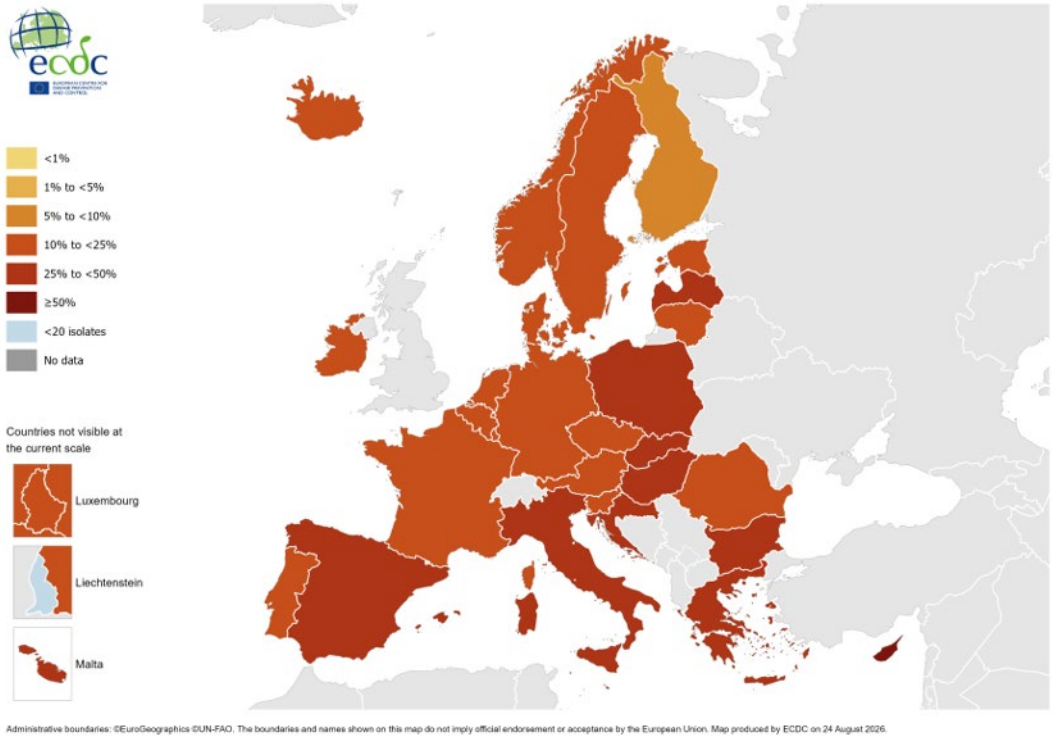


Figure 2. ***Escherichia coli*****. Percentage of invasive isolates resistant to third-generation cephalosporins (cefotaxime/ceftriaxone/ceftazidime), by country, EU/EEA, 2025**

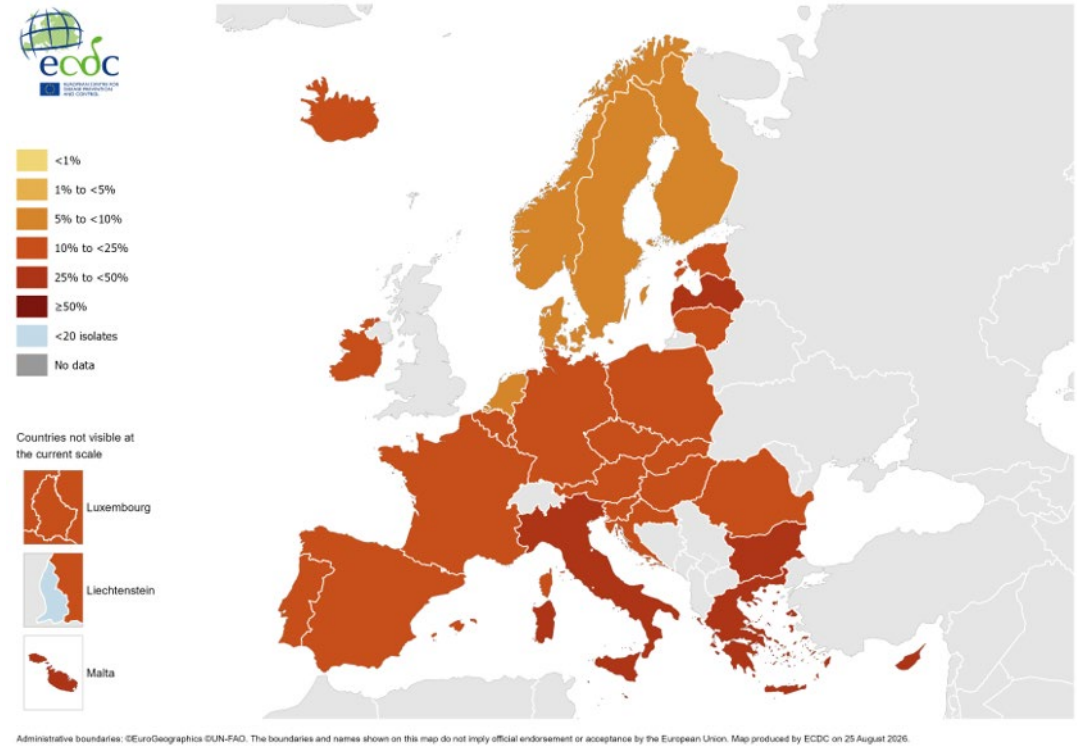


Figure 3. ***Escherichia coli*****. Percentage of invasive isolates resistant to carbapenems (imipenem/meropenem), by country, EU/EEA, 2025**

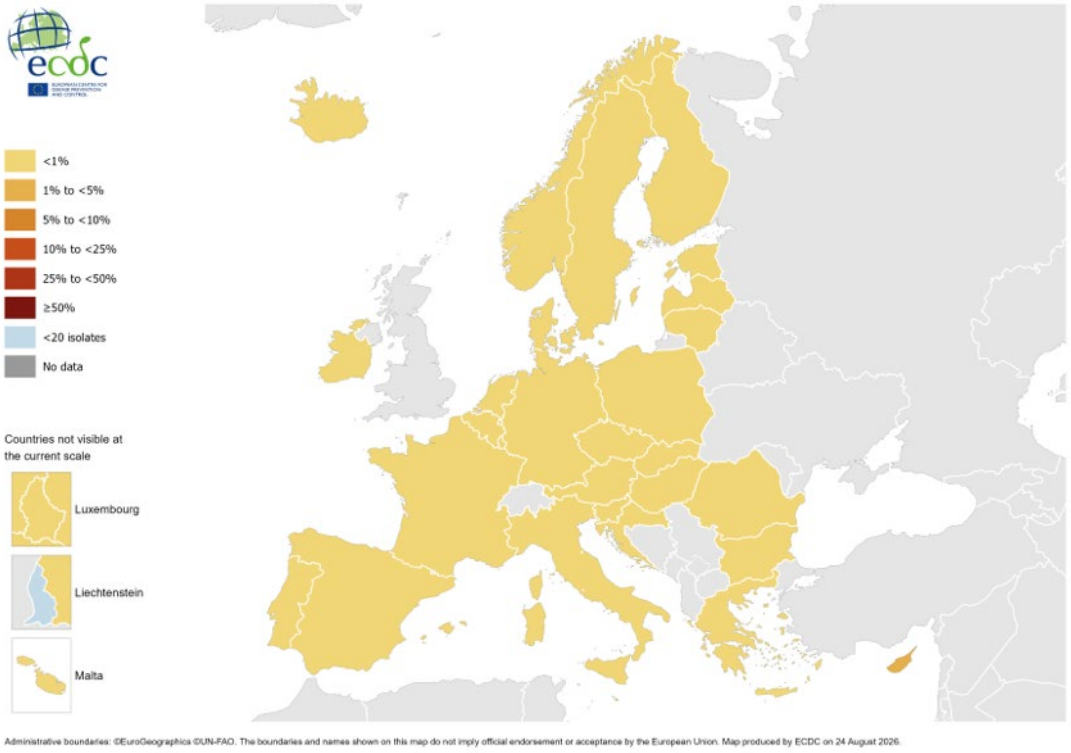


Table 10. ***Klebsiella pneumoniae.*** **Total number of invasive isolates tested (n = 62 068)[a] and AMR percentage (%) per phenotype, EU/EEA, 2025**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups [d]	**38 121**	**61.4**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**5 638**	**9.1**
Third-generation cephalosporins	3 378	5.4
Fluoroquinolones	1 986	3.2
Other antimicrobial groups	274	0.4
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**5 425**	**8.7**
Third-generation cephalosporins + fluoroquinolones	3 891	6.3
Third-generation cephalosporins + aminoglycosides	720	1.2
Other antimicrobial group combinations	814	1.3
Resistance to three antimicrobial groups		
Total (any three-group combinations)	**7 220**	**11.6**
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	5 403	8.7
Third-generation cephalosporins + fluoroquinolones + carbapenems	1 696	2.7
Other antimicrobial group combinations	121	0.2
Resistance to four antimicrobial groups		
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	**5 664**	**9.1**

[a] *Only isolates with complete susceptibility information for third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin) were included in the analysis. This represented 91% (62 068/68 345) of all reported* K. pneumoniae *isolates.*

[b] *Only AMR combinations >1% of the total are specified.*

[c] *Not adjusted for population differences in the reporting countries.*

[d] *Third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin).*

Figure 4. ***Klebsiella pneumoniae*. Percentage of invasive isolates resistant to third-generation cephalosporins (cefotaxime/ceftriaxone/ceftazidime), by country, EU/EEA, 2025**

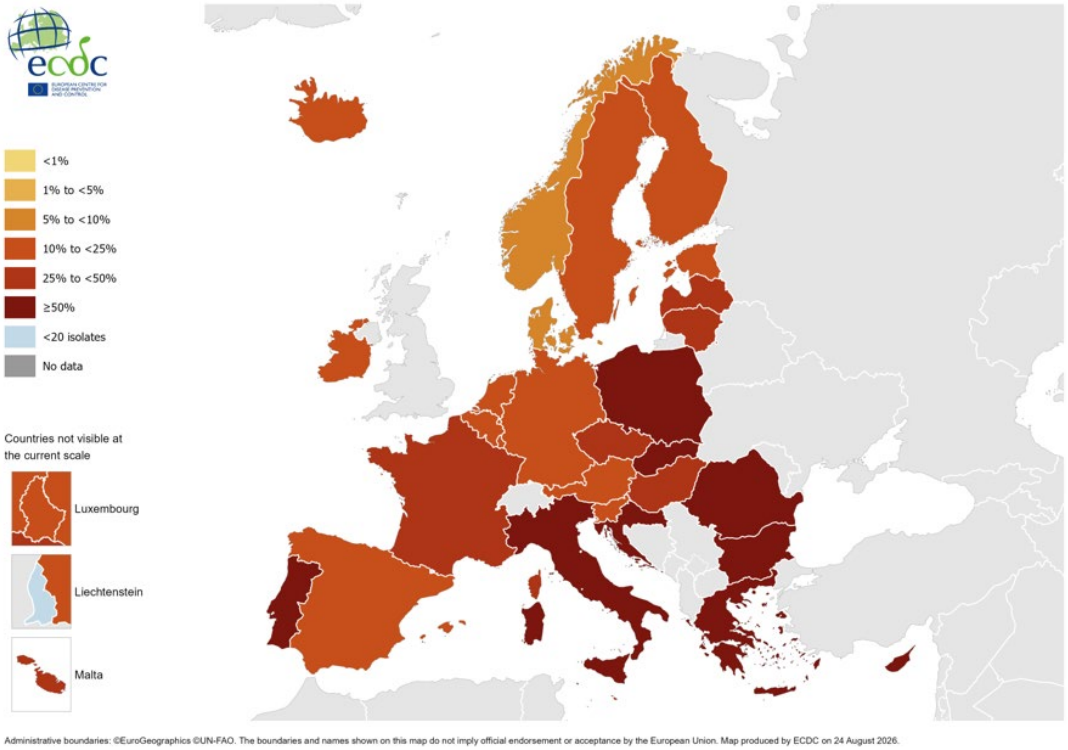


Figure 5. ***Klebsiella pneumoniae*. Percentage of invasive isolates resistant to carbapenems (imipenem/meropenem), by country, EU/EEA, 2025**

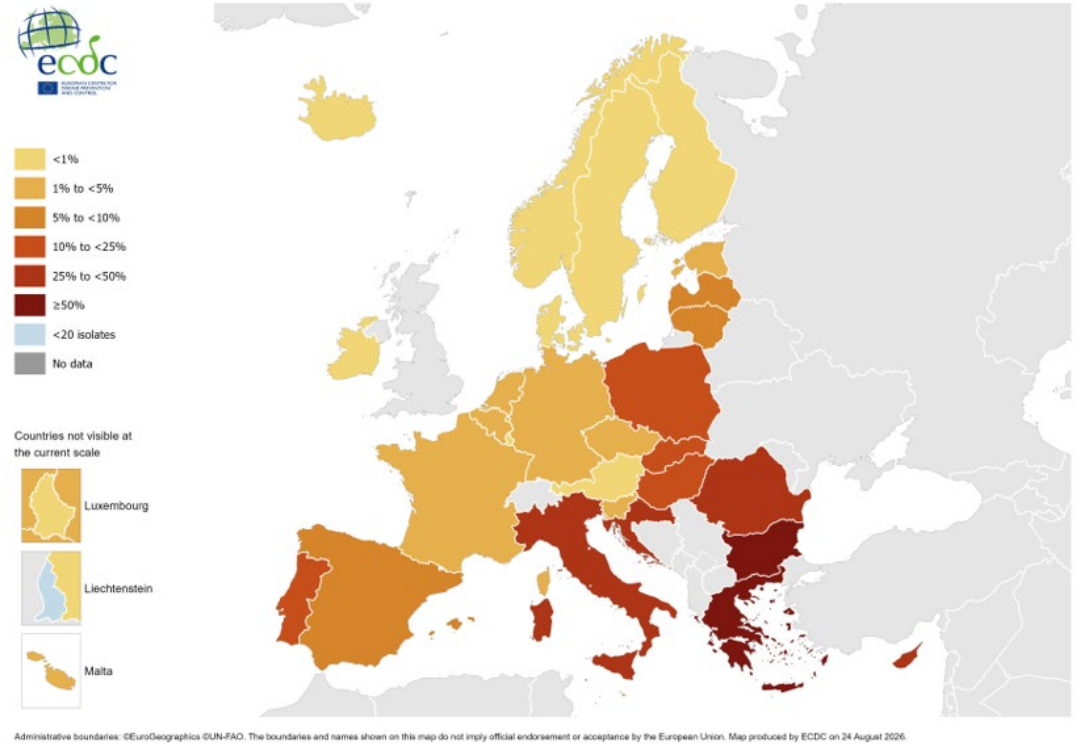


Table 11. ***Pseudomonas aeruginosa.*** **Total number of invasive isolates tested (n =22 162)[a] and AMR percentage (%) per phenotype, EU/EEA, 2025**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**15 626**	**70.5**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**2 738**	**12.4**
Carbapenems	1 174	5.3
Fluoroquinolones	889	4.0
Piperacillin-tazobactam	485	2.2
Other antimicrobial groups	190	0.9
Resistance to two antimicrobial groups		
Total (any two group combinations)	**1 797**	**8.1**
Piperacillin-tazobactam + ceftazidime	985	4.4
Fluoroquinolones + carbapenems	285	1.3
Other antimicrobial group combinations	527	2.4
Resistance to three antimicrobial groups		
Total (any three group combinations)	**761**	**3.4**
Piperacillin-tazobactam + ceftazidime + carbapenems	320	1.4
Other antimicrobial group combinations	441	2.0
Resistance to four antimicrobial groups		
Total (any four group combinations)	**491**	**2.2**
Piperacillin-tazobactam + fluoroquinolones + ceftazidime + carbapenems	291	1.3
Other antimicrobial group combinations	200	0.9
Resistance to five antimicrobial groups		
Piperacillin-tazobactam + fluoroquinolones + ceftazidime + aminoglycosides + carbapenems	**749**	**3.4**

[a] *Only isolates with complete susceptibility information for piperacillin-tazobactam, ceftazidime, carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (tobramycin) were included in the analysis. This represented 72% (22 162/30 675) of all reported* P. aeruginosa *isolates.*

[b] *Only AMR combinations >1% of the total are specified.*

[c] *Not adjusted for population differences in the reporting countries.*

[d] *Piperacillin-tazobactam, ceftazidime, carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (tobramycin).*

Figure 6. ***Pseudomonas aeruginosa*****. Percentage of invasive isolates with resistance to carbapenems (imipenem/meropenem), by country, EU/EEA, 2025**

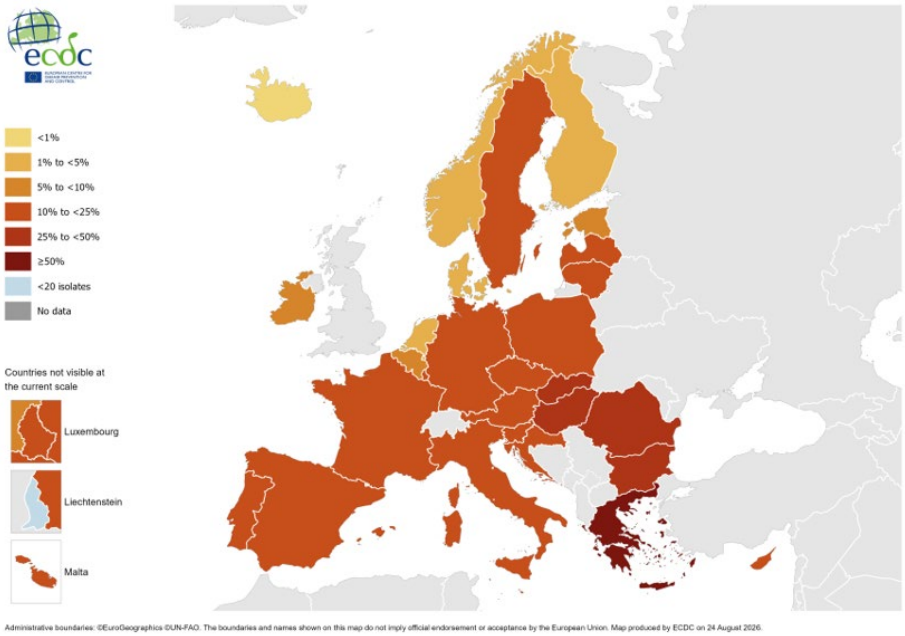


Table 12. ***Acinetobacter*** **species. Total number of invasive isolates tested (n =8 920)[a] and AMR percentage (%) per phenotype, EU/EEA, 2025**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**4 023**	**45.1**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**262**	**2.9**
Aminoglycosides	118	1.3
Fluoroquinolones	114	1.3
Other antimicrobial groups	30	0.3
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**455**	**5.1**
Fluoroquinolones + carbapenems	368	4.1
Other antimicrobial group combinations	87	1.0
Resistance to three antimicrobial groups		
Fluoroquinolones + aminoglycosides + carbapenems	**4 180**	**46.9**

[a] Only isolates with complete susceptibility information for carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (gentamicin or tobramycin) were included in the analysis. This represented 89% (8 920/10 070) of all reported Acinetobacter *spp. isolates.*
[b] Only AMR combinations >1% of the total are specified.
[c] Not adjusted for population differences in the reporting countries.
[d] Carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (gentamicin or tobramycin).

Figure 7. ***Acinetobacter*** **species. Percentage of invasive isolates with resistance to carbapenems (imipenem/meropenem), by country, EU/EEA, 2025**

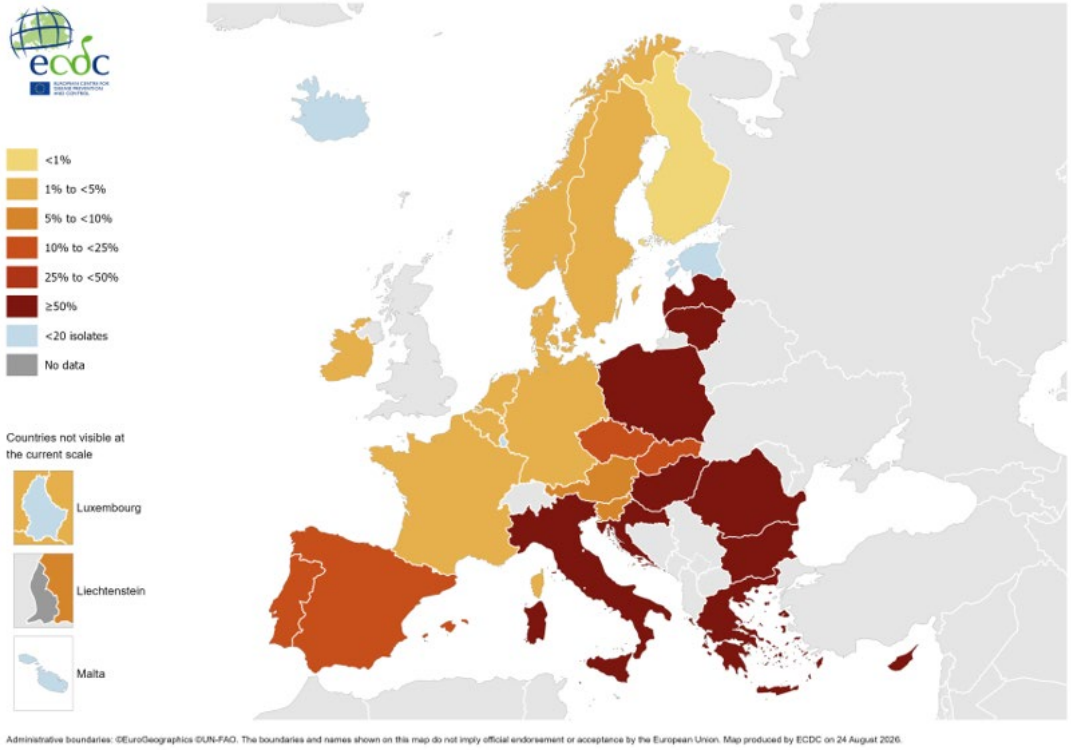


Table 13. ***Staphylococcus aureus.*** **Total number of invasive isolates tested (n =79 996)[a] and AMR percentage (%) per phenotype, EU/EEA, 2025**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**66 955**	**83.7**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**7 052**	**8.8**
Fluoroquinolones	3 295	4.1
Meticillin/MRSA	3 027	3.8
Other antimicrobial groups	730	0.9
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**5 630**	**7.0**
Meticillin/MRSA + fluoroquinolones	5 457	6.8
Other resistance combinations	173	0.2
Resistance to three antimicrobial groups		
Meticillin/MRSA + fluoroquinolones + rifampicin	**359**	**0.4**

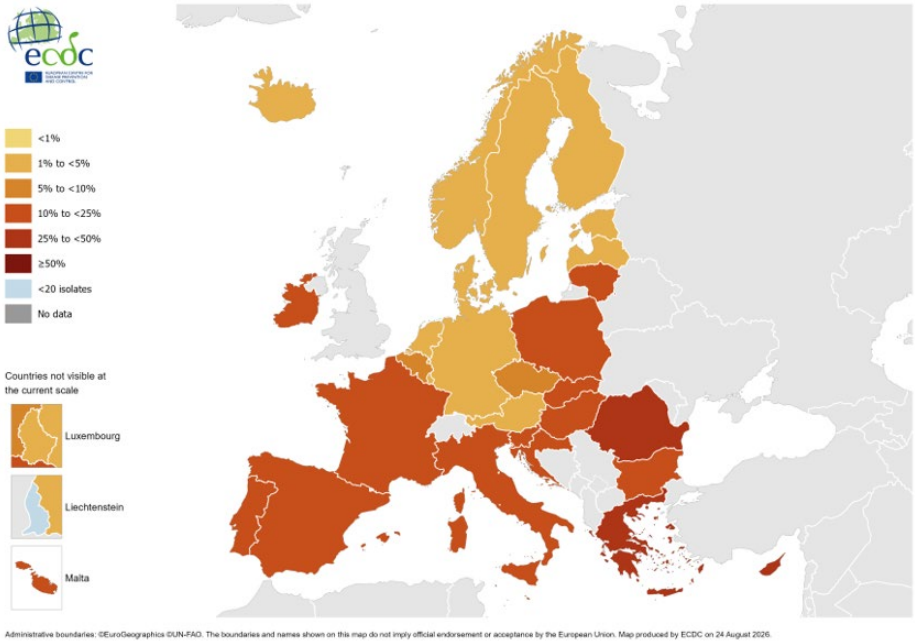
[a] *Only isolates with complete susceptibility information for MRSA, fluoroquinolones and rifampicin were included in the analysis. This represented 74% (79 996/107 904) of all reported* S. aureus *isolates. MRSA is based on AST results for cefoxitin, or if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene by PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA. For fluoroquinolones (ciprofloxacin or levofloxacin) AST results for norfloxacin are also accepted if neither ciprofloxacin nor levofloxacin results are available.*

[b] *Only AMR combinations >1% of the total are specified.*

[c] *Not adjusted for population differences in the reporting countries.*

[d] *MRSA, fluoroquinolones and rifampicin. MRSA is based on AST results for cefoxitin, or if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene by PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA. For fluoroquinolones (ciprofloxacin or levofloxacin) AST results for norfloxacin are also accepted if neither ciprofloxacin nor levofloxacin results are available.*

Figure 8. ***Staphylococcus aureus.*** **Percentage of invasive isolates resistant to meticillin (MRSA)[a], by country, EU/EEA, 2025**



[a] *For EARS-Net, MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene by PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

Table 14. ***Streptococcus pneumoniae.*** **Total number of invasive isolates tested (n = 16 779)[a] and percentage non-wild-type/AMR (%) per phenotype, EU/EEA, 2025**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**13 184**	**78.6**
Single non-wild-type/resistance (to indicated antimicrobial groups)		
Total (any single resistance)	**2 204**	**13.1**
Macrolides	1 224	7.3
Penicillin non-wild-type[e]	923	5.5
Other antimicrobial groups	57	0.3
Non-wild-type/resistance to two antimicrobial groups		
Total (any two-group combinations)	**1 294**	**7.7**
Penicillin non-wild-type + macrolides	1 240	7.4
Other antimicrobial group combinations	54	0.3
Non-wild-type/resistance to three antimicrobial groups		
Total (any three-group combinations)	**75**	**0.4**
Other antimicrobial group combinations	75	0.4
Non-wild-type/resistance to four antimicrobial groups		
Penicillin non-wild-type + third-generation cephalosporins + fluoroquinolones + macrolides	**22**	**0.1**

[a] *Only isolates with complete susceptibility information for penicillins (based on penicillin or, if unavailable, oxacillin), third-generation cephalosporins (cefotaxime or ceftriaxone) and fluoroquinolones (levofloxacin or moxifloxacin - AST results for norfloxacin are also accepted if neither levofloxacin nor moxifloxacin results are available) and macrolides (azithromycin, clarithromycin or erythromycin) were included in the analysis. This represented 67% (16 779/24 891) of all reported* S. pneumoniae *isolates.*

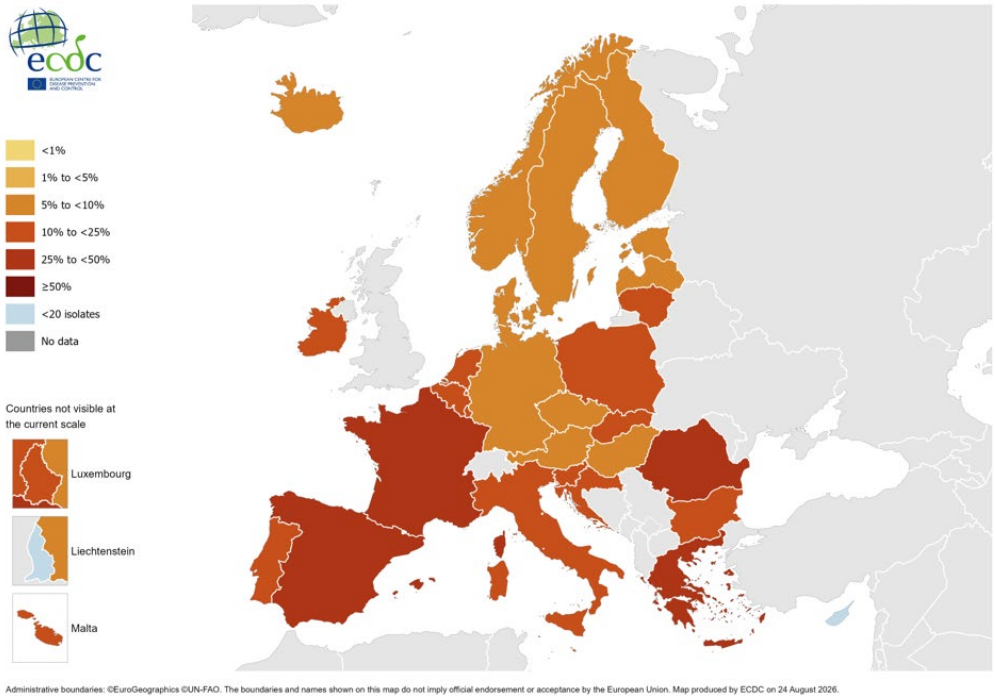
[b] *Only AMR combinations >1% of the total are specified.*

[c] *Not adjusted for population differences in the reporting countries.*

[d] *Penicillins (based on penicillin or, if unavailable, oxacillin), third-generation cephalosporins (cefotaxime or ceftriaxone) and fluoroquinolones (levofloxacin or moxifloxacin - AST results for norfloxacin are also accepted if neither levofloxacin nor moxifloxacin results are available) and macrolides (azithromycin, clarithromycin or erythromycin) were included in the analysis.*

[e] *For* S. pneumoniae*, the term 'penicillin non-wild-type' is used in this report, referring to* S. pneumoniae *isolates reported by local laboratories as 'susceptible, increased exposure' (I) or resistant (R) to penicillin, assuming MIC for benzylpenicillin above that for wild-type isolates (>0.06 mg/L). This cut-off is also the EUCAST S-breakpoint for all indications (the R-breakpoint is variable depending on type of infection). The qualitative susceptibility categories (S/I/R) as reported by the laboratory are used, since quantitative susceptibility information is missing for a large part of the data.*

Figure 9. ***Streptococcus pneumoniae*****. Percentage of penicillin[a] non-wild type[b] invasive isolates, by country, EU/EEA, 2025**



[a] *Penicillin results are based on penicillin or, if unavailable, oxacillin.*

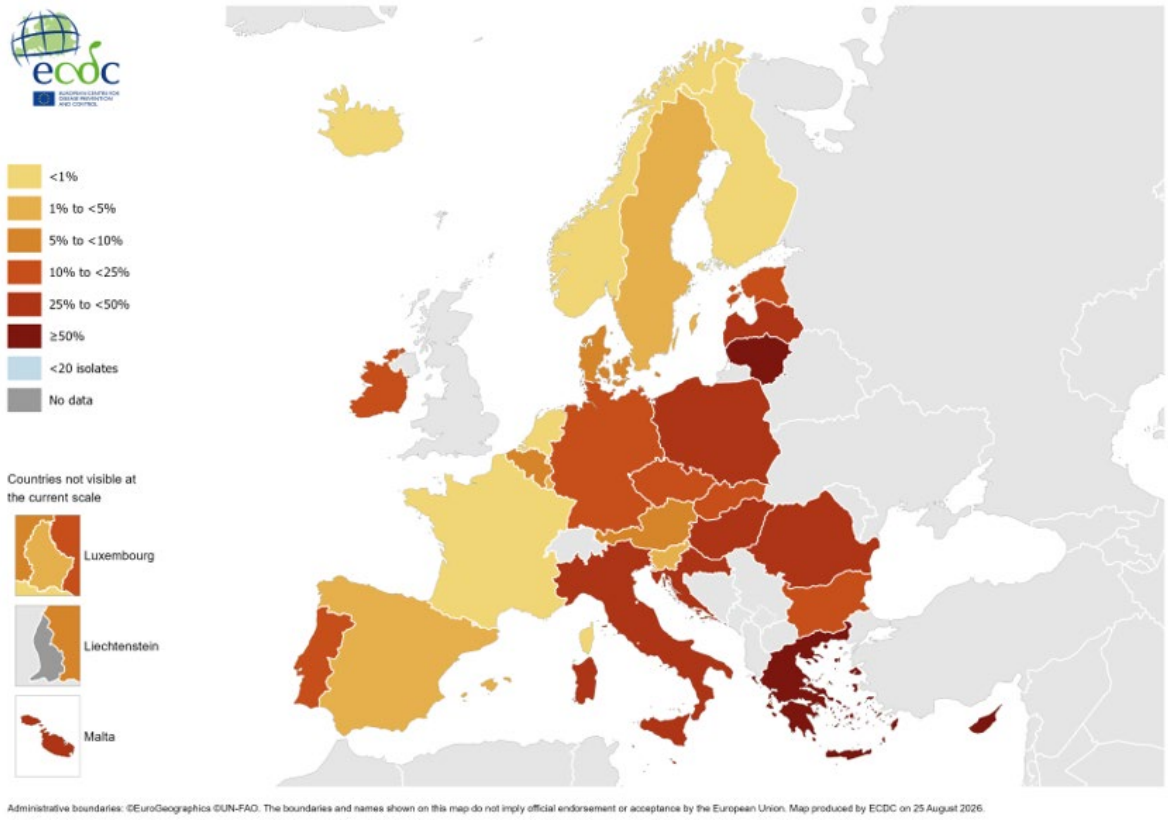
[b] *For* S. pneumoniae*, the term 'penicillin non-wild-type' is used in this report, referring to* S. pneumoniae *isolates reported by local laboratories as 'susceptible, increased exposure' (I) or resistant (R) to penicillin, assuming MIC for benzylpenicillin above that for wild-type isolates (>0.06 mg/L). This cut-off is also the EUCAST S-breakpoint for all indications (the R-breakpoint is variable depending on type of infection). The qualitative susceptibility categories (S/I/R) as reported by the laboratory are used, since quantitative susceptibility information is missing for a large part of the data.*

Table 15. ***Enterococcus faecium.*** **Total number of invasive isolates tested (n = 14 328)[a] and AMR percentage (%) per phenotype, EU/EEA, 2025**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**1 057**	**7.4**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**4 663**	**32.5**
Aminopenicillins	4 549	31.7
Other antimicrobial groups	114	0.8
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**6 790**	**47.4**
Aminopenicillins + gentamicin (high level resistance)	5 624	39.3
Aminopenicillins + vancomycin	1 138	7.9
Other resistance combinations	28	0.2
Resistance to three antimicrobial groups		
Aminopenicillins + gentamicin (high level resistance) + vancomycin	**1 818**	**12.7**

[a] *Only isolates with complete susceptibility information for aminopenicillins (ampicillin or amoxicillin), gentamicin (high-level resistance) and vancomycin were included in the analysis. This represented 49% (14 328/28 994) of all reported* E. faecium *isolates.*
[b] *Only AMR combinations >1% of the total are specified.*
[c] *Not adjusted for population differences in the reporting countries.*
[d] *Aminopenicillins (ampicillin or amoxicillin), gentamicin (high-level resistance) and vancomycin.*

Figure 10. ***Enterococcus faecium*****. Percentage of invasive isolates resistant to vancomycin, by country, EU/EEA, 2025**



Annex 1. Participating institutions

Country	Participating institutions	Web link
Austria	Federal Ministry of Social Affairs, Health, Care and Consumer Protection	www.sozialministerium.at
	Ordensklinikum Linz, Elisabethinen	www.ordensklinikum.at
Belgium	Sciensano	www.sciensano.be
Bulgaria	National Center of Infectious and Parasitic Diseases	https://ncipd.org/index.php?option=com_content&view=featured&Itemid=730&lang=en
Croatia	Reference Center for Antimicrobial Resistance Surveillance University Hospital for Infectious Diseases (Dr Fran Mihaljević), Zagreb	https://bfm.hr/referentni-centar-za-pracenje-rezistencijebakterija-na-antibotike
Cyprus	Microbiology Department, Nicosia General Hospital	https://shso.org.cy/clinic/mikroviologiko
Czechia	National Institute of Public Health	www.szu.gov.cz
	National Reference Laboratory for Antibiotics	https://szu.gov.cz/odborna-centra-a-pracoviste/centrum-epidemiologie-a-mikrobiologie/oddeleni-bakterialni-rezistence-na-antibiotika-a-sbirka-kultur/nrl-pro-antibiotika
Denmark	Statens Serum Institut	https://www.ssi.dk
	Danish Study Group for Antimicrobial Resistance Surveillance (DANRES)	www.danmap.org
Estonia	Estonian Health Board	https://www.terviseamet.ee/et
	East-Tallinn Central Hospital	https://itk.ee
	Tartu University Hospital	https://www.kliinikum.ee/partnerile/uhendlabor
Finland	Finnish Institute for Health and Welfare, Department of Health Security	www.thl.fi
	Finnish Study Group for Antimicrobial Resistance (FiRe)	www.finres.fi
	Finnish Hospital Infection Program (SIRO)	https://thl.fi/en/web/infectious-diseases-and-vaccinations/diseases-and-disease-control/healthcare-associated-infections
France	Santé Publique France	www.santepubliquefrance.fr
	Since 2020:	
	Surveillance and Prevention of Antimicrobial RESistance in hospital settings (SPARES)	https://www.preventioninfection.fr
	National Reference Centre for Pneumococci	www.cnr-pneumo.com
	Up to 2019:	
	French National Observatory for the Epidemiology of Bacterial Resistance to Antimicrobials (ONERBA) through three participating networks:	www.onerba.org
	Azay-Résistance	
	Île-de-France	
	Réussir	
Germany	Robert Koch Institute	www.rki.de
Greece	National Public Health Organization, Central Public Health Laboratory	https://eody.gov.gr/en
Hungary	National Center for Public Health and Pharmacy	www.nngyk.gov.hu
Iceland	National University Hospital of Iceland	https://www.landspitali.is
	Centre for Health Security and Infectious Disease Control	https://www.landlaeknir.is
	Akureyri hospital	www.sak.is
Ireland	Health Protection Surveillance Centre	www.hpsc.ie
Italy	National Institute of Health	www.iss.it
Latvia	Centre for Disease Prevention and Control, Latvia	www.spkc.gov.lv
Liechtenstein	Liechtensteinisches Landesspital	https://www.landesspital.li
	Laboratory Dr Risch[a]	https://www.risch.ch/de
	The Swiss Center for Antibiotic Resistance (ANRESIS)[b]	https://www.anresis.ch

Country	Participating institutions	Web link
Lithuania	National Public Health Surveillance Laboratory	www.nvspl.lt
	Institute of Hygiene	www.hi.lt
Luxembourg	National Health Laboratory	https://lns.lu
	Microbiology Laboratory, Centre Hospitalier de Luxembourg	https://www.chl.lu/fr/service/laboratoire-de-bacteriologie-microbiologie
Malta	Malta Mater Dei Hospital, Msida	https://healthservices.gov.mt/en/MDH/Pages/Home.aspx
Netherlands	National Institute for Public Health and the Environment	www.rivm.nl
Norway	University Hospital of North Norway	https://www.unn.no/fag-og-forskning/norm-norsk-overvakingssystem-for-antibiotikaresistens-hos-mikrober
	Norwegian Institute of Public Health	https://www.fhi.no
	St Olav University Hospital, Trondheim	https://www.stolav.no
Poland	National Medicines Institute, Department of Epidemiology and Clinical Microbiology	https://www.nil.gov.pl
	National Reference Centre for Susceptibility Testing	https://korld.nil.gov.pl
Portugal	National Institute of Health Doutor Ricardo Jorge	https://www.insa.min-saude.pt
	Directorate-General of Health	https://www.dgs.pt
Romania	National Institute of Public Health	www.insp.gov.ro
Slovakia	National Reference Centre for Antimicrobial Resistance	https://www.uvzsr.sk
	Public Health Authority of the Slovak Republic	https://www.uvzsr.sk
	Regional Public Health Authority Banska Bystrica	https://www.uvzsr.sk
Slovenia	National Institute of Public Health	www.nijz.si
	Medical Faculty, University of Ljubljana	https://imi.si
	National Laboratory of Health, Environment and Food	https://www.nlzoh.si
Spain	Health Institute Carlos lll	www.isciii.es
	National Centre for Microbiology	https://cnm.isciii.es
	CIBERinfect	https://www.ciberinfec.es
Sweden	The Public Health Agency of Sweden	www.folkhalsomyndigheten.se

[a] *Liechtenstein uses Laboratory Dr Risch as a participating institution at national level.*
[b] *Liechtenstein uses the Swiss Center for Antibiotic Resistance as a participating institution at national level.*