



UK Health
Security
Agency

English surveillance programme for antimicrobial utilisation and resistance (ESPAUR) report 2024 to 2025

Annexe

Contents

Chapter 2. Antimicrobial resistance	3
Methods and caveats annexe.....	3
Antifungal resistance	16
Antiviral resistance	17
Antiparasitic resistance.....	19
Additional data sources	19
Statistical analyses	20
AMR resources.....	20
Supplementary analyses	21
Chapter 3. Antimicrobial consumption.....	23
Antimicrobial consumption: data sources	23
Classification of prescribing data	24
Denominators	25
Other community settings categories	26
Secondary care data quality	27
Trusts definitions	28
Antiviral consumption	31
Antiparasitic consumption.....	32
Chapter 4. Antimicrobial stewardship.....	33
Chapter 5. NHS England: improvement and assurance schemes	33
Chapter 6. Professional and public education and training	34
Antibiotic Guardian	34
Chapter 7. Research insights and knowledge mobilisation	37
List of publications	37
Chapter 8. ESPAUR oversight group members' activities and actions to tackle AMR – mapping to the National Action Plan	48
Chapter 9. Knowledge mobilisation of ESPAUR report: evaluation of feedback from report users.....	48
References.....	49
About the UK Health Security Agency	50

Chapter 2. Antimicrobial resistance

Methods and caveats annexe

Antibacterial resistance

Data on the antibiotic susceptibility of pathogens causing bacteraemia was obtained from SGSS (Second Generation Surveillance System), a national database maintained by UK Health Security Agency (UKHSA) that contains laboratory data supplied electronically by approximately 98% of hospital microbiology laboratories in England. SGSS comprises 2 modules, a communicable disease reporting (CDR; formerly CoSurv/LabBase2) module and an antimicrobial resistance (AMR; formerly AmSurv) module. The AMR module contains comprehensive antibiogram information as it includes results for all antibiotics tested (including results suppressed from clinical reports) for isolates from all clinical sources. For trends included within this report, resistance data between 1 January 2019 to 31 December 2024 is taken from the AMR module.

Hospital microbiology laboratories have reported antimicrobial susceptibility test results as 'susceptible', 'susceptible, increased exposure' or 'resistant'. These categories were defined as follows as per the European Committee on Antimicrobial Susceptibility Testing ([EUCAST](#)):

1. Susceptible, standard dosing regimen (S): a bacterial strain is said to be susceptible to a given antibiotic when there is a high likelihood of therapeutic success using a standard dosing regimen.
2. Susceptible, increased exposure (I): a bacterial strain is said to be susceptible, increased exposure' when there is a high likelihood of therapeutic success because exposure to the agent is increased by adjusting the dosing regimen or by its concentration at the site of infection.
3. Resistant (R): a bacterial strain is said to be resistant to a given antibiotic when there is a high likelihood of therapeutic failure even when there is increased exposure.

For the whole time period, values are presented with only resistant episodes included in the numerator, as per the definition of susceptibility test results used by the European Committee on Antimicrobial Susceptibility Testing (EUCAST), [updated in January 2019](#). Breakpoints can change over time, and this has implications for interpretation of resistance trends spanning breakpoint changes. See [ESPAUR 2023 to 2024 report box 2.3](#) for further explanation.

As patients may have more than one positive blood culture taken, blood cultures taken from the same patient that yielded growth of the same pathogen during a rolling 14-day period from the initial positive blood culture were regarded as comprising the same episode of infection and were de-duplicated, retaining the worst-case scenario susceptibility result for each antibiotic tested (resistant > intermediate > susceptible). Combining patient results into one infection

episode is limited by the provision of key identifiers by reporting laboratories, so some episodes may be counted more than once if these identifiers enabling grouping and de-duplication are not provided or are provided incorrectly.

Antibiotic groupings used in the bacteraemia antimicrobial susceptibility analyses within the report are shown in [Annexe Table 2.1](#).

Annexe Table 2.1. Antibiotic class groupings

Antibiotic class groupings	Antibiotic
Third-generation cephalosporins	cefotaxime, ceftazidime, cefpodoxime or ceftriaxone, unless otherwise indicated
Carbapenems	meropenem or imipenem, except where neither were tested, in which cases results for ertapenem were used if available; the exception to this is for <i>Pseudomonas spp.</i> where ertapenem was not used
Aminoglycosides	gentamicin or amikacin
Fluoroquinolones	ciprofloxacin, unless otherwise defined
Glycopeptides	vancomycin or teicoplanin
Macrolides	azithromycin, clarithromycin or erythromycin

Data on the incidence of *Escherichia coli* (*E. coli*) and *Staphylococcus aureus* (*S. aureus*) bacteraemia was extracted from the national mandatory surveillance schemes while data on the incidence of other pathogens was derived from cases reported to the AMR module of SGSS. As the latter data was provided on a voluntary basis, case ascertainment will be incomplete.

SGSS and the mandatory surveillance Data Capture System are live reporting databases, and therefore data is subject to change and may differ to other published outputs.

Data on additional bacterial pathogens causing hospital bacteraemia in England can be found in [Chapter 2 data tables](#).

Incidence trends, age and sex distributions and antibiotic resistance trends are presented based on SGSS AMR module data. This data continues the series previously published in separate annual voluntary surveillance bacteraemia reports (published in the Health Protection Report series).

Limitations and caveats

In England, the mandatory surveillance scheme for *E. coli* bacteraemia does not include susceptibility testing data, which is collected through a parallel voluntary laboratory reporting system. Comparison of the incidence reported between the 2 systems indicated that the

ascertainment achieved in the laboratory reporting system was 91% in 2024 (90% in 2023; [Annexe Table 2.2](#)) and varied by local geography across the country (ranging between 75% and 99%; [Annexe Table 2.3](#)).

Annexe Table 2.2. Ascertainment factor applied to estimate total number of resistant bloodstream infections

Year	Mandatory <i>E. coli</i> bacteraemia reports	SGSS AMR <i>E. coli</i> bacteraemia reports	% ascertainment	Ascertainment factor
2019	43,742	37,967	87%	1.152
2020	37,899	31,545	83%	1.201
2021	37,864	32,942	87%	1.149
2022	38,495	33,690	88%	1.143
2023	41,225	37,102	90%	1.111
2024	43,545	39,794	91%	1.094

Annexe Table 2.3. Regional ascertainment factor applied to estimate total number of resistant bloodstream infections 2024

Region	Mandatory <i>E. coli</i> bacteraemia reports	SGSS AMR <i>E. coli</i> bacteraemia reports	% ascertainment	Ascertainment factor
East Midlands	3,761	3,712	99%	1.013
East of England	4,696	4,307	92%	1.090
London	5,793	5,077	88%	1.141
North East	2,650	1,985	75%	1.335
North West	6,367	5,757	90%	1.106
South East	6,767	6,259	92%	1.081
South West	4,210	4,060	96%	1.037
West Midlands	4,496	4,358	97%	1.032
Yorkshire and Humber	4,805	4,274	89%	1.124

Since April 2017 reporting of bacteraemia caused by *Klebsiella* spp. and *Pseudomonas aeruginosa* was also [mandatory](#). Reviews of ascertainment between the mandatory and voluntary surveillance schemes for each pathogen were assessed for 2021 as 83% (*Klebsiella* spp.) and 85%, for *P. aeruginosa*.

Rapid molecular techniques are used to identify the *mecA* gene (meticillin-resistant *S. aureus* (MRSA) indicator) avoiding the requirement to undertake susceptibility testing for isoxazolympenicillins (such as oxacillin). This information is not captured in the SGSS data. [Figure 2.1](#) and [Figure 2.2](#) in the main report present the mandatory surveillance results for MRSA bacteraemia which represents a more accurate burden of MRSA in England. Whereas [Figure 2.9](#) (resistance differences between MRSA and meticillin-susceptible *S. aureus* (MSSA)) is using SGSS AMR data, where MRSA is defined as *S. aureus* reported as resistant to meticillin, oxacillin, ceftioxin or flucloxacillin. The ascertainment factor for *S. aureus* reports in SGSS AMR was 1.111 in 2024.

EUCAST does not provide daptomycin clinical breakpoints for *E. faecium* and *E. faecalis*, but rather lists the breakpoint as 'Insufficient Evidence', in-part due to the dosing regimes which far exceed licensed doses. Although daptomycin is increasingly used for enterococcal bacteraemia and endocarditis, especially in the context of vancomycin resistance, uncertainties remain particularly with the inability of even the highest published doses to achieve adequate exposure against all wild-type enterococcal isolates (1). Although minimum inhibitory concentration (MIC) distributions and epidemiological cut-off values are frequently used to predict likelihood of clinical success, as the local method of susceptibility testing cannot be verified, daptomycin MIC cannot be categorised and therefore caution should be used when interpreting the results.

Estimating the burden of antibiotic-resistant bloodstream infections

Data used to update the pathogen and antimicrobial summaries in the ESPAUR report was utilised to generate a metric of the estimated burden of resistant bacteraemia in England. The total number of resistant infections is generated by calculating the proportion of each pathogen that were reported as resistant to one or more specific antibiotics and ensuring that that infection report is not counted in any subsequent antibiotic combinations to avoid double counting. A full list of pathogen and antibiotic combinations is shown in [Annexe Table 2.4](#). The pathogen and antibiotic combinations used for the ESPAUR AMR burden metric include all of those used to calculate the UK Government's 2024 to 2029 AMR National Action Plan AMR burden metric for human health target 1a, plus additional combinations – the differences between these metrics are detailed in [Annexe Table 2.4](#).

For each year, the ascertainment of cases of *E. coli* bacteraemia reported on a voluntary basis to the AMR module of SGSS was estimated by comparison with mandatory surveillance reports ([Annexe Table 2.2](#)). This value was then applied to the other pathogens under surveillance to estimate the total number of bacteraemia for each pathogen each year (except for *S. aureus*, where the mandatory surveillance totals for both MRSA and MSSA were used). The same method with region-specific numbers was used to calculate the regional AMR burden (regional numbers and ascertainment factors are listed in the [data tables accompanying the report](#)).

For 2024, the AMR burden from bacteraemia was reported by ethnic group and by indices of multiple deprivation (IMD). As the mandatory surveillance scheme does not include ethnicity

and deprivation information, incidence data of all pathogens was derived from cases reported to the AMR module of SGSS.

Annexe Table 2.4. Bacteria and antibiotic resistance categories included in the AMR burden analysis within the ESPAUR report; ESPAUR AMR bacteraemia burden combinations and National Action Plan (NAP) estimate combinations

Bacteria	Antibiotic resistance	ESPAUR AMR bacteraemia burden	NAP estimate AMR burden
<i>Escherichia coli</i>	Carbapenem-resistant	✓	✓
	Third-generation cephalosporin-resistant (excluding isolates also resistant to carbapenems)	✓	✓
	Aminoglycoside-resistant (excluding isolates also resistant to carbapenem and/or third-generation cephalosporin)	✓	
	Fluoroquinolone-resistant (excluding isolates also resistant to carbapenem and/or third-generation cephalosporin and/or aminoglycoside)	✓	
<i>Klebsiella pneumoniae</i>	Carbapenem-resistant	✓	✓
	Third-generation cephalosporin-resistant (excluding isolates also resistant to carbapenem)	✓	✓
	Aminoglycoside-resistant (excluding isolates also resistant to carbapenem and/or third-generation cephalosporin)	✓	
	Fluoroquinolone-resistant (excluding isolates also resistant to carbapenem and/or third-generation cephalosporin and/or aminoglycoside)	✓	
	Carbapenem-resistant	✓	

Bacteria	Antibiotic resistance	ESPAUR AMR bacteraemia burden	NAP estimate AMR burden
<i>Klebsiella oxytoca</i>	Third-generation cephalosporin-resistant (excluding isolates also resistant to carbapenem)	✓	
	Aminoglycoside-resistant (excluding isolates also resistant to carbapenem and/or third-generation cephalosporin)	✓	
	Fluoroquinolone-resistant (excluding isolates also resistant to carbapenem and/or third-generation cephalosporin and/or aminoglycoside)	✓	
<i>Acinetobacter spp.</i>	Carbapenem-resistant	✓	✓
	Aminoglycoside- and fluoroquinolone-resistant (excluding isolates also resistant to carbapenem)	✓	✓
<i>Pseudomonas spp.</i>	Carbapenem-resistant	✓	✓ [*]
	Resistant to 3 or more antimicrobial groups (excluding isolates also resistant to carbapenem)	✓	✓ [*]
<i>Enterococcus spp.</i>	Glycopeptide-resistant	✓	✓ ^{**}
<i>Staphylococcus aureus</i>	Methicillin-resistant	✓	✓
<i>Streptococcus pneumoniae</i>	Penicillin- and macrolide-resistant (excluding isolates only resistant to penicillin)	✓	✓
	Penicillin-resistant (excluding isolates also resistant to macrolides)	✓	✓

* The NAP estimate AMR burden includes *Pseudomonas aeruginosa* only and not other *Pseudomonas* species.

** The NAP estimate AMR burden includes *E. faecalis* and *E. faecium* only and not other *Enterococcus* species.

Acquired carbapenemase-producing Gram-negative bacteria

Acquired carbapenemase-producing Gram-negative organisms (CPO) continue to pose a significant public health concern in terms of threat to global health and economic stability (2).

Carbapenems constitute some of the most effective and broadest-spectrum antibiotics available and are typically reserved for severe and multi-drug-resistant infections. Acquired carbapenemases are enzymes which inactivate carbapenems and most other -lactam antibiotics, including penicillins and cephalosporins, and can result in infections with severely limited treatment options. Many carbapenemase genes are found on mobile genetic elements and are thus easily transferable between species.

The prominent carbapenemase families, termed the 'big 5', and constituting >98% of carbapenemase mechanisms overall, are KPC, NDM, OXA-48-like, VIM and IMP, and are increasingly found in species such as *E. coli*, *K. pneumoniae* and *Enterobacter cloacae* complex. However, novel mechanisms of resistance are increasingly being detected.

Developing local laboratory capacity to detect the 'big 5' carbapenemase families has been a key part of the national response, and a change in referral criteria to the Antimicrobial Resistance and Healthcare Associated Infections (AMRHAI) Reference Unit with a focus on invasive isolates and mechanistic uncertainty in the context of certain resistant determinants, has seen a decrease in nationally referred isolates (presented later in the Chapter).

Data on confirmed CPOs was obtained from both the Antimicrobial Resistance and Healthcare-Associated Infections (AMRHAI) Reference Unit and from the Antimicrobial Resistance (AMR) module of SGSS (see the [Antibacterial resistance methods](#) section for details).

As patients may have more than one positive specimen taken, specimens taken from the same patient that yielded growth of the same pathogen and carbapenem resistance mechanism within a 52-week period from the initial positive specimen were regarded as comprising the same episode of infection and were de-duplicated. CPO positive referred isolates and local laboratory isolates were combined for this de-duplication process, with resistance mechanism results from the AMRHAI Reference Unit retained preferentially where patient specimen overlap occurred. A summary of the distribution of the carbapenemase families covered by the AMRHAI Reference Unit (including those outside the 'big 5' families) is presented in [Annexe Table 2.5](#), below. The local laboratory data presented only includes results from the 'big 5' carbapenemase families.

UKHSA strongly recommends that all diagnostic laboratories should be able to detect the 4 carbapenemase families in bold (the 'big 4'). The following table uses these symbols: ¥ = combinations of mechanism and species would not be considered as exceptional results. A = intrinsic to *A. baumannii* and only expressed when associated with an insertion element; B = almost exclusively reported in *Enterobacter spp.* with less than a handful of reports in other genera; C = reported only in *Serratia marcescens*.

Where an 'exceptional' carbapenemase and species combination result (cells without a ¥ symbol in Annexe Table 2.5) has been identified, isolates should be sent to [AMRHAI Reference Unit](#) for confirmation.

Annexe Table 2.5. Distribution of carbapenemase genes covered by AMRHAI Reference Unit molecular assay (based on AMRHAI data)

Carbapenemase family	Associated with common 'host' organism		
	Enterobacterales	<i>Pseudomonas spp.</i>	<i>Acinetobacter spp.</i>
KPC	¥	<10D	<10D
OXA-48-like	¥	<50E	0
NDM	¥	¥	¥
VIM	¥	¥	<10D
IMP	¥	¥	¥
IMI/NMC-A	¥ B	0	0
GES	¥	¥	<10D
FRI	<10D	0	0
SME	<10 ^C ¥C	0	0
DIM	0	<50E	0
GIM	<10D	<10D	0
SIM	0	<10D	0
SPM	0	<10D	0
OXA-23-like	<50E	0	¥
OXA-40-like	0	0	¥
OXA-51-like ^A	0	0	¥
OXA-58-like	0	0	¥

¥ = combinations of mechanism and genus are not considered exceptional.

B = almost exclusively reported in *Enterobacter* spp. with less than a handful of reports in other genera.

C = reported only in *Serratia marcescens*.

D = fewer than 10 in total ever confirmed by AMRHAI Reference Unit.

E = fewer than 50 in total ever confirmed by AMRHAI Reference Unit

Notification data

Following the inclusion of carbapenemase screening in the notification schedule, a mechanism to combine reference laboratory referrals with local laboratory-confirmed carbapenemases was implemented. Data presented in the Antimicrobial resistance chapter in [the main ESPAUR report](#) includes analyses on counts of combined clinical infection and routine screening samples reported by laboratories using the recommended molecular or immunochromatographic methods to both SGSS and the AMRHAI Reference Unit. This differs slightly from the weekly

case totals included within the causative agents of [notified diseases reports](#) which currently only include local laboratory reports.

For the purpose of the ESPAUR report and for the notification data, specimen reports of a positive CPO fall into 3 specimen type categories: sterile site, 'screening' and 'everything else'. A full list of the specimen types and how they are grouped is available in the [data tables accompanying this report](#), but at a high level:

- sterile site group specimens include blood, CSF and bone and joint specimens
- screening group specimens include faecal, rectal swab, skin swab specimen
- the other specimens include urine, upper respiratory, catheter and lower genital tract specimens

Timeline of CPE activities

The [Antimicrobial Resistance and Healthcare Associated Infections \(AMRHAI\) Reference Unit](#) within UKHSA received and confirmed an increasing number of CPO year-on-year since 2006. Amongst Enterobacterales sent for referral in 2006, 4 were identified as carbapenemase producers compared to more than 4,000 identified in 2018. In response to the observed increase, UKHSA (then Public Health England (PHE)) established an incident control team in 2013 and implemented a number of initiatives aimed at preventing and controlling the spread of CPO.

The timeline of CPO activities included:

- October 2000 – AMRHAI Reference Unit published 'Carbapenemases: a problem in waiting?'
- 2003 – first VIM-producing Enterobacterales (*Klebsiella* sp.)
- 2003 – first IMP-producing Enterobacterales (*Klebsiella* sp.)
- December 2005 – resistance alert issued 'Carbapenem-resistant Enterobacteriaceae'
- November 2007 – first OXA-48-producing Enterobacterales (*K. pneumoniae*)
- January 2008 – first KPC-producing Enterobacterales (*K. pneumoniae*)
- October 2008 – first NDM-producing Enterobacterales (*K. pneumoniae*)
- January 2009 – resistance alert issued 'CPE in the UK: multi-faceted emergence'
- June 2009 – first KPC-producing *K. pneumoniae* identified in Manchester
- July 2009 – resistance alert issued 'CPE in the UK: NDM- β -lactamase: repeated importation from Indian subcontinent'
- mid-2009 – start of KPC outbreak in Manchester
- 2011 – the Health Protection Agency (HPA, forerunner to PHE) and the Advisory Committee on Antimicrobial Resistance and Healthcare Associated Infection (ARHAI) publish guidance on detection, control and treatment of carbapenem resistant infections

- March 2013 – UK Standard for Microbiological Investigation (SMI) for detection of carbapenemases published
- November 2013 – PHE Level 3 Incident Control Team established
- December 2013 – acute trust toolkit for CPE published
- March 2014 – Patient Safety Alert addressing rising trends and outbreaks in CPE
- May 2015 – Electronic Reporting System (ERS) for the enhanced surveillance of carbapenemase-producing Gram-negative bacteria launched
- June 2015 – non-acute and community settings CPE toolkit published
- July 2016 – ERS upgraded to accept carbapenemase producers identified by diagnostic laboratories
- February 2017 – UK component of ECDC-funded ‘European Survey on Carbapenemase-producing Enterobacteriaceae (EuSCAPE)’ project published
- April 2018 – AMRHAI Reference Unit introduce charging for detection of KPC, NDM, OXA-48-like and VIM
- July 2018 – PHE conducts national survey on carbapenemase testing methods performed by diagnostic laboratories
- August 2018 – evaluation of the acute trust toolkit for CPE published
- January 2019 – AMRHAI requests diagnostic laboratories refer only locally-confirmed CPO from sterile sites
- January 2019 – evaluation of the ERS published
- 1 May 2019 – ESR closed
- 1 October 2020 – CPO was made notifiable
- April 2022 – CPE point prevalence survey in intensive care units (ICUs) in England
- September 2022 – update of CPE Framework guidance

Skin or soft tissue infection (SSTIs) in people in prison

Patient postcode from the AMR module of SSGS and patient alternate postcode from the CDR module of SGSS were used to identify adults (those aged 18+ years) in prison. To account for potential delays in updating addresses, this analysis captures those with prison postcodes listed as their postcode at the time of their specimen as well as those that had a non-prison postcode at the time of their specimen but had at least one sample reported into SGSS while registered at a prison postcode between 1 April 2019 and 31 March 2024. The method of identifying the prison population by using postcodes has been employed in other studies (3) and was also validated by using IIS (Immunisation Information system) to cross check the current population identifiable by using prison postcode against the published MoJ population as at September 2024. Whilst it is acknowledged that this may have limitations in identifying the population for example where a postcode may have been wrongly entered or where a site might use more than one postcode, it was the best available method to ascertain cases and can be improved upon in future analyses by matching whole address fields to UPRN SGSS. Isolates recorded as ‘skin’ or ‘wound’ samples in SGSS where either *Staphylococcus aureus* or *Streptococcus* Group A, C, or G were extracted and analysed using 14-day rolling episode grouping and worst-case scenario methodology, as described above. Antibiotics included in the analysis are as described in [Annexe Table 2.6](#).

Annexe Table 2.6. Antimicrobials included in SSTI in prisons analysis

Antimicrobial group	Antimicrobials
Fluoroquinolones	Levofloxacin, delafloxacin, moxifloxacin or ciprofloxacin; exception to this is for Group A streptococci where ciprofloxacin is not used.
Glycopeptides	Vancomycin or teicoplanin
Macrolides	Azithromycin, clarithromycin, or erythromycin

Rates of infection were calculated by dividing the total number of infections over person-years. Mid-year population figures for England broken down by sex were used to calculate the denominators. This was taken from [Ministry of Justice published data](#). The calculation of the rate is made on the basis of person-years, therefore using snapshots in this way, rather than estimating the total number of people who had been in prison during the period is seen as a defensible approach.

Surveillance of antimicrobial resistance in urine isolates

Data on susceptibility of pathogens with specimen group as 'URINE/KIDNEY' was obtained from the SGSS AMR module for this section. Episode grouping using 14-day rolling windows and worst-case scenario methodology was applied, as described above. The figures in this section contain Wilson binomial 95% confidence intervals, which were calculated using the number resistant and the number tested for the organism-antimicrobial combination., these organism-antimicrobial combinations w Proportion of episodes tested was calculated and when <50%, these organism-antimicrobial combinations were presented with shaded bars to denote lower representativeness.

Surveillance of antimicrobial resistance in *Neisseria gonorrhoeae*

Surveillance of antibiotic resistance in *Neisseria gonorrhoeae* is monitored through the Gonococcal Resistance to Antimicrobials Surveillance Programme (GRASP), which comprises a suite of surveillance systems to detect and monitor AMR in *N. gonorrhoeae* and to record potential treatment failures. Trend data is derived from the national sentinel surveillance system, which collects gonococcal isolates from consecutive patients attending a network of 26 participating sexual health services (SHSs) (24 in England, 2 in Wales) over a 2- to 3-month period each year. Gonococcal isolates are referred to the UKHSA sexually transmitted infection (STI) reference laboratory (STIRL) for antimicrobial susceptibility testing and the results are linked to patient demographic, clinical and behavioural data for analysis of antimicrobial susceptibility trends in patient sub-groups.

Surveillance of antibiotic resistance in *Mycoplasma genitalium*

Surveillance of antimicrobial resistance in *M. genitalium* in England is monitored through the *M. genitalium* Antimicrobial Resistance Surveillance (MARS) Programme. Pilot collections for this programme were conducted in 2019 (4) and 2020 (5), before MARS was launched as an annual programme in [2023](#) (6).

From 1 March to 30 June, *M. genitalium*-positive clinical specimens are collected from routine patient care at participating sexual health services (SHSs) and sent to the UKHSA Sexually Transmitted Infections Reference Laboratory. Specimens are tested for molecular markers predictive of macrolide and fluoroquinolone resistance in the *M. genitalium* 23S rRNA and *parC* genes, respectively.

Antimicrobial susceptibility data is combined with enhanced data including demographic data collected as part of routine surveillance from GUMCAD, as well as behavioural and clinical information provided by recruited SHS clinicians.

The MARS programme estimates the prevalence of macrolide and fluoroquinolone resistance and determines the demographic, behavioural and clinical factors associated with resistance.

Tuberculosis

Data for AMR in tuberculosis data for 2001 to 2024 was extracted from the Enhanced Tuberculosis Surveillance system (ETS). More detail on the methods and data sources are described in the [Tuberculosis in England annual report](#).

Critical antibiotic resistance in foodborne bacteria and Extensively drug-resistant *Shigella* spp.

Surveillance of antibiotic resistance in foodborne bacteria is undertaken by the UKHSA [Gastrointestinal Bacterial Reference Unit](#). Antibiotic resistance data for referred samples in England is derived through whole genome sequencing (WGS), identifying genes that confer resistance. Isolates were sequenced using Illumina technologies and antimicrobial resistance was profiled using a mapping-based approach using the in-house processor, [GeneFinder](#). Specific genes that conferred resistance to tetracycline, carbapenems and colistin were investigated *in silico*, without phenotypic confirmation of expression of resistance. Single nucleotide polymorphism (SNP) single linkage clusters were assigned using [SnapperDB](#).

Antifungal resistance

Routine surveillance

Data on the laboratory reports of yeast species from 2019 to 2023 was obtained from UKHSA's SGSS, as described in the [Antibacterial resistance section](#) of Chapter 2. The SGSS CDR module was used to obtain incidence trends of fungaemia (fungal bloodstream infections) and

the species distribution of yeasts, the SGSS AMR module data was used for assessing the antifungal susceptibility.

As previously reported, several taxonomic revisions to species previously classified in *Candida* have been implemented in the period covered by this report. As a result, this report has expanded from *Candida* to include further yeast species causing fungaemia. This may mean rates of fungaemia may not reflect what has been reported in previous reports. A full list of species causing fungaemia identified from SGSS can be found as part of the monomicrobial and polymicrobial data tables included in the [Chapter 2 data tables](#) accompanying this report.

Recent taxonomic changes better reflect true lineages and is significant. For example, *Nakaseomyces glabratus*, unlike most *Candida* species, demonstrates reduced susceptibility to fluconazole. *P. kudriavzevii*, in common with other *Pichia* species, is innately resistant to fluconazole and *Clavispora lusitaniae* sometimes demonstrates the rare phenomenon amongst *Candida* species of innate or emergent resistance to amphotericin B.

In previous [ESPAUR reports](#), hospital microbiology laboratories antifungal susceptibility test results were grouped into 'reduced-susceptibility'. For the purpose of this report, antifungal susceptibility test results reported as 'susceptible', 'intermediate' or 'resistant', as determined locally, are presented alongside a proportion that are resistant.

The breakpoint criteria for categorising clinical isolates as susceptible, intermediate or resistant to individual antifungals have changed over time, the classification presented is the same as at the time of the specimen and has not subsequently been adjusted. Antifungal resistance for yeast species is focused on 3 antifungal drugs (amphotericin B, caspofungin and fluconazole). These drugs represent 3 different classes of antifungal drug and are the most frequently tested for and used.

As patients may have more than one positive blood culture taken, blood cultures taken from the same patient that yielded growth of the same pathogen during a rolling 14-day period from the initial positive blood culture were regarded as comprising the same episode of infection and were de-duplicated.

Antiviral resistance

Influenza virus

UKHSA screens influenza virus positive samples for mutations in the virus neuraminidase (NA) and the cap-dependent endonuclease (PA) genes, which are known to confer neuraminidase inhibitor or baloxavir resistance, respectively. The samples are primarily obtained for surveillance; however, diagnostic testing is also performed on patient samples with a suspected antiviral-resistant strain.

Influenza virus susceptibility to the neuraminidase inhibitor class of antivirals has been monitored routinely in the UK since 2005 using a combination of phenotypic and genotypic testing. The current influenza antiviral susceptibility surveillance strategy is a genotypic only approach.

Results are reported in the [National flu and COVID-19 surveillance reports: 2024 to 2025 season](#) during the active influenza season and summarised in the [influenza annual report](#) for each flu season.

[UKHSA guidelines for treatment and prophylaxis of Influenza virus](#)

Human immunodeficiency virus (HIV)

The detection of HIV resistance in drug-naïve people indicates the transmission of drug-resistant variants, an important occurrence which limits first-line regimen options. Tracking drug resistance in the treatment-experienced population provides an insight into the causes of treatment failure. HIV sequences generated as part of routine clinical care by the UKHSA and NHS laboratories are collected by the UK HIV Genomics Database at UKHSA. This Database, previously called the UK HIV Drug Resistance Database, was hosted by University College London until 2019, but was moved to UKHSA in 2024 and aims to provide regular updates on HIV drug resistance. The data used here comes from 2 UKHSA labs, which perform HIV genotyping on behalf of multiple hospitals across the UK, and have contributed data up to 2024. We are still in the process of collecting data from other NHS labs from 2020 onwards, following the Database relaunch at UKHSA.

Hepatitis C virus (HCV)

Recommended first line Direct Acting Antiviral (DAA) combinations in the UK usually contain an NS5A inhibitor with either an NS5B polymerase inhibitor or NS3 protease inhibitor. Two antiviral combinations are available with activity against almost all viral strains common in the UK, sofosbuvir-velpatasvir and glecaprevir-pibrentasvir. The success of DAA drug roll-out underpins the UK's commitment to WHO HCV elimination targets.

Testing for HCV drug resistance is not universally recommended prior to initiating DAA therapy, as there is no or minimal impact of resistance on cure rates in DAA-naïve individuals in many scenarios. The European Association for the Study of the Liver (EASL) and the American Association for the Study of Liver Diseases (AASLD) have produced guidelines on particular scenarios when resistance testing may be considered or recommended. There is currently no role for phenotypic resistance testing in clinical management, as this is costly, laborious and available only within research contexts.

There is no national database of HCV resistance in the UK. However, the UKHSA Antiviral Unit provides a HCV genotyping and resistance testing service for the NHS. Since 2019, resistance testing has been carried out by whole genome sequencing, which identifies the viral genotype and subtype, as well as the resistance profile of the NS3, NS5A and NS5B genes, in a single

test. UKHSA also coordinates the English HCV Treatment Registry which contains information on treatment status that is whether DAA-naïve or previously exposed to DAAs, and can be linked to HCV sequence data.

Antiparasitic resistance

As part of the surveillance and resistance monitoring functions of the UKHSA Malaria Reference Laboratory (MRL) suspected treatment failure in cases of imported malaria is investigated by molecular genotyping of parasite genes implicated in reduced antimalarial susceptibility. Additional *in vitro* drug susceptibility testing of a subset of imported parasite infections is provided by colleagues in the malaria research laboratories at the London School of Hygiene and Tropical Medicine. Artemisinin combination therapy (ACT) consists of a member of the rapid-acting artemisinin family of compounds plus a partner drug from a different chemical class with a longer-half-life.

Additional data sources

Population data used in the chapter was taken from the Office for National Statistics annual [mid-year population estimates](#) published data for the corresponding geographic region and year. Geographies were assigned to infection episodes based on patient postcode where available, where not available the reporting laboratory postcode was used. The postcodes were then assigned to regions or Integrated Care Boards and presented at this level. The number of infection episodes with a reported 'ZZ' postcode, indicating no fixed abode, was 1,490 (0.3% of total episodes) between 2019 and 2024.

A [SPINE trace](#) was performed on records of patient episodes to identify those with reported 30-day all-cause mortality. Case fatality rates were calculated at 30 days in line with the [30 day all-cause mortality following MRSA, MSSA and Gram-negative bacteraemia and C. difficile infections, 2022 to 2023 report](#) protocol. Gram-negative bacteraemia case fatality rates includes *K. pneumoniae* only and not other *Klebsiella* species.

The [index of multiple deprivation](#) (IMD) is a way of summarising how deprived a particular geographical area is based on a set of factors that includes levels of income, employment, education and levels of crime within that area. Episodes were linked to IMD using patient postcode (or GP or laboratory postcode where patient postcode was unavailable) and the IMD quintile score was identified by the lower super output area in which the patient resided.

The [Office for Health Improvements and Disparities](#) developed a method for [assigning ethnic group](#) based on hospital admissions data. As different ethnicities may be recorded in different treatment episodes, the method selected a single ethnic group from a patient's HES records. Episodes were linked to ethnic group using patient NHS number and date of birth.

Statistical analyses

P-values were calculated to assess the change in resistance over time, these were generated using an unadjusted binomial regression model for each drug and bug combination. A significant change is defined by a p-value less than 0.05 ($p < 0.05$).

Trends in incidence and resistance are shown at national, regional and IMD quintile level for England. Incidence rates are calculated per 100,000 population per year using the Office for National Statistics [mid-year population estimates](#). At the time of writing, 2024 estimates were not yet available and therefore 2023 was used as a proxy for 2024.

Binomial confidence intervals were calculated to 95% for the percentage resistance for the ethnic group analysis.

To enable fairer comparisons between ethnic groups and IMD quintiles, direct standardisation was used to adjust for the known differences in the age and sex distribution of the population in England. Age-sex specific weights were calculated using [mid-year population estimates](#) (the 'standard population') and applied to the crude age-sex stratum-specific rates. The age-sex standardised rates represent the rates that would be observed if all populations within ethnic groups and IMD quintiles had the same demographic structure as the standard population. These rates were produced using the [dstdize](#) command in Stata.

Analyses were completed using Stata v15/v17 (StataCorp) and RStudio (R version 4.4.0).

AMR resources

This will group together the locations and names of other AMR-relevant publications that UKHSA and others produce to help people know that there is more information available, including:

- [Antimicrobial resistance | UKHSA data dashboard](#)
- [quarterly reports on acquired carbapenemase-producing organisms identified in human samples in England](#)
- [Mycoplasma genitalium antimicrobial resistance surveillance \(MARS\)](#)
- [Gonococcal resistance to antimicrobials surveillance programme report](#)
- [Notifications of infectious diseases \(NOIDs\)](#)
- [Escherichia coli \(E. coli\): guidance, data and analysis](#)
- [Pseudomonas aeruginosa: guidance, data and analysis](#)
- [Klebsiella species: guidance, data and analysis](#)
- [Clostridium difficile: guidance, data and analysis](#)
- [Staphylococcus aureus: guidance, data and analysis](#)
- [MRSA, MSSA, Gram-negative and CDI quarterly report \(official statistics\)](#)

- [MRSA, MSSA, Gram-negative bacteraemia and CDI; independent sector \(annual official statistics\)](#)
- [Laboratory surveillance of paediatric bloodstream infections and antimicrobial resistance in England](#)
- [Pyogenic and non-pyogenic streptococcal bacteraemia annual data from voluntary surveillance](#)
- [Fingertips public health UKHSA data: AMR local indicators](#)
- [Third UK One Health Report: joint report on antibiotic use, antibiotic sales and antibiotic resistance](#)
- [Point prevalence survey of healthcare-associated infections and antimicrobial use in European acute care hospitals 2016 to 2017](#)
- [Central Asian and European Surveillance of Antimicrobial Resistance \(CAESAR\) data](#)
- [GLASS \(Global Antimicrobial Resistance and Use Surveillance System\) AMR routine data surveillance](#)
- [podcast: Infection Control Matters on Apple Podcasts](#)
- [the European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2021 to 2022](#)
- [Tuberculosis in England: national quarterly reports](#)
- [TB diagnosis, microbiology and drug resistance in England](#)
- [Enteric fever \(typhoid and paratyphoid\) England, Wales and Northern Ireland](#)
- [National flu and COVID-19 surveillance reports: 2022 to 2023 season](#)

Supplementary analyses

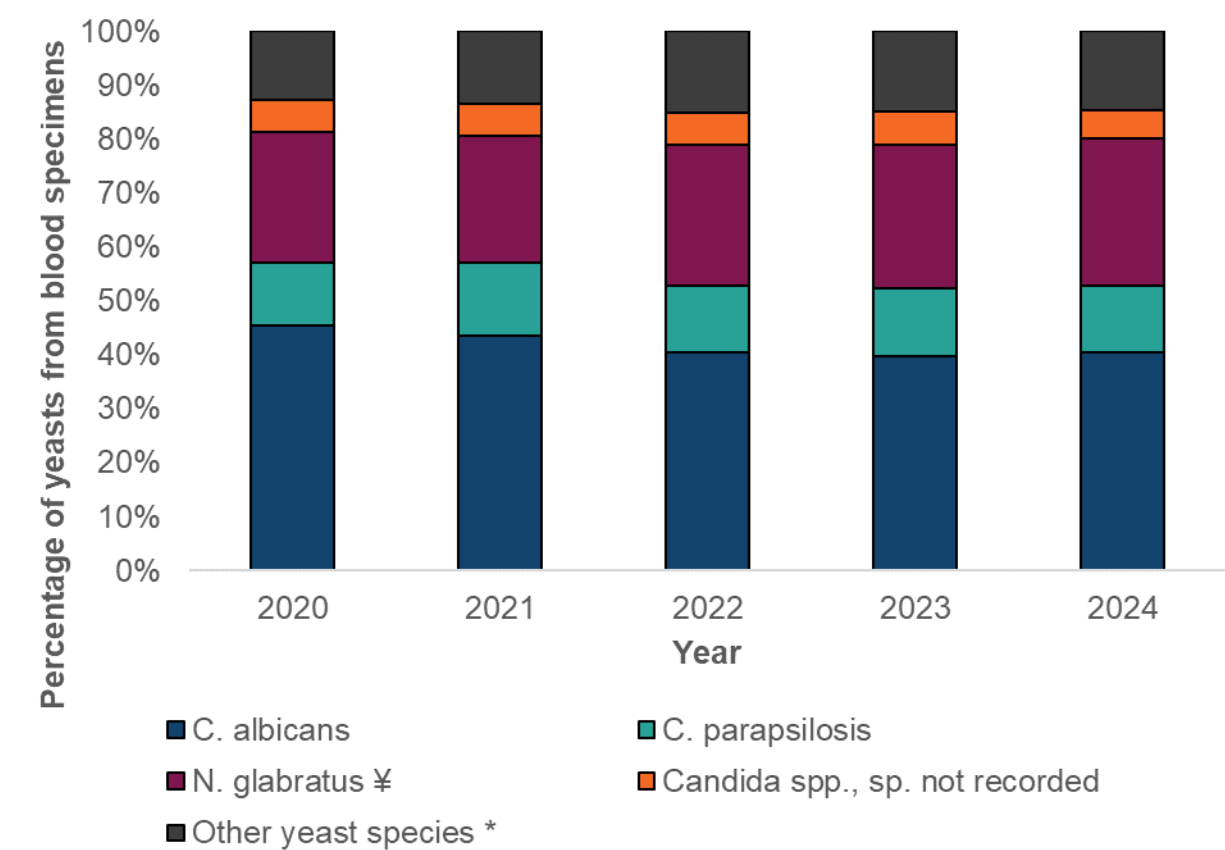
Antifungal resistance

[Incidence of fungaemia by region, and species frequency](#)

[Annexe Figure 2.1](#), below, shows *Candida albicans* was the most frequently isolated yeast species across the 5-year period, accounting for 40% of fungaemia in 2024 (909 out of 2,247). In common with many other surveillance studies the second most frequently reported species was *Nakaseomyces glabratus* (formerly *Candida glabrata*), which was identified in 27% (611) of fungaemia episodes in 2024.

Regionally, variation in incidence of fungaemia can be seen. The region with the highest rate of fungaemia in 2024 was the North West (4.6 per 100,000 population). The lowest recorded rate was the South East (3.1 per 100,000 population). Further regional data for incidence from 2020 to 2024 can be found in the 'Laboratory surveillance of fungaemia due to yeasts in England: 2024' Health Protection Report.

Annexe Figure 2.1. Reports of yeasts from blood isolates by species, 2020 to 2024



¥ Nakaseomyces glabratus (formerly Candida glabrata)

* for all other yeast species and genera please see the [Chapter 2 data tables accompanying this report](#)

Chapter 3. Antimicrobial consumption

All data presented in this chapter in tables can be accessed in the 'Chapter 3 data tables' and all figures can be accessed via the downloadable slide set, both available from [the ESPAUR report web page](#).

Antimicrobial consumption: data sources

Primary care

Information on prescribing of antimicrobials in the community was obtained from the UKHSA Antibiotic Prescribing Data Warehouse, a project initiated by the ESPAUR Oversight Group. Data is sourced from the NHS Digital database and are extracted each month as a snapshot in time from the GP Payments system.

Age group data for primary care was obtained from ePACT2 from NHS BSA.

Primary care prescribing data includes antimicrobials prescribed from general practice and other community settings such as out-of-hours services and walk-in centres. The full list of primary care prescribing settings is provided in [Annex table 3.1](#).

Secondary care

Information on the use of antimicrobials in secondary care was obtained from IQVIA (formerly QuintilesIMS, formed from the merger of IMS Health and Quintiles). The database held by IQVIA contains information from 99% of NHS hospital pharmacy systems for drugs dispensed to individual patients and wards.

Data from all NHS acute trusts was included and organisational changes is reflected up to the latest year of data provided in the report. Trusts can amend their prescribing data for up to a period of 2 years, hence data for the last 2 years is provisional and is subject to change.

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Dental care

Information on the use of antibiotics prescribed in NHS dental surgeries was obtained from NHS BSA through a data request.

Private care

Information on the use of antimicrobials in the private sector obtained from IQVIA. The data held by IQVIA comprises the following settings:

Sales into Private Hospitals and Private Pharmacies from IQVIA Supply Chain Manager (SCM). This dataset captures the flow of medicines from manufacturers through wholesalers to outlet locations. The data specifically includes sales into private hospitals and private pharmacies only. It excludes products supplied directly by some manufacturers or distributed via Third Party Logistics (3PL) providers. The sales into private pharmacies data includes sales into those pharmacies that dispense purely private medications and do not have a contract to dispense NHS prescriptions.

Private Prescriptions Dispensed in Community Pharmacy from IQVIA Prescription Based Services (PBS). This dataset reflects medicines dispensed to patients in community pharmacies based on private prescriptions, as recorded in Patient Medical Record (PMR) systems. It excludes medicines dispensed under NHS-reimbursed FP10 prescriptions. The Private Prescriptions Dispensed in Community Pharmacy includes pharmacies that have a contract to dispense NHS prescriptions but also from time to time may dispense private prescriptions. This includes small, medium and large chains as well as independent pharmacies.

Private Usage within NHS Hospitals from IQVIA Hospital Pharmacy Audit (HPA). This dataset provides information on medicines dispensed in NHS hospital settings, based on data from hospital pharmacy stock control systems. The data is limited to medicines issued by private wards within NHS hospitals and is dependent on accurate recording by hospital pharmacy teams.

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Classification of prescribing data

The classification of antimicrobials for this report is based on the Anatomical Therapeutic Chemical / Daily Defined Dose (ATC/DDD) index 2023 managed by the World Health Organization (WHO) at [Collaborating Centre for Drug Statistics Methodology](#).

Data for antibiotics covered all agents in the ATC group 'J01', (antibiotics for systemic use) and 4 additional oral agents outside the 'J01' group used to treat *Clostridioides difficile* infections, fidaxomicin (A07AA12), metronidazole (P01AB01), tinidazole (P01AB02) and vancomycin (A07AA09).

Data for antifungals covered all agents in the ATC group 'J02', (antimycotics for systemic use) and one additional systemic antifungal outside the 'J02' group, terbinafine (D01BA02).

Third level pharmacological sub-grouping within ATC group 'J01'

Penicillins ('beta-lactam antibacterials, penicillins') include extended-spectrum penicillins, beta-lactamase sensitive and resistant penicillins, and beta-lactamase inhibitors either alone or in combination with penicillins.

'Other beta-lactam antibacterials' includes cephalosporins, carbapenems, and monobactams. Anti-*Clostridioides difficile* (formerly *Clostridium difficile*) agents include: oral vancomycin (ATC code: A07AA09) and fidaxomicin (ATC code: A07AA12). Oral metronidazole (ATC code: P01AB01) has been separated from this group, as opposed to previous years, following feedback from stakeholders.

'Other antimicrobials' (ATC 3rd level pharmacological subgroup 'J01X') includes glycopeptides, polymyxins, steroid antibacterials, imidazole derivatives, nitrofurans derivatives, and other antimicrobials: fosfomicin, methenamine, linezolid, daptomycin and tedizolid.

The broad-spectrum antibiotics includes Co-amoxiclav J01CR02, Cefaclor J01DC04, Cefadroxil J01DB05, Cefalexin J01DB01, Cefixime J01DD08, Cefotaxime J01DD01, Cefoxitin J01DC01, Cefpodoxime J01DD13, Cefradine J01DB09, Ceftazidime J01DD02, Ceftriaxone J01DD04, Cefuroxime J01DC02, Cefazolin J01DB04, Cefotaxime J01DD01, Ceftazidime/avibactam J01DD52, Cefepime J01DE01, Ceftaroline fosamil J01DI02, Ceftobiprole medocaril J01DI01, Ceftolozane/tazobactam J01DI54, Ofloxacin J01MA01, Ciprofloxacin J01MA02, Norfloxacin J01MA06, Levofloxacin J01MA12, Moxifloxacin J01MA14

ATC and DDD methodology

The ATC system aims to identify the active therapeutic ingredient of all human medicines and assigns drugs a measure of use known as the DDD, which is the assumed average maintenance dose per day for a drug used for its main indication in adults. It is important to note however that while the DDD is used as a unit of measurement of drug use, it does not necessarily reflect the recommended or prescribed daily doses used in practice as therapeutic doses for individual patients may vary depending on characteristics such as age, weight, ethnic differences, type and severity of disease and pharmacokinetic considerations.

Denominators

Mid-year populations (inhabitants) for each year were extracted from the [Office for National Statistics](#) (ONS). Hospital admission data for each year was extracted from [Hospital Episode Statistics](#) (HES) from NHS Digital. Please note that population estimates for 2023 were used as a proxy for the 2024 data, as data at the time of extraction was available only for 2023. Similarly HES 2023 admissions were used as a proxy for 2024.

In addition, hospital admissions by speciality were extracted from NHS digital for the financial year 2022 to 2023. Where antibiotic use in NHS acute hospital trusts has been calculated by

speciality, measured using hospital admissions as the denominator, data (both numerator and denominator data) has not been included for 11 trusts, as outline in the data quality section below. Please note that admissions by speciality are usually published annually by NHS Digital, 2022 to 2023 data was the latest available at the time of reporting.

Other community settings categories

Annexe Table 3.1. Mapping of community settings to the setting categories used within the report

Other community settings	Setting category
Walk-in centre	Walk-in centre
Out-of-hours	Out-of-hours
WIC and OOH practice	Out-of-hours
Public health service	PH service
Community health service	Community service
Hospital service	Hospital
Optometry service	Other
Urgent and emergency care	Urgent care
Hospice	Hospice
Care home or nursing home	Nursing home
Border Force	No data reported
Young offender institution	Custody
Secure training centre	No data reported
Secure children's home	Custody
Immigration removal centre	Custody
Court	No data reported
Police custody	No data reported
Sexual assault referral centre	Other
Other: justice estate	No data reported
Prison	Custody
Secure Training Centre	Other
Other	Other

Secondary care data quality

Lack of data quality and completeness originating from both the secondary care dispensing and hospital admission data were identified. These data quality issues pertained to several trusts and where not addressed, would have otherwise impacted the comparability over the time period of secondary care consumption.

It was estimated that the 2019 to 2024 totals for England were missing data for approximately 1.3% of DDDs, and approximately 0.4% of hospital admissions. This should be taken into consideration when interpreting trends in this report.

Common issues affecting data quality and completeness include the migration to new electronic patient record systems affecting admissions and pharmacy dispensing data flow, other notable anomalies have resulted from changes to admission coding. An outline of the trust-specific issues that have been identified is provided below.

Dispensing data completeness and accuracy

There are several acute teaching trusts where data are largely incomplete in the pharmacy dispensing database. One trust is missing an approximate 250,000 DDDs per year in 2021 and 2022. A second trust is missing approximately 1.25 million DDDs per year in 2023 and 2024. A third trust is missing approximately 1.5 million DDDs per year in 2024. A fourth is missing approximately 1.2 million DDDs in 2024. A fifth trust is missing approximately one million DDDs per year in 2020 and 2021. As these trusts account for a large proportion of the acute teaching DDDs, the decision was made to include these trusts DDDs. However, for those metrics calculated per 1,000 hospital admissions, and the period had missing DDDs, the equivalent trusts admissions data was also excluded. A final acute teaching trust was removed entirely from analysis following termination of their data flow to IQVIA.

Dispensing and admissions data completeness and accuracy

Due to technical issues, one acute large-sized trust was unable to submit hospital admissions data between July 2022 and March 2023. Data is also missing from this trust in the pharmacy dispensing database for 2023. Proxy hospital admissions data has been calculated for this trust for the affected months, using the mean hospital admissions for each respective month from unaffected same months across the 5-year period report period. Proxy hospital admissions data was calculated for this trust by averaging the admissions for each month from 2019 to present. The average for each month was then applied to the relevant month affected during the July 2022 to March 2023 period. Where the dispensing data for this trust is missing, the admissions data has been excluded during those months.

Admissions data completeness and accuracy

From April 2021, there was a change to how NHS Digital reported patient admissions data. This meant that day-case patients at an acute specialist trust were included in the admissions data, leading to a significant increase in the total number of admissions observed for this trust. Admissions subsequently returned to pre-April 2021 rates, as of April 2023. This had a significant effect on the trends for those metrics which are calculated per 1,000 hospital admissions for this trust, therefore a proxy measure was used for the affected period. This was calculated by averaging admissions for each month from 2019 to present (admissions for this trust remained stable throughout the COVID-19 pandemic and are thus included). The average for each month was then applied to the relevant month affected during the April 2021 to March 2023 period.

A small acute trust has seen a decline in admissions across 2023 and 2024, affecting an estimated 18,000 admissions. It is believed this is due to a change in the coding of same day emergency care contacts. A proxy for the affected months has been applied using data from the previous unaffected year.

A medium acute trust were missing admissions from July to December of 2024, the reasons for which are unclear. A proxy for the affected months was applied for the respective months using data from 2023.

A small acute trust saw a decline in their admissions from 2022 to 2023 affecting an estimated 48,000 admissions. A monthly proxy was applied using data from the previous unaffected year. For secondary care metrics reporting admissions data by consultant speciality, the admissions data as provided by NHS Digital is aggregated across all trusts. This means that the exclusions described above are not applicable to these metrics and admissions will be higher than calculated for other metrics.

Trusts definitions

[Trusts definitions](#) in the ESPAUR report are based on the [Estates Returns Information Collection](#) (ERIC) ([Annex Table 3.2](#)).

Annex table 3.2. Definitions of trust type (source: ERIC)

Trust	Definition
Acute small, medium or large	Sites that provides a range of inpatient medical care and other related services for surgery, acute medical conditions or injuries (usually for short-term illnesses or conditions). Treatment centres providing inpatient facilities are classed as general acute hospitals.

Trust	Definition
Acute teaching	Sites that are a hospital that provides clinical education and training to future and current health professionals. Teaching hospitals work closely with medical students throughout their period of matriculation, and especially during their clerkship (internship) years.
Acute specialist	Sites that undertake a single specialist function, inclusive of oncology, orthopaedics, dental hospital, maternity hospital, children's hospital, and cardio or thoracic. This category excludes specialist hospitals in the mental health or learning disabilities sector.
Acute multiservice	Sites where 2 or more functions are provided by the same provider. Such functions would include any combination of single speciality, acute services, community services, mental health services and learning disabilities services.

Department speciality

Annex table 3.3. Department speciality to department group look-up table for antibiotic consumption

Department speciality	Department group
Mixed outpatient clinics	AE / Non-specific out-patient department
Aseptic unit	AE / Non-specific out-patient department
A&E	AE / Non-specific out-patient department
Psychogeriatric	Geriatrics
Geriatrics	Geriatrics
Intensive care	Intensive care unit
Dermatology	General medicine
Respiratory, chest or asthma clinic	General medicine
Cardiology	General medicine
Gastroenterology	General medicine
Coronary care	General medicine
Rheumatology	General medicine
Thoracic or chest medicine	General medicine

Department speciality	Department group
General medicine	General medicine
Endocrinology	General medicine
Obstetrics and gynaecology	Obstetrics and gynaecology
Fertility and genetics	Obstetrics and gynaecology
Orthopaedics	Orthopaedics
Trauma and Orthopaedics	Orthopaedics
Pain clinic	Other
Radiology	Other
Radiology and Imaging	Other
Physiotherapy	Other
Physically disabled	Other
Rehabilitation or long stay unit	Other
Pathology lab	Other
Mental handicap	Other
Occupational health	Other
Learning disabilities	Other
Child adolescent psychiatry	Other
Other wards or units	Other
Psychiatry and mental illness	Other
Psychiatric day Hospital	Other
Paediatric ICU	Paediatrics
Neonatal unit	Paediatrics
Paediatric or paediatric surgery	Paediatrics
Acute internal medicine	Specialist medicine
Medical oncology	Specialist medicine
Clinical oncology (Radiotherapy)	Specialist medicine
AIDS unit	Specialist medicine
Infectious disease or Isolation	Specialist medicine
Renal medicine	Specialist medicine
Liver or Pancreatic unit	Specialist medicine
Neurology	Specialist medicine
GUM	Specialist medicine

Department speciality	Department group
GU Medicine or HIV	Specialist medicine
GU/VD/STD/AIDS	Specialist medicine
Haematology	Specialist medicine
GUM medicine	Specialist medicine
Liver (failure) unit	Specialist medicine
Transplantation unit	Specialist surgery
ENT	Specialist surgery
Cardio-thoracic surgery	Specialist surgery
Plastic surgery	Specialist surgery
Burn and Plastic surgery	Specialist surgery
Oral surgery	Specialist surgery
Vascular surgery	Specialist surgery
Ophthalmology	Specialist surgery
Urology	Specialist surgery
Neurosurgery	Specialist surgery
General surgery	General surgery
Breast treatment and care	General surgery
Day case theatres	General surgery
Theatre and anaesthetics	General surgery

Antiviral consumption

Data sources

COVID-19 therapeutics usage data for the primary care was obtained from ePACT2, and for the secondary care was sourced from IQVIA further details on IQVIA data is available on secondary care section of this annex. As data on the number of patients eligible to receive COVID-19 therapeutics was unavailable to UKHSA, COVID-19 case counts were used as the denominator and were sourced from the [UKHSA COVID-19 dashboard](#).

Data analysis

Total DDDs from 1 January 2020 to 31 December 2024 by therapy were included for (Molnupiravir (Lagevrio®), Nirmatrelvir plus ritonavir (Paxlovid®), Remdesivir (Veklury®) and Sotrovimab (Xevudy®). Rates of DDDs were estimated by dividing the number of DDDs by the COVID-19 case numbers (per 1,000) over the specified time period.

Rates by region were estimated by dividing the COVID-19 case numbers (per 1,000) which were extracted from the [UKHSA COVID-19 dashboard](#) by each region over the specified time period.

STATA 18 and R was used in all medicines supply data analysis.

Antiparasitic consumption

Data sources

Antiparasitic usage data for the primary care was obtained from ePACT2, and for the secondary care was sourced from Rx-Info (Define). Private care antiparasitic usage data was included in the report for the first time this year. Private care data was obtained from IQVIA, and includes antiparasitic sales into private hospitals and private pharmacies, private prescriptions dispensed in community pharmacy, and private usage within NHS hospitals.

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Data analysis

Total rates of antiparasitic consumption were calculated using the ONS Mid-year population (inhabitants) denominator, as above.

Chapter 4. Antimicrobial stewardship

None

Chapter 5. NHS England: improvement and assurance schemes

None

Chapter 6. Professional and public education and training

Antibiotic Guardian

Annexe Table 6.1. A summary of Antibiotic Guardian pledges made on the main pledge page by pharmacy teams each year, from 2014 to 2024, with breakdown of the sub-category of pledger. These sub-categories were not available in 2014 and the 'Community pharmacist' sub-category was introduced in 2018

Year	Pharmacy teams pledges	Pharmacy team pledge sub-category						
		Academic pharmacist	Community pharmacist	Pharmacy assistant	Pharmacy technician	Primary care pharmacist	Secondary care pharmacist	Unknown
2014	1,300	N/A	N/A	N/A	N/A	N/A	N/A	0
2015	1,338	30	0	85	270	398	551	0
2016	2,111	75	0	145	409	654	756	0
2017	3,021	81	0	357	544	861	901	0
2018	1,627	30	245	163	317	350	496	0
2019	2,410	42	807	242	403	299	574	0
2020	28,701	125	10,145	13,214	3,166	1,359	394	0
2021	27,684	47	8,856	13,900	2,885	1,223	392	0
2022	9,747	43	3,059	4,755	965	547	378	0
2023	14,896	84	4,063	8,010	1,454	717	325	243
2024	8,628	43	2,451	4,492	964	436	242	0

Annexe Table 6.2. Summary of the organisational AMS pledge activity from January to December 2024, broken down by the type of organisation, from across UK

Organisation type	Number of registrations in 2024
GP practice	47
Hospital (secondary care)	10
NHS primary care	9
Private healthcare	7
Community pharmacy company	6
NHS trust or health and social care trust (NI)	6
Other	5
Community pharmacy premises	3
National NHS organisation	3
Regional NHS organisation (for example health boards, ICBs, local commissioning group)	3
University	3
Government (national)	1
Veterinary and animal care	1
Total	104

Antibiotic Guardian Shared Learning and Awards – June 2025

Annexe Table 6.3. A summary of the number of entries received per category for the Antibiotic Guardian shared learning and awards event 2024 to 2025 and then number shortlisted for

Category	Number of entries	Number of shortlisted entries
Animal health, agriculture and food supply	2	2
Children and family	3	3
Community communications	8	4
Diagnostic stewardship	2	2
Innovation and technology	10	4
Multi-country collaboration	8	8
Prescribing stewardship	21	8
Public engagement	4	3

Research	2	2
Das Pillay antimicrobial stewardship memorial award	5	3
Health student of the year	3	3
Infection prevention and control	4	3
Tackling health inequalities	3	3
Total	75	48

Annexe Table 6.4. A summary of the number of entries received for the Antibiotic Guardian shared learning and awards event since its inception

Year	Number of entries
2016	79
2017	50
2018	84
2019	77
2020	103
2022 to 2023	62
2024 to 2025	75
Total	530

Chapter 7. Research insights and knowledge mobilisation

List of publications

A list of peer-reviewed publications from April 2024 to March 2025:

Aluzaitė, Kristina, Marta O Soares, Catherine Hewitt, Julie Robotham, Chris Painter, and Beth Woods. 2025. 'Economic evaluation of interventions to reduce antimicrobial resistance: a systematic literature review of methods', *PharmacoEconomics*: 1-16.

Amin-Chowdhury, Zahin, Marta Bertran, Fariyo Abdullahi, Carmen L Sheppard, Seyi D Eletu, David J Litt, Norman K Fry, and Shamez N Ladhani. 2025. 'Risk of invasive pneumococcal disease during pregnancy and postpartum and association with adverse maternal and foetal outcomes: A prospective cohort study, England, 2014-19', *Journal of Infection*, 90: 106363.

Ayorinde, A, I Ghosh, J Shaikh, V Adetunji, A Brown, M Jordan, E Gilham, D Todkill, and D Ashiru-Oredope. 2023. 'Improving healthcare professionals' interactions with patients to tackle antimicrobial resistance', *European Journal of Public Health*, 33: ckad160. 1424.

Bender, Rose Grace, Sarah Brooke Sirota, Lucien R Swetschinski, Regina-Mae Villanueva Dominguez, Amanda Novotney, Eve E Wool, Kevin S Ikuta, Avina Vongpradith, Emma Lynn Best Rogowski, and Matthew Doxey. 2024. 'Global, regional, and national incidence and mortality burden of non-COVID-19 lower respiratory infections and aetiologies, 1990–2021: a systematic analysis from the Global Burden of Disease Study 2021', *The Lancet Infectious Diseases*, 24: 974-1002.

Bertagnolio, Silvia, Zlatina Dobрева, Chad M Centner, Ioana Diana Olaru, Daniele Donà, Stefano Burzo, Benedikt D Huttner, Antoine Chaillon, Nebiat Gebreselassie, and Teodora Wi. 2024. 'WHO global research priorities for antimicrobial resistance in human health', *The Lancet Microbe*, 5.

Blum, Maxim, Jeroen Geurtsen, Eva Herweijer, Michal Sarnecki, Bart Spiessens, Gil Reynolds Diogo, Peter Hermans, Simon Thelwall, Alex Bhattacharya, and Thomas Verstraeten. 2025. 'Epidemiology of invasive *Escherichia coli* disease in adults in England, 2013–2017', *Epidemiology and Infection*, 153: e4.

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Chapter 8. ESPAUR oversight group members' activities and actions to tackle AMR – mapping to the National Action Plan

None.

Chapter 9. Knowledge mobilisation of ESPAUR report: evaluation of feedback from report users

None.

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