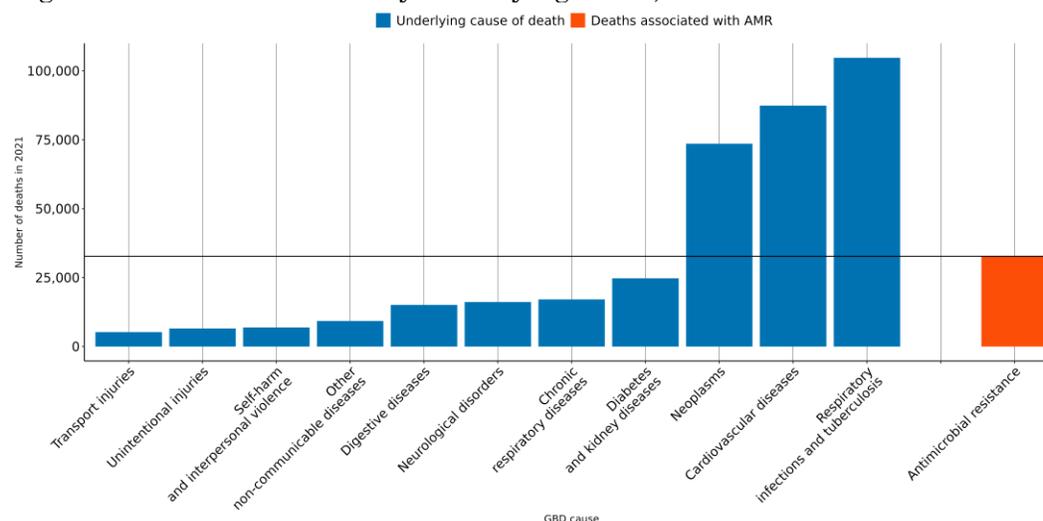


The burden of antimicrobial resistance (AMR) in Argentina

Executive summary

- Antimicrobial Resistance (AMR) is a major global health threat, over **8,000 lives** have been lost each year since 1990 in Argentina due to AMR.
- In 2021, there were an estimated **8,320 UI (7,580-9,060)** deaths attributable to AMR and **32,700 UI (30,300-35,200)** deaths associated with AMR in this location.
- The largest number of deaths associated with AMR in 2021 occurred among those aged **70+** in the country.
- Among the most deadly pathogen-drug combinations in 2021 were *Staphylococcus aureus* resistant to methicillin, *Klebsiella pneumoniae* resistant to carbapenems and *Acinetobacter baumannii* resistant to carbapenems.

Figure 1 Number of deaths by underlying cause, and those associated with AMR in 2021



- In 2021, the number of deaths associated with AMR (orange bar in *figure 2*) were high compared to the most relevant underlying causes of death (depicted in blue) in the country. AMR associated deaths occur within multiple Global Burden of Disease (GBD) causes of death and AMR is not an underlying cause of death by itself.
- At the [2024 United Nations General Assembly high level meeting on antimicrobial resistance](#), country members agreed to aim for a **10% reduction** compared to 2019 baseline (**from 4.95 to 4.45 million**) in the global number of deaths associated with AMR by 2030. But [our forecast](#) indicates that in absence of concerted action, deaths associated with AMR could reach **5.5 million** (UI 4.8 - 6.2) if current trends continue. For Argentina, a 10% reduction means to decrease the number of deaths associated with AMR to **35,800**, but currently the trend for this country could reach up to **44,000 UI [36,100-51,600]** AMR-associated deaths in 2030.

AMR in Argentina

Key takeaways

- Antimicrobial Resistance (AMR) is a major global health threat, over *a million lives* have been lost each year since 1990.
- Globally, 4.71 (95% Uncertainty Interval (UI) 4.2-5.2) million deaths were associated with bacterial drug-resistant infections in 2021.
- And 1.14 (UI 1 - 1.3) million deaths were attributable to bacterial drug-resistant infection in the same year.
- *39 (UI 33 - 46) million deaths* directly attributable to bacterial AMR are projected to occur between 2025-2050 unless concerted action is taken. This equates to three deaths every minute.

Figure 2 Comparing 30 years of infection related deaths, and those associated with and attributable to AMR in Argentina between 1990 and 2019.



- To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#)
- In **Argentina** in 2021, there were an estimated **8,320 UI (7,580-9,060)** deaths attributable to AMR and **32,700 UI (30,300-35,200)** deaths associated with AMR. Here “*attributable deaths*” are considered to be those that would have been prevented had the drug-resistant bacteria causing the infections not been drug-resistant. “*Associated deaths*” are considered to be those that would not have occurred had the infections been prevented entirely.
- Across 204 countries, **Argentina has the 102nd highest** age-standardized mortality rate associated with AMR in 2021.
- *Table 1* shows the bacteria which caused most deaths in 2021 (↑ indicates an increasing estimated annual rate between 1990-2021, ↓ indicates a decreasing annual trend), and *table 2* shows the pathogen-drug combinations which caused most deaths in 2021.

Table 1. Bacteria which cause most deaths in 2021 (Number of deaths in parenthesis)

	Overall susceptible and resistant	Associated	Attributable
Burden rank	Staphylococcus aureus 11,300 UI (10,500-12,200) ↑	Staphylococcus aureus 6,690 UI (5,820-7,570) ↑	Staphylococcus aureus 2,010 UI (1,720-2,300) ↑
	Streptococcus pneumoniae 7,560 UI (6,940-8,180) ↑	Escherichia coli 5,640 UI (5,100-6,180) ↑	Klebsiella pneumoniae 1,400 UI (1,240-1,560) ↑
	Escherichia coli 7,510 UI (6,920-8,100) ↑	Klebsiella pneumoniae 4,730 UI (4,350-5,110) ↑	Escherichia coli 1,030 UI (852-1,200) ↑
	Klebsiella pneumoniae 5,980 UI (5,530-6,430) ↑	Streptococcus pneumoniae 4,100 UI (3,730-4,470) ↓	Acinetobacter baumannii 997 UI (898-1,100) ↓
	Pseudomonas aeruginosa 5,830 UI (5,410-6,260) ↑	Pseudomonas aeruginosa 3,730 UI (3,390-4,070) ↑	Pseudomonas aeruginosa 964 UI (819-1,110) ↑
	Acinetobacter baumannii 2,520 UI (2,350-2,700) ↓	Acinetobacter baumannii 2,460 UI (2,290-2,630) ↓	Streptococcus pneumoniae 789 UI (656-923) ↑
	Group A Streptococcus 1,860 UI (1,670-2,050) ↑	Enterobacter spp. 976 UI (904-1,050) ↑	Enterococcus faecium 268 UI (234-301) ↑
	Enterococcus faecalis 1,510 UI (1,400-1,630) ↑	Enterococcus faecium 913 UI (844-983) ↑	Enterobacter spp. 257 UI (231-282) ↑
	Proteus spp. 1,500 UI (1,380-1,630) ↑	Proteus spp. 903 UI (799-1,010) ↑	Serratia spp. 153 UI (135-171) ↑
	Enterobacter spp. 1,430 UI (1,330-1,530) ↑	Serratia spp. 595 UI (516-674) ↓	Proteus spp. 137 UI (108-165) ↑

Annualized rate of change (1990-2021) <-3% -1.5% to 0% 1.5% to 3% >5.0%
-3% to -1.5% 0% to 1.5% 3% to 5%

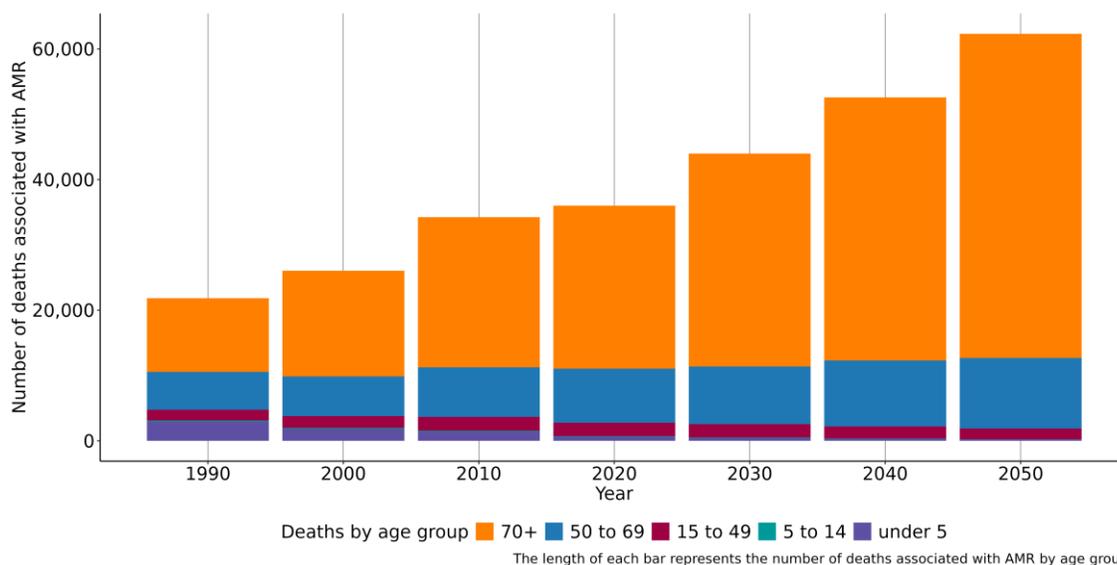
Table 2. Combinations which cause most deaths in 2021 (Number of deaths in parenthesis)

	Associated	Attributable
Burden Rank	Staphylococcus aureus Methicillin 6,120 UI (5,090-7,150) ↑	Staphylococcus aureus Methicillin 1,670 UI (1,380-1,950) ↑
	Escherichia coli Aminopenicillin 5,200 UI (4,640-5,760) ↑	Acinetobacter baumannii Carbapenems 547 UI (449-646) ↑
	Klebsiella pneumoniae Fluoroquinolones 3,770 UI (3,410-4,130) ↑	Klebsiella pneumoniae Carbapenems 501 UI (397-605) ↑
	Klebsiella pneumoniae Aminoglycosides 3,690 UI (3,240-4,130) ↑	Streptococcus pneumoniae Carbapenems 444 UI (294-593) ↑
	Staphylococcus aureus Macrolides 3,430 UI (3,010-3,860) ↑	Pseudomonas aeruginosa Carbapenems 402 UI (278-527) ↑
	Klebsiella pneumoniae Beta-Lactam/Lactamase Inhib. 3,340 UI (2,740-3,950) ↑	Klebsiella pneumoniae Fluoroquinolones 323 UI (233-413) ↑
	Klebsiella pneumoniae TMP-SMX 3,310 UI (2,950-3,670) ↑	Acinetobacter baumannii Fluoroquinolones 301 UI (247-354) ↑
	Escherichia coli TMP-SMX 3,240 UI (2,640-3,840) ↑	Klebsiella pneumoniae Aminoglycosides 282 UI (214-350) ↑
	Klebsiella pneumoniae 3GC 3,200 UI (2,880-3,510) ↑	Pseudomonas aeruginosa Fluoroquinolones 239 UI (162-316) ↑
	Escherichia coli Fluoroquinolones 3,080 UI (2,650-3,500) ↑	Escherichia coli Fluoroquinolones 214 UI (124-304) ↑

Annualized rate of change (1990-2021) <-3% -1.5% to 0% 1.5% to 3% >5.0%
-3% to -1.5% 0% to 1.5% 3% to 5%

- Independently of antimicrobial resistance, the infectious syndromes accounting for the most deaths in 2021 were as follows (estimated thousands of deaths in parenthesis) lower respiratory infection (excl. COVID) (38,600 UI (35,000-42,100)), bloodstream infections (19,700 UI (18,300-21,100)), urinary tract infections and pyelonephritis (6,580 UI (5,900-7,260)), peritoneal and intra-abdominal infections (5,220 UI (4,770-5,680)) and infections of the skin and subcutaneous systems (4,590 UI (4,050-5,130)).

Figure 3. Number of deaths associated with AMR by age group between 1990-2020 and 2050 projection



- In Argentina, people aged 70+ saw the largest number of deaths associated with AMR both in 1990 and 2021, which indicates that 70+ continues to be particularly vulnerable to infections which are resistant to antibiotics. In 2021, the number of deaths associated with AMR among the 70+ was 22,600 UI (20,400-24,800), whereas the mortality rate per 100,000 was 634 UI (573-696).

Data sources for Argentina

In total, 520 million individual records or isolates covering 19,513 study-location-years were used as input data to our estimation process. The subset of input data for this country is shown below.

Table 3. Data inputs for Argentina by source type

Source type	Years	Sample size	Sample size units
Antibiotic use	2010-2021	1,028	Study-year datapoints
Microbial or laboratory data without outcome	1990-2021	817,315	Isolates
Microbial or laboratory data with outcome	1990-2021	6,193	Isolates
Literature studies	1990-2021	17,103	Cases/isolates/susceptibility tests
Single drug resistance profile data	1990-2021	1,752,765	Antibiotic susceptibility test

More information

About GRAM:

The purpose of the Global Research on AntiMicrobial resistance (GRAM) project is to **generate accurate and timely estimates of the magnitude and trends in antimicrobial resistance (AMR) burden** across the world, which can be used to inform treatment guidelines and agendas for decision-making and research, detect emerging problems and monitor trends to inform global strategies, as well as facilitate the assessment of interventions over time.

GRAM is the flagship project of the University of Oxford–IHME Strategic Partnership. GRAM was launched with support from the United Kingdom Department of Health and Social Care’s Fleming Fund, and the Wellcome Trust.

All resources:

For all resources on AMR analysis at IHME, visit <https://www.healthdata.org/antimicrobial-resistance>.

To look at these and more visualization interactively visit [Measuring Infectious Causes and Resistance Outcomes for Burden Estimation \(MICROBE\)](#).

Data sources:

To download the list of data input sources by country, and AMR results by region, visit the [Global Health Data Exchange \(GHDx\)](#).

Contact us:

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