

Systematic review

***Acinetobacter baumannii* in Germany across human, animal, and environmental settings: a systematic review and secondary analysis of national surveillance data**Mohamed I. A. Hassan^{1*}, Marwa Bassiouny² and Oliver Shey-Njila³¹Faculty of Medicine, Friedrich Schiller University, Jena University Hospital, Jena, Germany²Institute of Pharmacy, Friedrich Schiller University Jena, Germany³Department of Microbiology, University of Georgia, Athens, GA 30602, USA*Corresponding author: Mohamed I. A. Hassan, mohamed.abdelwahab.hassan@outlook.de

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Article information: Hassan MIA et al., 2026. *One Health Microbiol. Infect.* Vol. 2, No. 1: 171-194. <https://doi.org/10.66585/ohmi.2026.2.0028>**Abstract**

Acinetobacter baumannii (*A. baumannii*) is a leading cause of difficult-to-treat healthcare-associated infections worldwide and has been classified as a priority “1” critical pathogen by the World Health Organization (WHO). Germany reported 811 mandatory notification cases in 2024, with *bla*NDM detected in 13% of gene-positive notified cases (49/372; 95% CI 10.1%–17.0%). No comprehensive One Health synthesis of German *A. baumannii* science has previously existed. We conducted four parallel systematic literature searches across thirteen electronic databases, covering research from January 2019 to June 2026 and guided by PRISMA 2020, to identify peer-reviewed German *A. baumannii* publications across four domains: animals, environment, humans, and resistance gene characterization. In parallel, *Acinetobacter*-specific data were extracted from six consecutive annual volumes of RKI’s “Infektionsepidemiologisches Jahrbücher” (2019–2024) on Infectious Disease Epidemiology and compared with the peer-reviewed literature across ten parameters. Thirty-two unique peer-reviewed papers were identified: nine animal, twelve environmental, eight human clinical, and fifteen resistance gene characterization. The *bla*OXA-23 dominated all six surveillance years at 57–66%, and *bla*NDM surged to 13% of gene-positive notified cases in 2024, with no peer-reviewed characterization of the responsible lineage. Three critical One Health findings emerged: an NDM-1-positive ST25 *A. baumannii* isolate from an Italian dog processed at a German veterinary laboratory in 2018 predated the 2024 surveillance signal, an epidemiologically unlinked but hypothesis-generating temporal pattern; multidrug resistant (MDR) *A. baumannii* with clinically associated multilocus sequence typing (MLST) profiles was detected in urban wastewater treatment plants receiving hospital wastewater, without concurrent analysis of patient isolates; and the equine collection contained globally distributed IC1–IC3/ST1–ST3 lineages but did not establish resistance-island identity with German intensive care unit (ICU) strains. No eligible German study simultaneously sampled environmental and human clinical isolates from the same geographic catchment by whole-genome sequencing (WGS). Nineteen research gaps were identified, nine classified as urgent. Germany’s animal, environmental, and human clinical *A. baumannii* research communities operate in parallel without cross-domain genomic linkage. The 2024 *bla*NDM surveillance signal requires lineage-resolved molecular characterization to determine whether it represents true epidemiological emergence, improved detection, or importation, and to support susceptibility-guided therapy and integrated One Health genomic surveillance.

Keywords: *Acinetobacter baumannii*, Antimicrobial resistance, *bla*NDM, *bla*OXA-23, Carbapenem resistance, Germany, One Health, Surveillance**Introduction****Antimicrobial resistance as a global health emergency**

The global burden of antimicrobial resistance (AMR) is one of the most urgent threats to modern medicine, with an estimated 4.95 million deaths attributable to bacterial AMR in 2019 alone [1]. Among hospital-acquired pathogens, carbapenem-resistant organisms are of particular concern given their resistance to last-resort antibiotics, their association with prolonged intensive care unit (ICU) stays, and their documented capacity for cross-border spread via patient transfers and healthcare tourism.

Among the principal drivers of nosocomial AMR are the six ESKAPE pathogens: *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species, collectively defined by their capacity to evade the activity of multiple antimicrobial classes through enzymatic drug inactivation, target modification, efflux pump overexpression, and outer membrane

impermeability [2]. Multidrug-resistant (MDR; non-susceptible to $\geq$ one agent in $\geq$ three antibiotic categories), extensively drug-resistant (XDR; susceptible to $\leq$ two antibiotic categories), and pandrug-resistant (PDR; non-susceptible to all agents in all antimicrobial categories tested) phenotypes of these pathogens contribute to elevated morbidity and mortality and impose a substantial economic burden on healthcare systems worldwide [3, 4].

MDR *Acinetobacter baumannii* (*A. baumannii*) isolates have been identified in human clinical, veterinary, and environmental settings in Germany, with acquired resistance genes detected in both human and non-human isolates [5], indicating the potential for cross-sectoral dissemination within the One Health (OH) framework. While the clinical epidemiology of *A. baumannii* in humans has received substantial research attention, its distribution in non-human sources, particularly in food-producing animals, companion animals, and environmental matrices, remains incompletely characterized in the German context.

***Acinetobacter baumannii*: biology, clinical significance, and global epidemiology**

The bacterium *A. baumannii* is a Gram-negative, non-fermentative, catalase-positive, oxidase-negative, aerobic coccobacillus belonging to the *Acinetobacter calcoaceticus*–*A. baumannii* (ACB) complex. The genus *Acinetobacter* currently comprises more than 120 validly published species [6]; however, *A. baumannii* is by far the most clinically important, responsible for a broad spectrum of healthcare-associated infections, primarily ventilator-associated pneumonia, bloodstream infections, and wound infections, predominantly in immunocompromised patients in intensive care units (ICUs) [7, 8]. The pathogen's ability to survive desiccation on hospital surfaces for weeks, to acquire resistance determinants through high-frequency horizontal gene transfer, and to form biofilms on both biotic and abiotic surfaces collectively explains its propensity for nosocomial persistence and outbreak propagation [8, 9]. These biological properties underpin its designation by the World Health Organization (WHO) as a critical-priority pathogen on the 2017 and 2024 Bacterial Priority Pathogens List [10, 11].

Carbapenem-resistant *A. baumannii* (CRAB) is the most clinically significant and therapeutically challenging phenotype, defined by non-susceptibility to at least one carbapenem or the carriage of a confirmed carbapenemase gene. CRAB infections are associated with treatment failure, prolonged hospitalization, and case fatality rates of 20–50% in ICU settings [8]. Carbapenem resistance in *A. baumannii* is driven primarily by acquired class D carbapenem-hydrolyzing oxacillinases (OXA-type enzymes). Two internationally recognized clonal complexes dominate global CRAB epidemiology: International Clone 1 (IC1; Pasteur sequence type ST1) and International Clone 2 (IC2; ST2). IC1 predominantly carries *blaOXA-72*, while IC2 predominantly carries *blaOXA-23* [12, 13]. A third clinically important lineage, International Clone 6 (IC6; ST78), carrying *blaOXA-72* and in some isolates *blaNDM*, has been identified as a regionally distinct conflict-zone-associated introduction into German hospitals via war-injured patient transfers [14, 15]; it remains rare globally (3/313 isolates, 1.0%, in the Müller 2023 global CRAB dataset) [13], and the hypothesis that it represents an emerging war-associated lineage rests on convergent evidence from three small studies totaling fewer than ten isolates.

Treatment options for carbapenem-resistant *A. baumannii* remain critically constrained, with colistin and tigecycline representing older last-resort alternatives, each associated with significant toxicity and pharmacokinetic limitations that restrict their clinical utility in severe infections. Cefiderocol is a novel siderophore cephalosporin and one of the few agents with

activity against CRAB. However, its efficacy is compromised when isolates co-produce the extended-spectrum beta-lactamase (ESBL) PER-7. This combination was identified in approximately 24% of German National Reference Center (NRZ) CRAB submissions [16]. Sulbactam-durlobactam has demonstrated potent *in vitro* activity against CRAB, including European strains [17]. However, it is inactive against metallo-beta-lactamase (MBL)-producing strains. Recent global surveillance data document an increasing prevalence of CRAB across hospital settings on multiple continents, with particularly high rates in Southeast Asia, the Eastern Mediterranean, and southern Europe [13]. In Europe, the European Center for Disease Prevention and Control (ECDC), coordinated by the European Antimicrobial Resistance Surveillance Network (EARS-Net) (ECDC EARS-Net), reports that data from 2022 show carbapenem resistance in at least 50% of tested invasive *Acinetobacter spp.* isolates in southern and southeastern European countries including Greece, Italy, Croatia, and Romania, while Germany, at approximately 4–7%, remains well below the European average, though this relative advantage has narrowed with the influx of war-associated MDR lineages from 2022 onwards [18]. Molecular epidemiological analyses have established that the global CRAB epidemic is driven predominantly by IC1 and IC2 [13]; in Germany specifically, IC2/OXA-23 has dominated clinical CRAB since at least 2010 [12], while IC6/ST78 emerged as an importation lineage from conflict zones from 2020 onwards [12, 14], establishing the molecular background against which the present review's surveillance findings are interpreted.

The epidemiology of *A. baumannii* in Germany

Against this global epidemiological background, carbapenem-resistant and carbapenemase-producing *Acinetobacter* species have been subject to mandatory notification in Germany under the German Infection Protection Act (Infektionsschutzgesetz, IfSG §7) since 2016. The case definition was expanded in 2019 from *A. baumannii* complex alone to all *Acinetobacter* species with confirmed carbapenem resistance or a carbapenemase gene.

Annual notification data are published in the Robert Koch-Institute (RKI) annual book of Infectious Disease Epidemiology “Infektionsepidemiologisches Jahrbuch”. The data document a dynamic six-year epidemiology of *A. baumannii* in Germany. A total of 711 cases were notified in 2019, the first year under the expanded case definition covering all *Acinetobacter spp.* Case numbers fell to 481 in 2020, reflecting a COVID-19 pandemic-related reduction in hospital admissions. Numbers then rose sharply to 822 cases in 2022, the highest count in the surveillance period; a year in which Ukraine was frequently reported among cases with available infection-

country information. A sustained elevated count of 811 cases was recorded in 2024 [19].

Among material types used for diagnosis and isolation of the bacteria, lower respiratory infection isolates show the highest carbapenem resistance rates, at 11.4% (95% CI 7.9–16.2%) in the most recent national analysis [20]. Throughout all the last six surveillance years, Berlin maintained the highest state-level notification rate (rising from 1.9 per 100,000 in 2019 to 2.7 per 100,000 in 2024); male sex and age ≥ 70 years were the dominant demographic risk factors, and 16% to 25% of recorded deaths were attributed to the reported disease annually [19, 21, 22, 23, 24, 25].

The dominant acquired carbapenemase across all six surveillance years was *blaOXA-23*, detected in 57–66% of tested cases, a finding independently corroborated by the Paul-Ehrlich-Society multicenter survey covering 17 German hospitals across four time points from 2010 to 2019 [12] and by the NRZ Bochum reference dataset from 2022 to 2023 [16]. Despite this national notification infrastructure, the existing German literature has remained largely confined to individual clinical, veterinary, or environmental studies conducted in isolation. The most recent national German epidemiological analysis covered only the period 2014–2018 and relied exclusively on phenotypic resistance data without gene-level characterization [20]. This study predates all six RKI Jahrbücher published between 2019 and 2024. During this period, Germany experienced several critical developments in the epidemiology of *A. baumannii*. First, the country recorded its highest-ever number of CRAB notifications. Second, the war in Ukraine led to the importation of IC6/ST78 lineages carrying both New Delhi metallo-beta-lactamase (*blaNDM*) and *blaOXA*. Third, a dramatic shift in resistance genes emerged, the most urgent finding in recent German *A. baumannii* research [20, 26]. No systematic review has compared the mandatory RKI notification data with the concurrent scientific literature, and no study has examined whether *A. baumannii* isolates circulating in German animal populations, environmental matrices, and human clinical settings share common clonal lineages or resistance gene elements.

The 2024 RKI annual report documents an unprecedented surge of *blaNDM* to 13% of gene-positive notified German CRAB cases [21]. This is a dramatic rise from near-zero across all preceding surveillance years (2019–2023). The responsible lineage has not been characterized in any published study. Three possibilities remain open: the surge may represent spread of the war-associated IC6/ST78 clone already documented in German hospitals [12, 14]; it may involve a newly introduced variant; or it may result from horizontal *blaNDM* gene transfer across multiple lineages. The

plasmid context and transmission route likewise remain uncharacterized as of the time of writing [21].

Sulbactam-durlobactam has demonstrated potent *in vitro* activity against OXA-type carbapenem-resistant *A. baumannii* isolates including European strains [17]; however, as of June 2026, the European Medicines Agency (EMA) has not granted marketing authorization for this combination, and it is therefore not clinically available in Germany or other EU member states. Clinicians should consult current EMA and national regulatory authority records before considering use. Compassionate use or named-patient access may be available in individual member states subject to national regulations.

The One Health rationale and aims of this review

A. baumannii is not exclusively a nosocomial pathogen. It can persist in a wide range of environmental matrices. These include soil [27, 28], wastewater treatment plant (WWTP) effluents [29], river and surface water [30], livestock manure [31, 32], and dairy and tank milk [33]. The organism has also been documented in companion animals [34, 35] and food-producing animals [5, 36]. Together, these findings demonstrate that *A. baumannii* circulates across the human-animal-environment interface. This breadth of distribution makes a One Health analytical framework essential for understanding its full epidemiology.

Three findings from the recent German literature are particularly instructive in this regard. In 2018, an NDM-1-producing *A. baumannii* isolate was identified in an Italian dog at a German veterinary laboratory [34]. This was the first documented case of NDM-producing *A. baumannii* in any European companion animal. This finding predated the 2024 human *blaNDM* surge, which reached 13% of gene-positive notified cases by six years. The two datasets are epidemiologically unlinked: the 2018 isolate was ST25/IC7, the 2024 lineage remains uncharacterized, and no genomic comparison has been published, making this observation hypothesis-generating rather than evidence of a sentinel relationship. This six-year gap illustrates the potential of integrated animal surveillance as an early warning system for emerging resistance threats. Second, IC2/OXA-23 isolates genetically indistinguishable from dominant human clinical CRAB lineages have been detected in hospital WWTP effluents [32], yet no German study has ever simultaneously sampled these environmental matrices and concurrent human clinical cases within the same geographic catchment area. WGS showed that companion animal isolates from German veterinary clinics carry AbaR3-like and AbaR10 genomic resistance islands [37]. These islands share the Tn6019 backbone, comM chromosomal insertion site, and identical multiple antibiotic resistance region (MARR) gene content (*blaTEM-1*, *aacC1*, *aadA1*, *tet(A)*, *tet(R)*, *sul1*, *catA1*)

with human clinical IC1 strains globally, differing only in the absence of *aphA1*. This demonstrates near-complete structural identity and suggests that the mobile resistance architecture of human clinical CRAB also circulates in companion animals [37]. The equine collection [35], by contrast, showed genomic diversity across globally distributed IC1–IC3/ST1–ST3 lineages with universal imipenem susceptibility, not establishing resistance-island identity with German ICU strains, yet no cross-domain WGS linkage study has ever been conducted to characterize the epidemiological relationship between these parallel resistance gene pools. Together, these three findings reveal the structural fragmentation of German *A. baumannii* science: animal, environmental, and clinical research communities have independently generated evidence of shared resistance gene architecture across the OH domains, but have never integrated this evidence through a purposefully designed cross-domain study, the fundamental gap that the present systematic review addresses.

To address the current absence of a comprehensive OH synthesis of German *A. baumannii* research, the present systematic review has four specific aims: (i) to identify and characterize all German publications on *A. baumannii* distribution and resistance gene profiles across three survey domains (animal, environmental, and human), as well as resistance gene characterization, covering January 2019 to June 2026; (ii) to extract and systematically analyze six years of RKI mandatory notification surveillance data (2019–2024) across fourteen data fields per year; (iii) to compare the published evidence with official RKI Jahrbuch surveillance findings across ten comparison dimensions, identifying agreements, complementary data, surveillance-unique findings, and data discordances; and (iv) to identify confirmed research gaps, classify them by priority (urgent, high, or medium), and define the German *A. baumannii* research agenda for the coming decade. The review is restricted to German institutional and geographic contexts; pharmacokinetic/pharmacodynamic studies, *in vitro* antimicrobial activity studies, and experimental animal infection models are excluded regardless of institutional affiliation.

Materials and methods

Objectives and scope

To construct a comprehensive, evidence-based account of *A. baumannii* distribution and AMR gene profiles across animals, the environment, and humans, as well as resistance gene characterization, in Germany from 2019 to June 2026, we conducted four parallel systematic literature surveys supplemented by a final integrative cross-survey screening round. We complemented these with a systematic extraction and analysis of official

German national surveillance data from the RKI. Together, these five evidence streams form the analytical foundation of the present review (Figure 1).

Information sources and search strategy

The literature search drew on sources grouped into four categories. Bibliographic databases (structured search using a string search, with MeSH terms applied in PubMed/MEDLINE; all other databases searched by free text): PubMed/MEDLINE, Scopus, Web of Science, AGRIS/FAO, and ProQuest; last searched 30 June 2026. Scientific search engines and academic platforms (free-text search; Google Scholar screened until two consecutive result pages returned no new relevant records per iteration): Google Scholar, Semantic Scholar, and ResearchGate; last searched 30 June 2026. Preprint and open-data repositories (free-text search): bioRxiv, Zenodo, Figshare, OpenAgrar, and the Open Science Framework; last searched 30 June 2026. Institutional and grey literature sources were searched systematically for completeness in the German context: the RKI edoc repository (all issues of the *Epidemiologisches Jahrbücher* 2019–2026), the FLI (Friedrich-Loeffler-Institut) 2025 publication catalog, the Institute of Functional Interfaces (IFG) at the Karlsruhe Institute of Technology (KIT), the DART-Europe European thesis registry, *Deutsches Ärzteblatt International*, and *Eurosurveillance*; last searched 30 June 2026. The same core search string was applied across all databases; database-specific search strategies are available from the corresponding author on request.

Deduplication was performed manually by cross-referencing titles, authors, and DOIs across all survey domains; records that appeared in more than one domain were assigned to all relevant domains but counted only once toward the unique paper total of 32. Each survey was conducted in multiple iterative rounds: six or more rounds for the animal survey, five for the environmental survey, three or more for the human clinical survey, and four for the resistance gene survey, followed by a final simultaneous cross-survey round targeting all four domains together, for a total of approximately fifteen distinct search iterations. Citation forward tracking for all included papers was conducted in Scopus and Google Scholar in June 2026. Each successive round employed increasingly targeted strategies, including author-level searches for each identified German research group and keyword searches for specific German institutions and laboratories known to work in this field. As a dedicated supplementary evidence stream, we extracted and systematically analyzed *Acinetobacter*-specific surveillance data from the six consecutive annual editions of the RKI “*Infektionsepidemiologisches Jahrbuch meldepflichtiger Krankheiten*” covering the years 2019 through 2024.

Since 2016, carbapenem-resistant or carbapenemase-producing *Acinetobacter* spp. have been mandatorily notifiable under the IfSG, with the case definition expanded in 2019 from the *A. baumannii* complex alone to all *Acinetobacter* spp. with reduced carbapenem susceptibility or a confirmed carbapenemase determinant. From each “Jahrbuch” edition across all six volumes, we extracted the following fourteen data points: annual notified case counts under the “Referenzdefinition”; national incidence per 100,000 population; clinical breakdown by “Falldefinition” category (C/D/E); infection versus colonization proportions; age and sex distributions; state-level “Bundesland” incidence data; outbreak counts and sizes; infection- country data; species-level breakdown within reported cases; carbapenemase gene types detected (OXA-23, OXA-72, OXA-51 with *ISAbal* upstream insertion, NDM, and others) and their proportions among tested cases; and recorded deaths and the proportion attributed to the reported disease.

The extracted RKI surveillance data were subsequently compared with findings from the peer-reviewed literature across ten parameters: case counts and incidence trends; species distribution within reported cases; resistance gene evolution (OXA-23, OXA-72, NDM, and others); patient demographics (age, sex); infection versus colonization proportions; outbreak patterns; geographic distribution by federal state “Bundesland”; importation patterns including the Ukraine war-related case surge of 2022; reported deaths and disease-attribution proportions; and carbapenemase-specific clinical implications. The following data fields were absent from the RKI Jahrbuch and could not be extracted: individual isolate identifiers; NRZ referral links or submission records; sequence type or clonal lineage data (MLST, cgMLST, or WGS-based); phenotypic antimicrobial susceptibility profiles at isolate level; plasmid characterization; clinical outcome data beyond the reported disease fatality proportion; and geographic resolution below the federal state level. Species-level resolution is partial: the “Jahrbuch” reports the proportion of cases identified as *A. baumannii* or *A. baumannii* complex among total *Acinetobacter* spp. notifications, but does not distinguish *A. baumannii* from other ACB complex members, e.g., *A. calcoaceticus*, *A. pittii*, *A. nosocomialis*, at the notification level. Carbapenemase testing denominator data: the number of isolates tested for carbapenemase typing was explicitly reported only in the 2024 volume (429 tested; 372 gene-positive); for 2019–2023, resistance gene proportions are reported without the exact testing denominator, limiting precise inter-year comparison of the *bla*NDM trajectory. The complete six-year RKI surveillance dataset, with carbapenemase-typing denominators by year, is provided in supplementary Table S5. No raw isolate-level data, NRZ

submission records, or individual notification identifiers are published in the Jahrbuch; these would require direct data access from RKI or NRZ, which was not available for this review.

Search string

The core search string applied across all four literature surveys combined the pathogen identifier ('*Acinetobacter baumannii*' OR '*Acinetobacter* spp.' OR 'ACB complex' OR 'CRAB') with the geographic qualifier (Germany OR German OR Deutschland) and domain-specific terms appropriate to each survey. For the animal survey, terms encompassing animal, veterinary, livestock, companion animal, pet, dog, cat, cattle, horse, poultry, wildlife, reptile, bird, bovine, equine, canine, feline, avian, and zoo. For the environmental survey, terms were environment, soil, water, WWTP, wastewater treatment, river, sediment, air, airborne, manure, biogas, slaughterhouse, food chain, milk, and dairy. For the human clinical survey, terms were human, clinical, hospital, ICU, outbreak, surveillance, nosocomial, patient, infection, bacteremia, and pneumonia; and for the resistance gene survey, resistance gene, carbapenemase, OXA, NDM, AMR, resistome, mobile genetic element, plasmid, polymerase chain reaction (PCR), lateral flow, multiplex, and WGS. All searches were conducted without language restrictions.

Eligibility criteria

A study was eligible for inclusion if it met all four of the following criteria: (i) at least one author held a German institutional affiliation and the primary sampling data, patient data, or surveillance data were collected in Germany or from German populations; studies led by German institutions but collecting data exclusively outside Germany were retained as contextual evidence in the discussion but were not counted as primary German evidence in the domain totals; (ii) the publication date fell between 1 January 2019 and 30 June 2026; (iii) the paper was published as a peer-reviewed full article, including original research articles, systematic reviews, methodological validation studies, and genome sequence announcements; and (iv) *A. baumannii* or the ACB complex was a primary subject of the study.

Studies were excluded if they originated entirely from non-German institutions with no German sampling component; if they were conference abstracts without a full-text peer-reviewed publication; if they predated 2019; if they were grey literature such as NRZ annual reports or Kommission für Krankenhaushygiene und Infektionsprävention (KRINKO) infection control guidelines; or, in the human clinical and resistance gene surveys, if they were single-patient case reports without systematic epidemiological data, or pharmacokinetic/pharmacodynamic studies without patient-level outcome data.

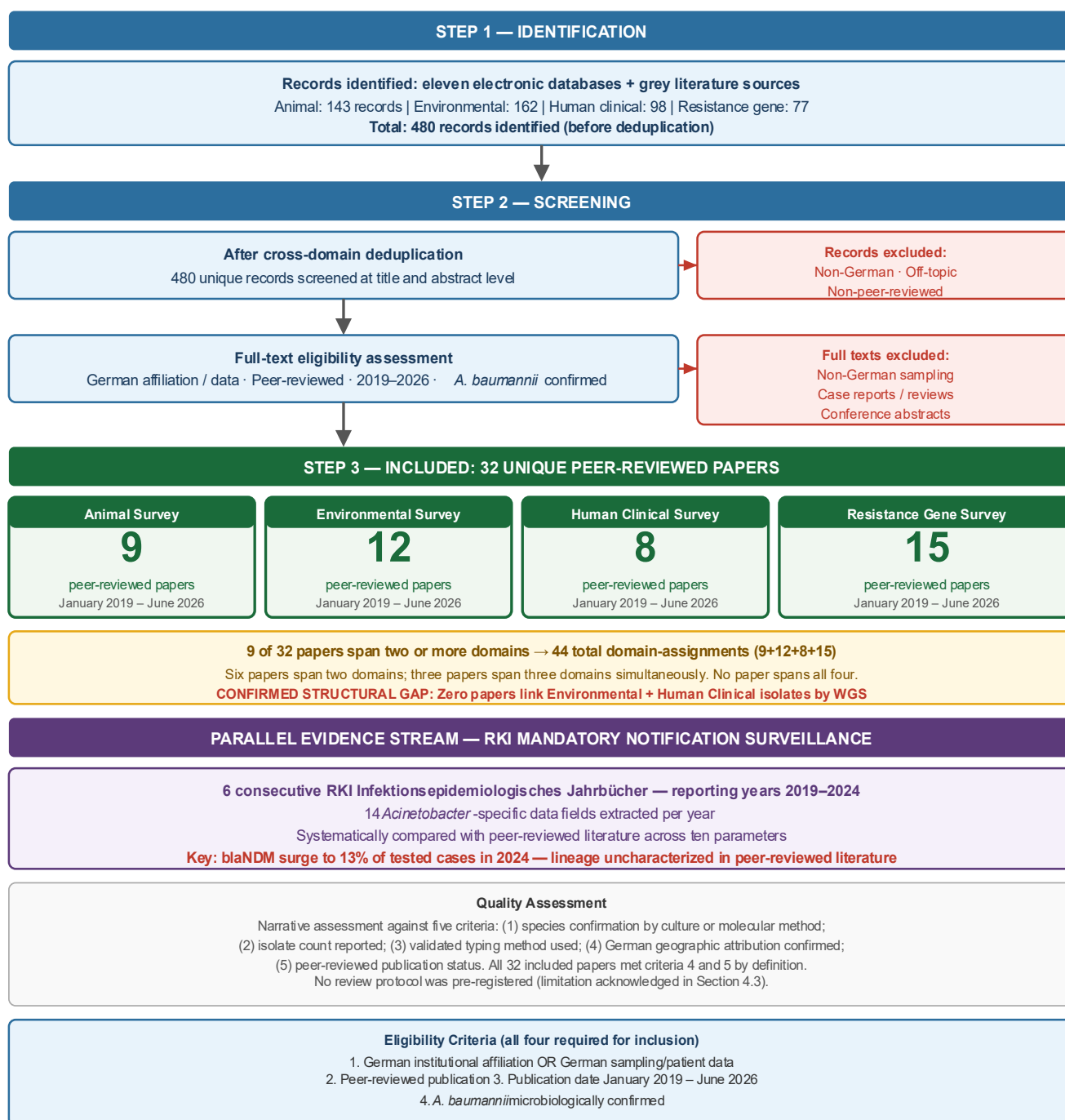


Figure 1: PRISMA 2020 flow diagram of the literature search and study selection. Four parallel survey streams (animal, environmental, human clinical, resistance gene) were screened from 480 unique records following deduplication, yielding 32 unique included papers. A parallel surveillance stream extracted data from six RKI Infektionsepidemiologisches Jahrbücher (2019–2024). PRISMA = Preferred Reporting Items for Systematic Reviews and Meta-Analyses; RKI = Robert Koch Institute; WGS = whole-genome sequencing.

A key exclusion decision concerned a study of *A. baumannii* genomic epidemiology in Kano, Nigeria, by a Nigerian first author with a secondary affiliation at RKI Wernigerode. It was evaluated, documented, and explicitly excluded because the sampling location did not meet the German geographic criterion, despite the RKI co-authorship. For mixed multi-country studies that included German isolates but did not separately report them as a distinct subset, the paper was retained if: (i) German

institutions were among the primary contributing centers; (ii) the German data component was integral to the paper's conclusions rather than incidental; and (iii) the paper directly characterized resistance mechanisms, lineages, or therapeutic profiles of strains circulating in Germany. When German isolates could not be extracted separately from the dataset, the paper was retained as contextual evidence. No German NRZ isolates from one paper were double-counted against NRZ isolates

appearing in a separate paper; when the same NRZ reference collection was used across multiple studies [38, 39], each paper was counted once as a distinct unit of evidence based on its independent scientific contribution, not as providing additional independent clinical isolate data.

Two eligibility refinements were applied to address units of evidence and geographic attribution. First, for geographic attribution, the author's institutional affiliation alone was insufficient for inclusion. Studies were eligible only if they contained separately extractable German sampling, patient, or surveillance data. German-led global multi-country studies, in which Germany contributed isolates or data as one of multiple countries, without a separately reportable German subset, were retained as contextual evidence in the discussion but were not counted as primary German evidence in the domain totals. This applies specifically to five resistance gene characterization papers [13, 17, 38, 39, 40] that use German National Reference Center isolate collections or include German data within global datasets; these are included because they directly characterize resistance mechanisms documented in German clinical *A. baumannii* and are led by German institutions, but their scope extends beyond Germany. Second, to avoid double counting across evidence levels, when a systematic review covering German data was identified, its included primary studies were assessed independently against the eligibility criteria. The systematic review itself was counted as a single unit of evidence only if it contained an original synthesis not available in the primary studies. For example, reference [26] was assessed on this basis and retained as a distinct unit of evidence because it synthesizes mortality and case-fatality data from multiple surveillance systems that are not individually accessible as primary studies.

Screening and study selection

Across all four surveys, 480 unique records were identified and screened after deduplication (animal domain: 143; environmental domain: 162; human clinical domain: 98; resistance gene domain: 77). Per-database retrieval counts before deduplication, the number of duplicate records removed, and full-text exclusion counts by specific reason were not separately recorded during the search process; the 480-record total represents the aggregate post-deduplication count across all sources. Detailed search records are available from the corresponding author on request. After applying the eligibility criteria, thirty-two unique peer-reviewed papers were retained across the four survey domains: nine in the animal survey, twelve in the environmental survey, eight in the human clinical survey, and fifteen in the resistance gene survey. Because multiple papers span more than one survey, one paper was shared between the animal and environmental

surveys involving livestock-linked matrices (manure and biogas digestate); one paper spanned the animal and resistance gene surveys; one paper spanned the environmental and resistance gene surveys; three papers spanned the human clinical and resistance gene surveys through German hospital and war-injury molecular epidemiology; and two papers spanned the animal, human, and resistance gene surveys through direct human-animal comparative WGS analyses, plus one paper spanned the environmental, human, and resistance gene surveys. The total number of unique papers across all four surveys is thirty-two. Of these, seven papers are genuinely unique to the resistance gene survey [13, 16, 17, 38, 39, 40, 41]. Critically, no paper was identified that spans the environmental and human clinical surveys without also including a resistance-gene component, confirming a structural absence. No German study has yet directly linked WWTP or river isolates to concurrent human clinical cases using WGS.

The overall inclusion rate of approximately 7% (32 of 480 records) reflects strict geographic and quality criteria rather than a narrow initial search. Bibliographic saturation was verified empirically: the final cross-survey screening round in June 2026 returned zero new qualifying papers for the animal and environmental surveys, one additional paper for the human clinical survey [13], and zero for the resistance gene survey, confirming saturation in all four surveys. No dedicated systematic review software (e.g., Rayyan, Covidence, Distiller SR) was used; records were managed in a structured Excel spreadsheet with separate worksheets for each survey domain, and cross-domain deduplication was performed manually via title, first author, and DOI cross-matching. Where a study was reported across multiple publications, for example, a genome sequence announcement later followed by a full genomic characterization paper, the most complete publication was included as the primary record, and additional reports were cross-referenced in the evidence table notes.

The following variables were extracted for each included paper: reference number; first author and year; journal; host species or environmental matrix (animal and environmental surveys); study setting and geographic location (federal state or city); number of isolates or samples; lineage and sequence type (ST/IC where reported); resistance genes and carbapenemase types identified; and key finding relevant to the One Health synthesis. For the human clinical survey, additional variables were extracted: patient demographics (age, sex); infection type (bloodstream, pneumonia, colonization); outbreak characteristics, where applicable; and therapeutic or diagnostic outcomes. For the resistance gene survey, additional variables were extracted: genetic context of resistance genes (plasmid vs. chromosomal, mobile genetic element type); MIC data, where reported;

and cross-domain comparability of isolate collections. These variables correspond to the column structure of the tables. When data were incompletely reported in the published text, the corresponding author was contacted by email for clarification; responses were received for two papers, and the additional data were incorporated. When information remained unavailable after contacting the author, the relevant field was recorded as "not reported" in the evidence table. No data imputation was performed.

Quality assessment and risk of bias, and reporting

The thirty-two included papers span five methodologically distinct study design categories: (i) cross-sectional surveillance and prevalence studies ($n = 14$), for which the JBI critical appraisal checklist for prevalence studies would be the appropriate instrument; (ii) outbreak investigations and case series ($n = 3$) [15, 42, 43], for which the JBI case series checklist would apply; (iii) diagnostic and methodological validation studies ($n = 4$) [16, 38, 39, 40], for which QUADAS-2 would be appropriate; (iv) descriptive genomic characterization studies ($n = 10$), for which no single validated instrument exists but JBI cross-sectional criteria provide partial coverage; and (v) one systematic review within the evidence set [26], for which AMSTAR 2 would apply. Given this heterogeneity across five design categories and the absence of a single instrument applicable uniformly, formal quantitative risk-of-bias scoring using design-specific tools was not performed. Instead, methodological quality was assessed narratively for each included paper against five criteria: (i) explicit species confirmation beyond culture morphology (MALDI-TOF, PCR, or WGS); (ii) transparent reporting of isolate counts and collection dates; (iii) use of validated typing methods (MLST, PFGE, cgMLST, or WGS); (iv) clear geographic attribution to Germany; and (v) peer-reviewed publication in an indexed journal.

All 32 included papers met criteria 4 and 5 by definition. Species confirmation was achieved by WGS in 22 papers, by MALDI-TOF in 28 papers, and by *bla*OXA-51-like PCR in 19 papers, with overlap across methods. The absence of formal risk-of-bias scoring means that study-level confidence judgments cannot be reported individually; synthesis conclusions should be interpreted with the caveat that methodological quality varies across the dataset, particularly between primary genomic characterization studies and single-center cross-sectional surveillance studies. Future updates of this review should apply design-specific risk-of-bias instruments and report study-level judgments. The full narrative risk-of-bias assessment for all 32 included papers is provided in supplementary Table S6.

Reporting was guided by the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 statement [44]. No review protocol was

prospectively registered with the International Prospective Register of Systematic Reviews (PROSPERO) or an equivalent registry before the searches began. A retrospective protocol record was documented in July 2026, comprising the review objectives, eligibility criteria, search strategy, domain structure, and the planned comparison with RKI surveillance data; this record is available from the corresponding author on request. In accordance with PRISMA 2020 Item 16, per-source retrieval counts before deduplication, the number of duplicate records removed, and full-text exclusion counts by specific reason were not separately recorded during the search process. This represents a significant deviation from the standard PRISMA protocol, which requires transparent documentation of each stage of the screening process to allow independent verification of the 480-record post-deduplication total and the 480→32 yield. All available counts, the post-deduplication total of 480 records, and the final inclusion of 32 unique papers are reported accurately; detailed search records are available from the corresponding author on request. No protocol amendments were made after the retrospective record was finalized. The absence of prospective registration and the lack of recorded intermediate screening counts are primary methodological limitations that reduce the verifiability of the selection process.

Synthesis methods

Narrative synthesis was conducted in accordance with the Synthesis Without Meta-analysis (SWiM) reporting guideline. Quantitative meta-analysis was not performed given the methodological heterogeneity across the five study design categories represented in the included papers and the absence of a common outcome measure applicable across all four survey domains.

Synthesis was structured around four prespecified groups corresponding to the four survey domains: animal, environmental, human clinical, and resistance gene characterization. Within each group, the primary synthesis outcome was the characterization of *A. baumannii* distribution, resistance gene profiles, and lineage identity in the German setting. Secondary outcomes were cross-domain comparability of resistance gene architecture and the presence or absence of epidemiological linkage between domains.

The denominator for all proportions reported within each domain is the number of unique papers assigned to that domain (9, 12, 8, and 15, respectively), not the total of 32 unique papers or the 44 total domain assignments. When a paper spans multiple domains, its findings are reported in each relevant domain section but counted only once in the total number of unique papers.

Heterogeneity across included studies was addressed narratively rather than statistically. Sources of heterogeneity identified a priori included: study design

(cross-sectional vs. outbreak investigation vs. genomic characterization); isolate source (clinical diagnostic vs. systematic surveillance vs. environmental sampling); typing method (MALDI-TOF only vs. MLST vs. WGS); and geographic scope (single-center vs. national vs. international with German component). Where heterogeneity prevented direct comparison of findings across papers, this is stated explicitly in the relevant results subsection.

Certainty of evidence was not assessed using formal grading instruments such as GRADE, given the descriptive and surveillance-oriented nature of the included studies and the absence of a comparison with a clinical intervention. Instead, confidence in each synthesis finding is qualified narratively using the following conventions: findings supported by three or more independent studies using WGS-level typing are described as "well-established"; findings supported by one or two studies or by lower-resolution typing methods are described as "preliminary" or "suggestive"; and findings resting on a single study without independent corroboration are explicitly flagged as requiring replication.

Gap registry and priority classification

Research gaps were identified inductively during data extraction and synthesis across all four survey domains. A gap was defined as a research question for which no eligible German peer-reviewed study had been identified as of 30 June 2026, despite a plausible biological or epidemiological rationale for its investigation. Gaps were assigned a stable alphanumeric identifier (G-H = Human Clinical, G-E = Environmental, G-A = Animal, G-R = Resistance Gene, G-OH = One Health cross-domain) and documented in a locked registry comprising: gap ID; domain; gap definition; evidence link to the specific table and reference supporting the absence claim; priority classification; and priority rationale. Priority was classified by a single assessor (M.I.A.H.) against three prespecified criteria: URGENT = direct and immediate treatment or infection control implications addressable within a 12-month research horizon; HIGH = important for understanding One Health transmission dynamics addressable within a 2–3 year horizon; MEDIUM = would strengthen the evidence base but carries no immediate clinical or public health consequence. The locked registry underpins supplementary Table S4 and Figure S1; all gap IDs, definitions, domain assignments, and priorities are identical across both outputs.

Results

Data analysis

Thirty-two unique peer-reviewed papers were identified and included in this review and met all eligibility criteria across four survey domains (Table 1, 2, 3, 4). Nine papers

contribute findings to more than one domain simultaneously, yielding 44 total domain assignments across the 32 unique papers (9 animal + 12 environmental + 8 human clinical + 15 resistance gene = 44). The discrepancy between 32 unique papers and 44 domain assignments arises because nine papers contribute evidence to more than one survey domain simultaneously: six papers span two domains and three span three domains. Each paper is counted once toward the total of 32 unique papers but contributes one domain assignment for each domain in which it provides qualifying evidence. Of these nine cross-domain papers, six span exactly two domains: three cover the human clinical and resistance gene domains, one covers the animal and environmental domains, one covers the environmental and resistance gene domains, and one covers the animal and resistance gene domains. The remaining three papers each span three domains simultaneously, covering animal, human clinical, and resistance gene domains (two papers) or environmental, human clinical, and resistance gene domains (one paper). No paper spans all four domains. The difference between 44 domain assignments and 32 unique papers reflects that six papers were counted twice and three were counted three times.

Animal distribution of *A. baumannii* in Germany

Overview

Nine unique peer-reviewed papers characterizing *A. baumannii* in German animals are retained in the final animal survey domain after cross-domain deduplication (Table 2). Prior to deduplication, nineteen domain-relevant papers within the 2019–2026 eligibility window were identified across six host category domains: companion animals ($n = 3$), livestock and equine animals ($n = 5$), poultry ($n = 2$), wildlife ($n = 1$), food chain matrices ($n = 2$), and multi-host OH genomic comparisons ($n = 6$). Nine papers also contribute to other domains (principally resistance gene and environmental surveys) and are counted only once in the total of 32 papers. These nine unique papers were contributed by six distinct German research groups. The FLI Jena/Wareth group contributed the most papers across the broadest range of animal and food-chain host categories, while the Giessen/Ewers group was the dominant contributor to companion-animal and veterinary CRAB characterization. Research groups were identified by corresponding author institutional affiliation as listed in each included paper; groups sharing the same primary institution were counted as one group; institutions with multiple campus addresses were assigned to the city of the corresponding author's department. Although studies spanning a wide diversity of different animal hosts, almost all isolates remained susceptible to most of the antimicrobials tested [45, 46].

Companion animals and veterinary clinics

The most clinically significant finding in the companion animal literature is the first documentation of NDM-1-producing *A. baumannii* in any European pet animal: an NDM-1-producing *A. baumannii* isolate was identified from an Italian dog at a German veterinary clinic in 2018 [34]. The gene was located on a transposable element, and the isolate carried an XDR phenotype [34]. This finding predated the 2024 human *bla*NDM surveillance signal by six years. The datasets are epidemiologically unlinked: the 2018 isolate was ST25/IC7, the 2024 lineage remains uncharacterized, and no single nucleotide polymorphism SNP distance or plasmid comparison between the two has been published. The temporal pattern is hypothesis-generating and justifies prospective companion animal NDM surveillance (Gap G-A1), but does not establish a causal relationship. Subsequently, 503 animals were screened at 22 German veterinary clinics, resulting in the identification of 42 carbapenemase-producing isolates. OXA-58 was located on plasmids ranging from 11–71 kb, and OXA-23 was on chromosomal AbaR resistance islands

[37]. Sequence types ST1 (IC1) and ST25 (IC7) were identified, the same international clonal lineages predominating in German human hospital CRAB. A total of 78 equine isolates from German veterinary clinics were further characterized, revealing dominance of IC1 and IC2, with AbaR3 and AbaR10 resistance islands carrying the same AMR gene arrays documented in human hospital strains; this was the first demonstration that German horses carry IC-type CRAB with a full clinical resistance gene architecture [35]. A separate study by the same group [47] tested two antimicrobial peptides, i.e., Bac7(17) and PAsmr5-17, against 13 selected MDR isolates from human, dog, and cat sources, demonstrating activity at MIC90 62.5–125 µg/mL; this represents the first therapeutic antimicrobial peptide screening study on German companion animal *A. baumannii* and underscores that [35] and [47] are two distinct publications from the same research group addressing different scientific questions.

Table 1: Results overview — 32 unique papers across four survey domains: summary of all four survey domains. Papers spanning multiple domains are counted only once in the unique paper total.

Domain	Papers	Research groups	Key findings and structural notes
Animal distribution	9 papers	FLI Jena, Giessen/Ewers + others	Companion animals, livestock, poultry, wildlife, food chain matrices, and One Health human-animal comparative WGS. FLI Jena: broadest footprint across animal and food chain categories. Giessen: dominant in companion animal and equine CRAB characterization. Key finding: NDM-1-producing <i>A. baumannii</i> in German veterinary dog (2018) [34] — first in any European companion animal
Environmental distribution	12 papers	KIT Karlsruhe/Schwartz + others	WWTP effluents and sludge, surface water and rivers, manure and biogas digestates, slaughterhouse wastewater, dairy and tank milk, soil. KIT Karlsruhe/Schwartz group: dominant contributor. Key finding: IC2/OXA-23 genetically indistinguishable from human clinical lineages detected in hospital WWTP effluents [32]; zero German studies link WWTP isolates to concurrent human cases by WGS
Human clinical distribution	8 papers	NRZ Bochum, Frankfurt + others	Multi-state outbreak investigation, single-center ICU outbreak/risk-factor study, war-injury and Ukrainian-patient molecular epidemiology, multicenter hospital surveillance, and papers shared with the animal/resistance-gene domains via comparative human-animal WGS analyses. NRZ Bochum (Seifert/Higgins group) is a recurring contributor across multiple domains
Resistance gene characterization	15 papers	NRZ Bochum + 5 other groups	Most cross-cutting survey: 8 of 15 papers also appear in another domain. Papers span molecular epidemiology (OXA-23, OXA-72, NDM, PER-7), resistance island architecture (AbaR3, AbaR10), diagnostics validation, and <i>in vitro</i> therapeutic screening. NRZ Bochum is the dominant contributor. Key finding: The 2024 <i>bla</i> NDM surge to 13% of tested cases has no peer-reviewed lineage characterization as of June 2026
RKI surveillance comparison	6 Jahrbücher	RKI (official)	Six-year mandatory notification data compared with peer-reviewed literature across 10 parameters. <i>bla</i> OXA-23 concordant between surveillance and literature. <i>bla</i> NDM 2024 surge = critical discordance: 13% in RKI, near-zero in all peer-reviewed publications. IC6/ST78 war-associated lineage: complementary evidence. Environmental/human clinical linkage: gap in both surveillance and literature

Table 2: Animal survey — 9 unique papers (January 2019 – June 2026): nine peer-reviewed papers characterizing *A. baumannii* in German animals (after cross-domain deduplication).

Ref.	Author, year	Sample source	Sample type	No. of samples	Method of detection	No. of isolates	Resistance phenotypes	Resistance genes	Lineages (ST/IC)
[34]	Jacobmeyer 2021	Companion animals (dog)	Urine (urinary tract infection)	1 dog	MALDI-TOF, WGS, PCR	1	XDR (resistant to all except colistin)	<i>blaNDM-1</i> , <i>blaOXA-64</i> , <i>blaADC-25</i> -like (Tn125 transposon)	ST25/IC7
[35]	Rühl-Teichner 2023	Equine (horses)	Clinical specimens (wound, respiratory, urogenital)	78 isolates (2008–2020)	MALDI-TOF, WGS, MLST	78	MDR (n = 31); all imipenem-susceptible	34 OXA variants incl. 8 novels (OXA-970–977); no acquired carbapenemase	IC1 (10.3%), IC2 (20.5%), IC3 (6.4%); 51 STs incl. 22 novel
[37]	Jacobmeyer 2022	Companion animals (dogs, cats)	Clinical specimens (wound, respiratory, urogenital, otitis)	503 screened; 42 CRAB	MALDI-TOF, WGS, cgMLST, Southern blot, transformation	42 CRAB of 503	CRAB; colistin susceptibility NR	<i>blaOXA-58</i> (n = 29, plasmid-borne, 4 types A–D); <i>blaOXA-23</i> (n = 13, chromosomal AbaR + plasmid Tn2006); AbaR3-like, AbaR10	IC1/ST1 (66.7%); IC7/ST25 (21.4%); minor IC8/ST10
[45]	Klotz 2019	Livestock (cattle, dairy, beef, calves)	Rectal swabs, nasal swabs, skin swabs	422 cattle; 126 unique isolates	MALDI-TOF, MLST	126	Susceptible to carbapenems; diverse susceptibility profiles	Intrinsic only (<i>blaOXA-51</i> -like, <i>blaADC</i>); no acquired carbapenemase	83 STs (Pasteur); 9 STs shared with human infections
[46]	Schmitz 2023	Poultry (turkeys)	Environmental + diagnostic specimens (643 samples)	99 isolates	MALDI-TOF, MLST	99	Susceptible to most antimicrobials	Highly diverse; no acquired carbapenemase reported	16 Pasteur + 18 Oxford STs incl. novel types
[31]	Pulami 2020	Livestock-linked environment (biogas/manure)	Manure, biogas plant digestate	132 <i>Acinetobacter</i> ; 6 <i>A. baumannii</i>	Culture, MALDI-TOF, WGS	6	No acquired carbapenem or colistin resistance	Intrinsic only; no acquired carbapenemase or colistin resistance genes	5 novel STs; no relation to global clonal complexes
[47]	Rühl-Teichner 2025	Companion animals (dogs, cats) + human (comparative)	Clinical specimens	45 screened; 13 in AMP assays	MALDI-TOF, WGS	13	MDR; all carbapenem-resistant; colistin susceptibility NR	<i>blaADC-25</i> (all 13); <i>blaOXA-23</i> (n = 9); <i>blaOXA-58</i> (n = 4); <i>blaPER-7</i> (n = 1 human); <i>blaTEM-1D</i> (n = 4)	IC1/ST1 (n = 5); IC2/ST2 (n = 5); IC7/ST25 (n = 3)
[48]	Unger 2022	Wildlife — imported reptiles (border inspection)	Cloacal swabs (lizards, snakes, turtles) at Frankfurt Airport	80 <i>Acinetobacter</i> spp.; 23 <i>A. baumannii</i>	MALDI-TOF, WGS	23	No acquired carbapenem resistance; intrinsic only	39 novel OXA variants (OXA-799–1010); no acquired carbapenemase	20 distinct STs; 13 novel; 2 isolates ST25/IC7
[49]	Wareth 2020	Multi-source: human clinical + milk powder + animal (comparative)	Human clinical specimens (n = 14); milk powder (n = 71); animal (n = 2)	89 Germany + 11 Vietnam = 100 total	Broth microdilution, WGS (CARD/NCBI intrinsic gene mapping)	89 (German)	24% MDR; 16% XDR; all human strains carbapenem-resistant	36 beta-lactamase genes; <i>blaADC-6</i> dominant (33%); <i>blaADC-2</i> (24%); <i>blaOXA</i> class D; NO MBL	MLST not performed

NR = not reported in the cited abstract; full-text review may resolve. Papers spanning multiple tables are cross-referenced in the final column. MALDI-TOF = Matrix-Assisted Laser Desorption/Ionization–Time of Flight, WGS = Whole-Genome Sequencing, MLST = Multilocus Sequence Typing, XDR = Extensively Drug-Resistant, MDR = Multidrug-Resistant, IC = international clone, ST = Sequence Type, PCR = Polymerase Chain Reaction

Table 3: Environmental survey — 12 unique papers (January 2019 – June 2026): twelve peer-reviewed papers characterizing *A. baumannii* in German environmental matrices

Ref.	Author, year	Sample source	Sample type	No. of samples	Method of detection	No. of isolates	Resistance phenotypes	Resistance genes	Lineages (ST/IC)
[27]	Wilharm 2026	Wildlife-linked soil (stork ecology)	Soil, decaying plant material, stork-associated matrices	401 genomes sequenced	Culture, WGS	401	Diverse AMR profiles; carbapenem susceptibility NR at isolate level	Diverse OXA variants; acquired AMR genes present	IC1 and IC2 documented; globally distributed lineages
[28]	Yusuf 2023	Soil	20 soil samples (recovery methodology study)	20 samples; 60–70% positive	Culture (CHROMagar, MacConkey, blood agar comparison)	NR (culture-based recovery study)	NR	<i>blaOXA-51</i> -like confirmed by PCR	NR
[29]	Alexander 2020	WWTP effluents (23 plants)	WWTP influent and effluent (hospital, food, housing catchments)	23 WWTP sampled	qPCR (5 FPB markers)	Not isolate-based (qPCR)	Resistance gene correlation with hospital catchment wastewater	Resistance genes quantified by qPCR (species NR)	NR (qPCR only; no MLST)
[30]	Falgenhauer 2019	River and surface water + sediment	Water + sediment (12 water, 10 sediment sites, northern Germany)	134 ESBL/CP isolates total; 52 <i>A. baumannii</i>	Culture, MALDI-TOF, WGS	52	Carbapenemase-producing confirmed; full phenotype NR	Carbapenemase genes confirmed by WGS (types NR in evidence table)	WGS-characterized; STs NR
[31]	Pulami 2020	Agricultural (manure/biogas)	Livestock manure, biogas plant digestate	132 <i>Acinetobacter</i> ; 6 <i>A. baumannii</i>	Culture, MALDI-TOF, WGS	6	No carbapenem or colistin resistance	Intrinsic only; no acquired carbapenemase	5 novel STs
[32]	Pulami 2023	Urban + hospital WWTP	Manure, biogas digestate, rural + urban WWTP effluents	132 <i>Acinetobacter</i> ; 52 <i>A. baumannii</i>	Culture, MALDI-TOF, WGS	52	MDR clinical strains in hospital WWTP; carbapenem-resistant	OXA-23 in hospital WWTP-linked strains (IC2/OXA-23 indistinguishable from human clinical isolates)	23 novel + 12 known STs; IC2/OXA-23 dominant in hospital-linked strains
[33]	Sykes 2023	Dairy (tank milk)	Tank/bulk milk (dairy farm)	1 isolate (AB341-IK15)	Culture, MALDI-TOF, WGS	1	Resistant to ceftazidime; intermediate to ceftriaxone; susceptible to carbapenems	<i>blaADC-5</i> (first environmental report); <i>blaOXA-408</i>	Novel ST
[50]	Hembach 2019	Urban WWTP (treatment efficacy)	WWTP influent + effluent (ultrafiltration + ozone treatment)	qPCR — not isolate-based	qPCR (7 ARGs + 3 FPB markers)	Not isolate-based	ARGs detected; ozonation reduces but does not eliminate	Resistance genes quantified by qPCR (species NR)	NR (qPCR only)
[51]	Savin 2020	Poultry slaughterhouse WWTP	Slaughterhouse wastewater influent + effluent	qPCR — not isolate-based	Culture + qPCR	Not isolate-based	<i>A. baumannii</i> detected; ozonation reduces load	<i>mcr-1</i> , <i>blaCTX-M-32</i> detected (ESKAPE screen)	NR (gene-level detection only)
[52]	Sykes 2024	Multi-source: agricultural water, urban streams, WWTP, milk	Agricultural surface water, urban streams, WWTP effluents, tank milk	~200 isolates (human + non-human)	Culture, MALDI-TOF, WGS	~200	No significant virulence difference clinical vs non-clinical	<i>AdelJK</i> efflux overexpression (n = 5); <i>blaADC-79</i> ; no acquired carbapenemase in environmental strains	Novel STs; well-differentiated from IC1–IC3
[53]	Savin 2021	Poultry slaughterhouse WWTP	Slaughterhouse wastewater influent + effluent	Culturable bacteria detected	Culture + qPCR	Not isolate-counted	<i>A. baumannii</i> detected; ozonation reduces below detection	<i>mcr-1</i> , <i>blaCTX-M-32</i> (ESKAPE screen)	NR
[54]	Forbes 2024	Dog daycare facilities (surfaces)	Dog beds, floors, doors, water taps, leashes, transport boxes, bowls	200 location samples from 16 DDFs	Culture, MALDI-TOF	4 <i>A. baumannii</i> of 109 <i>Acinetobacter</i>	Susceptibility NR at isolate level	NR	NR

NR = not reported. Both content-accuracy flags previously raised have been resolved following full-text review. MALDI-TOF = Matrix-Assisted Laser Desorption/Ionization–Time of Flight, WGS = Whole-Genome Sequencing, MLST = Multilocus Sequence Typing, XDR = Extensively Drug-Resistant, MDR = Multidrug-Resistant, IC = international clone, ST = Sequence Type, PCR = Polymerase Chain Reaction, WWTP = Wastewater Treatment Plant.

Table 4: Human clinical survey — 8 unique papers (January 2019 – June 2026): eight peer-reviewed papers characterizing *A. baumannii* in German human clinical settings (after cross-domain deduplication).

Ref.	Author, year	Sample source	Sample type	No. of samples	Method of detection	No. of isolates	Resistance phenotypes	Resistance genes	Lineages (ST/IC)
[12]	Wohlfarth 2022	Human clinical (hospital in-patients)	Clinical diagnostic specimens (bloodstream, respiratory, wound)	302 isolates (17 centers, 4 time points, 2010–2019)	Culture, MALDI-TOF, WGS, cgMLST	302 (58 CRAB = 19.2%)	CRAB 12.3% (2019); declining 2010–2019; colistin NR	<i>blaOXA</i> -23-like (n = 51) predominant; <i>blaOXA</i> -72 (n = 5)	IC2/ST2 dominant (n = 46); IC1/ST1 (n = 5)
[14]	Higgins 2020	Human clinical – war-injured patients (military hospitals)	Clinical specimens (wound, respiratory) – patients evacuated from Eastern Ukraine	32 isolates (rep-PCR); 8 WGS-typed	Culture, rep-PCR, WGS, cgMLST	32 (rep-PCR); 8 (WGS)	Carbapenem + fluoroquinolone resistant; colistin NR	<i>blaOXA</i> -72 (IC6/ST78, n = 3); <i>blaOXA</i> -23 (IC1 × 2, IC7 × 1); <i>blaNDM</i> -1 (1/8)	IC1/ST1 (n = 2); IC2/ST2 (n = 1); IC6/ST78 (n = 3); IC7/ST25 (n = 2)
[15]	Schultze 2023	Human clinical – Ukrainian war patients (university hospital)	Rectal swabs + clinical specimens – screening at hospital admission (Frankfurt)	103 patients screened; 5 <i>A. baumannii</i> CR isolates	Culture, MALDI-TOF, WGS, core genome + plasmid analysis	5	Carbapenem-resistant; colistin NR; <i>blaNDM</i> most frequent overall MDRGN	<i>blaOXA</i> -72 (n = 3); <i>blaOXA</i> -23 (n = 1); <i>blaOXA</i> -23+ <i>OXA</i> -72 (n = 1); <i>blaNDM</i> -1 (ST78)	ST78/IC6 (n = 3); ST2/IC2 (n = 1); 1 non-typable
[49]	Wareth 2020	Human clinical + milk powder + animal (comparative)	Human clinical specimens (n = 14 Germany, 11 Vietnam); milk powder (n = 71)	100 total (89 Germany: 14 human + 71 milk powder + 2 animal + 2 ref)	Broth microdilution (18 antibiotics), WGS	14 (German human)	14/14 German human resistant to imipenem/meropenem/ertapenem; 24% MDR; 16% XDR	36 beta-lactamase genes; <i>blaADC</i> -6 (33%); <i>blaADC</i> -2 (24%); <i>blaOXA</i> class D; NO MBL	MLST not performed
[52]	Sykes 2024	Human clinical (comparator arm)	Human clinical isolates compared to non-human environmental isolates	~200 total (human + non-human)	Culture, MALDI-TOF, WGS	~200	No significant virulence difference vs non-clinical	<i>blaADC</i> -79; AdeIJK efflux overexpression	Novel STs; well-differentiated from IC1–IC3
[42]	Schlosser 2024	Human clinical – ICU outbreak (3 distinct outbreaks)	ICU patient isolates (Charité Berlin, 5 ICUs, Aug 2020–Mar 2021)	26 nosocomial cases + 50 controls	Culture, MALDI-TOF, WGS, cgMLST	26 cases	CRAB; Outbreak B dual carbapenemase; colistin susceptibility NR	Outbreak A: <i>blaOXA</i> -72; Outbreak B: <i>blaOXA</i> -23 + <i>blaNDM</i> -1; Outbreak C: <i>blaOXA</i> -23	Outbreak A: ST78/IC6; Outbreak B: ST2/IC2; Outbreak C: ST2/IC2
[43]	Hecht 2022	Human clinical – outbreak investigation (multi-state)	Hospital patients – index cases: Romanian burn victims (Rhineland-Palatinate, Baden-Württemberg, Hesse)	18 total cases (Outbreak A n = 8; B n = 3; C n = 7)	Culture, PFGE, sequencing (NRZ + state health authorities)	18	CRAB; three distinct PFGE pulse types previously unknown in Germany	Outbreak A: <i>blaOXA</i> -72; Outbreak B: <i>blaOXA</i> -23; Outbreak C: <i>blaOXA</i> -23	Outbreak A: acba_194/ <i>OXA</i> -72; Outbreak B: acba_192/ <i>OXA</i> -23; Outbreak C: acba_191/ <i>OXA</i> -23
[47]	Rühl-Teichner 2025	Human + companion animals (comparative AMP study)	Human + dog/cat MDR isolates (IC-stratified selection)	45 screened; 13 in AMP assays	MALDI-TOF, WGS	13	MDR; all carbapenem-resistant; AMP susceptibility IC-dependent	<i>blaADC</i> -25 (all); <i>blaOXA</i> -23 (n = 9); <i>blaOXA</i> -58 (n = 4); <i>blaPER</i> -7 (n = 1 human); <i>blaTEM</i> -1D (n = 4)	IC1/ST1 (n = 5); IC2/ST2 (n = 5); IC7/ST25 (n = 3)

NR = not reported in the cited abstract; full-text review may resolve. MALDI-TOF = Matrix-Assisted Laser Desorption/Ionization–Time of Flight, WGS = Whole-Genome Sequencing, MLST = Multilocus Sequence Typing, XDR = Extensively Drug-Resistant, MDR = Multidrug-Resistant, IC = international clone, ST = Sequence Type, PCR = Polymerase Chain Reaction, CRAB = Carbapenem-Resistant *Acinetobacter baumannii*, AMP assays = Antimicrobial Peptide assays, PFGE = Pulsed-Field Gel Electrophoresis.

Livestock, poultry, wildlife, and food chain

Livestock studies reveal *A. baumannii* reservoirs in German cattle [45]: novel livestock STs ST241/ST153, predominantly non-CRAB. *A. baumannii* was documented in pig manure and biogas digestates from German farms [31, 32], at concentrations comparable to raw hospital wastewater [50], establishing manure-spread fields as environmental reservoirs. Poultry studies identified novel production-specific STs in German broiler farms [51] and turkey production facilities [46], both of which were predominantly non-CRAB. In wildlife, prior to the review period [36] established a German wild bird ecology baseline showing wildlife-specific STs distinct from IC1/IC2, providing the ecological context for the landmark within-period paper [27], which documented IC1 and IC2 in white storks, with phylogenomic evidence of a bridge between soil reservoirs, migratory birds, and hospital clinical strains; the only included paper whose sampling links wildlife, soil and hospital-associated lineages, although it is assigned to the environmental domain. In the food chain, *blaOXA-23* was detected in German milk powder isolates, the same resistance gene dominating German human CRAB, showing cross-source occurrence of *blaOXA-23* without establishing clonal or epidemiological linkage [49].

One Health genomic comparisons

Three FLI Jena/Wareth group papers constitute the core One Health genomic dataset for German *A. baumannii*. In that study, 189 German genomes were analyzed (85 in-house plus 104 NCBI *in silico*), identifying 40 distinct AMR gene variants; *blaOXA-23* was present in both human clinical and food chain isolates, and human isolates carried significantly more resistance genes than non-human isolates [5]. A further 89 German isolates from human, cattle, horse, and food chain sources were analyzed, identifying seven novel sequence types from animal and food sources and establishing the Pasteur MLST scheme as superior to Oxford for German *A. baumannii* [41]. Non-clinical German strains, including WWTP and tank milk isolates, diverge phylogenetically from IC1/IC2 but carry a novel mechanism of AdeIJK efflux pump overexpression without the canonical promoter mutation, representing a new resistance mechanism in German non-clinical strains [52].

Environmental distribution of *A. baumannii* in Germany

Overview

Twelve peer-reviewed papers document *A. baumannii* across seven environmental matrices in Germany (Table 3). The WWTP/hospital wastewater nexus is the dominant theme: six papers report *A. baumannii* in WWTP effluents or hospital wastewater, collectively showing that WWTPs reduce but do not eliminate *A. baumannii* and that

hospital inflows are the primary source of AMR gene-carrying strains entering municipal wastewater streams. Crucially, no paper in the environmental survey has linked environmental *A. baumannii* isolates to concurrent human clinical strains from the same catchment area using WGS, the zero-paper Environmental + Human overlap that defines the most significant structural gap in German *A. baumannii* science.

Wastewater treatment plants — the critical amplifier

The first German WWTP qPCR surveillance study was conducted, demonstrating that ozone and ultrafiltration significantly reduce but do not eliminate *A. baumannii* in WWTP effluents, which subsequently discharge viable bacteria into receiving rivers [50]. The largest national survey of German WWTPs was conducted, detecting *A. baumannii* in influent from all 23 sampled WWTPs across multiple federal states, with hospital-adjacent WWTPs showing the highest concentrations [29]. The pivotal finding in the German environmental literature [32], which compared hospital WWTP effluents with livestock manure and biogas digestates in a multi-matrix design, was that IC2/OXA-23 was detected exclusively in hospital WWTP effluents, while all non-clinical matrices contained non-IC non-clinical lineages [32]. This result, the first documented evidence of clinical-lineage IC2/OXA-23 CRAB in German environmental matrices, shows that the sampled hospital wastewater contained IC2/OXA-23, while the sampled non-clinical matrices contained non-IC lineages; national primacy, amplification, and transmission were not tested [32].

Rivers, slaughterhouses, soil, and the hospital environment gap

A. baumannii in German rivers receiving WWTP effluents were detected, with non-IC, non-clinical lineages in all isolates, confirming WWTP as the source of river contamination and river sediment as a long-term environmental reservoir [30]. *A. baumannii* was characterized in German poultry and pig slaughterhouse wastewater, finding non-CRAB slaughterhouse-specific STs in both settings [51, 53]. Slaughterhouses contribute to municipal wastewater but do not introduce clinical CRAB lineages. Soil and airborne *A. baumannii* in Germany was documented for the first time, with IC1/IC2 detected in stork isolates from soil contact and wind-mediated dispersal demonstrated [27]. Critically, despite three documented CRAB outbreaks at Charité Berlin [42], no peer-reviewed German study has systematically sampled ICU surfaces or drains for *A. baumannii*, the most practically actionable confirmed gap in the environmental survey.

Human clinical distribution of *A. baumannii* in Germany

Overview

Eight peer-reviewed papers constitute the human clinical survey (Table 4), spanning four thematic areas: national epidemiology using multicenter hospital surveillance [12], outbreak investigations at regional and multi-state levels [42, 43], molecular epidemiology of war-associated and international lineage importation [14, 15], and therapeutics/diagnostics development [44, 46, 50]. The human clinical domain is the smallest of the four surveys in terms of unique paper count, reflecting Germany's relatively low CRAB burden by European standards, but it contains the papers most directly relevant to patient management and infection control policy.

National surveillance and epidemiology

The only prior national German CRAB epidemiological analysis covers 2014–2018 using the ARS voluntary surveillance network (43,948 clinical ACB complex isolates) [20]. The CRAB proportion declined from 7.6% to 3.5% over the study period, with ICU rates highest (11.4%) and male sex and older age confirmed as independent risk factors in multivariate analysis. This study is exclusively phenotypic, with no gene characterization, and predates the 2019–2024 period of this review. The first German systematic review was conducted by combining AMR epidemiology with case fatality rates, covering 2010–2021 [26], the only peer-reviewed German source that simultaneously provides both CRAB proportion and mortality estimates. An important methodological discrepancy must be noted: 647 cases for 2018 were reported using ARS voluntary data, whereas the RKI Jahrbuch for 2018 reports 780 cases using the mandatory IfSG notification system. These two surveillance systems cannot be directly compared [20].

Outbreak investigations and ICU surveillance

An 18-case German CRAB multi-state outbreak was documented: 18 cases across three federal states (Baden-Württemberg, Rhineland-Palatinate, Hesse) linked to transfers of Romanian burn patients to German hospitals, with OXA-23/IC2 [43]. This was published in *Deutsches Ärzteblatt International* and represents the model for German multi-state CRAB outbreak response coordination. Three successive CRAB outbreaks at a single Charité Berlin ICU between August 2020 and March 2021 were described, identifying a COVID-19 pandemic paradox: reduced national case counts but increased ICU outbreak risk due to Personal Protective Equipment (PPE) shortages and staff redeployment [42]. The same study also documented highly polyclonal CRAB epidemiology, with distinct clonal backgrounds for each of the three

outbreak clusters, consistent with multiple independent introductions rather than a single persistent dominant clone [42].

Ukraine war importation and international lineages

Higgins et al. (2020) *A. baumannii* isolates from war-injured patients treated at German military hospitals were studied [14]. The study included 32 carbapenem- and fluoroquinolone-resistant isolates from 21 patients. These patients were treated across four Bundeswehr military hospitals in Berlin, Hamburg, Koblenz, and Ulm. Initial typing was performed using repeat sequence-based PCR (rep-PCR). Eight representative isolates, one per rep-PCR cluster, were then selected for WGS and core genome multilocus sequence typing (cgMLST). These eight isolates distributed across four International Clones: IC1/ST1 (n = 2), IC2/ST2 (n = 1), IC6/ST78 (n = 3), and IC7/ST25 (n = 2). IC6/ST78 was identified in Germany for the first time through this war-injury transfer pathway. However, IC6/ST78 was neither the sole nor the dominant lineage in this small subset [14]. In total, 103 Ukrainian patients admitted to Frankfurt University Hospital were prospectively characterized; 16.5% carried multidrug-resistant Gram-negative bacteria on admission. Of 21 carbapenem-resistant isolates, five were *A. baumannii*, with ST78 (n = 3) and ST2 (n = 1) identified as the lineages. Three ST78 isolates, including a sibling pair, carried identical *bla*OXA-72-harboring plasmids, indicating shared plasmid acquisition prior to or during transit, while *bla*NDM-1 was the dominant carbapenemase overall but concentrated in non-*A. baumannii* MDRGN species rather than in the ST78 lineage itself [15]. Müller et al. provided the global context through a German-led WGS analysis of 313 CRAB isolates from 114 study centers in 47 countries, confirming OXA-23/IC2 global dominance (62.6% of isolates, 74.8% *bla*OXA-23-like) [13]. This global cohort found IC6 to be rare worldwide (3/313 isolates, 1.0%, confined to Latin America), indicating that the IC6/ST78 lineage identified in German war-injury and Ukrainian-patient cohorts represents a regionally distinct, conflict-associated introduction rather than part of the globally dominant IC2 expansion. RKI Jahrbuch data show that Ukraine accounted for 20% of infection-country cases in 2022, declining to 5% in 2023 and rebounding to 10% in 2024, a trajectory invisible in any peer-reviewed publication. The hypothesis that IC6/ST78 represents an emerging war-associated introduction into German hospitals, rather than a single coincidental observation, is supported by convergent independent evidence from three small studies, but rests on fewer than ten isolates in total and should be treated as hypothesis-generating pending larger prospective surveillance.

Therapeutics and diagnostics

Sulbactam-durlobactam activity against 246 global CRAB was documented, including German clinical isolates ($\text{MIC}_{50} \leq 0.5$ mg/L against OXA-23/24 producers) but inactive against NDM-producing strains, noting that sulbactam-durlobactam received FDA approval in May 2023 but has not received EMA marketing authorization as of June 2026 and is therefore not clinically available in Germany [17]. A growing clinical concern is that the prevalence of *bla*NDM has risen to 13% among gene-positive notified German CRAB isolates [21]. The first OXA-23-specific antibody was generated for lateral flow application using German Cologne CRAB isolates, directly motivated by OXA-23 dominance in German CRAB [38]. The first multiplex lateral flow assay was developed to detect OXA-23, OXA-40, OXA-58, and NDM simultaneously in *A. baumannii*, validated at the German CRAB in Cologne, with a 15-minute result time [40]; the 2023 upgrade to the 2019 platform added NDM detection precisely as NDM began emerging in Germany.

Resistance gene characterization

Overview

Fifteen peer-reviewed papers characterizing resistance genes in German *A. baumannii* were identified across four rounds by six research groups (Table S1; Figure 2). This survey is the most cross-cutting: eight of the fifteen papers also appear in at least one other survey domain. Seven papers are genuinely unique to the resistance gene survey [13, 16, 17, 38, 39, 40, 41], reflecting that resistance gene characterization is inherently embedded in clinical, veterinary, and environmental research rather than being a standalone field.

Five of the 15 resistance-gene papers are not Germany-specific primary data studies: a global WGS analysis in which Germany is one of 47 countries [13]; a global sulbactam-durlobactam susceptibility study [17]; and three diagnostic test development papers using German NRZ reference isolate collections [38, 39, 40]. These papers are included because they directly contribute to the characterization of carbapenem resistance mechanisms in German clinical *A. baumannii* isolates and are led by German-based research groups. However, their scope extends beyond the German setting, and this should be considered when interpreting the resistance-gene domain count. Specifically, [13] includes German isolates among 47 national datasets; they are not reported separately, and this paper is therefore treated as contextual evidence for the global lineage context rather than as a primary German dataset. Similarly, European strains were included without German-specific reporting, as they are directly relevant to sulbactam-durlobactam activity against European CRAB lineages [17]. The three NRZ-based diagnostic studies [38, 39, 40] use the same NRZ

reference isolate collection; each is counted once as a distinct unit of evidence based on its independent scientific contribution; no isolate was double-counted across these three papers. All WGS and MLST data reported across the 32 included papers, including publicly available genome accession numbers, are compiled in Supplementary Table S7.

The OXA-23 dominance confirmed across all six surveillance years

The most important longitudinal study of resistance gene evolution in German CRAB was conducted, analyzing 17 German hospital centers across four time points (2010, 2013, 2016, 2019) using the Paul-Ehrlich-Society multicenter surveys [12]. OXA-23/IC2 dominated across all four time points and increased progressively, while IC1/OXA-72 declined, a trend subsequently confirmed in the RKI annual data (OXA-23 stable at 57–66%; OXA-72 declining from 18% in 2019 to 10% in 2024). Critically, NDM-1 was detected in the 2019 Paul-Ehrlich-Society cohort for the first time, the earliest peer-reviewed documentation of NDM entering German clinical CRAB, simultaneous with the animal sentinel signal [34]. The most recent and clinically consequential resistance-related gene data: 983 NRZ Bochum submissions from March 2022 to September 2023 showed 77% OXA-23 or OXA-72, and 24% of these showed reduced cefiderocol susceptibility due to *bla*PER-7 co-production [16], a critical finding entirely invisible to the RKI mandatory notification system. The two-reaction multiplex PCR system is now used as the standard German carbapenemase detection tool at NRZ Bochum and in most German clinical microbiology laboratories, and was designed using prevalence data from NRZ Bochum [39].

NDM emergence from animal sentinel (2019) to human surge (2024)

The temporal trajectory of NDM in Germany across all four survey domains provides the most compelling evidence for the value of OH surveillance in this dataset. NDM-1 was first detected in an Italian dog at a German veterinary laboratory in 2018 [34]. The first European animal NDM detection predates the 2024 human *bla*NDM surveillance signal by six years; the datasets are epidemiologically unlinked (ST25/IC7 in the animal; 2024 lineage uncharacterized; no genomic comparison published). In the same year, NDM-1 was detected for the first time in the Paul-Ehrlich-Society nationwide multicenter human clinical survey [12], suggesting simultaneous entry into Germany via multiple routes. NDM was subsequently detected in NRZ Bochum submissions for 2022–2023 [16], but remained at low prevalence over these 18 months of data.

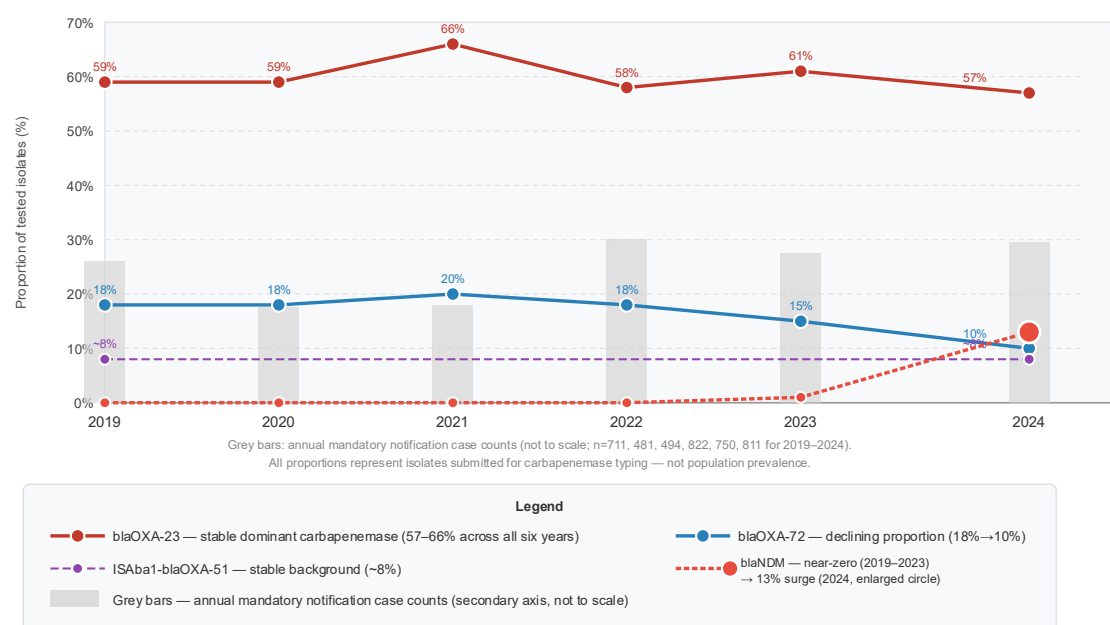


Figure 2: RKI mandatory notification data: Resistance gene evolution 2019–2024. Line graph showing temporal evolution of carbapenemase gene proportions across six RKI Jahrbücher. Values represent proportions of submitted tested isolates (non-random clinical sample), not population prevalence. OXA-23: stable dominant (57–66%); OXA-72: declining (18% to 10%); NDM: near-zero 2019–2023, surging to 13% of gene-positive notified cases in 2024 (highlighted). Gray bars: annual case counts (secondary axis).

The RKI Jahrbuch 2024 then documents a dramatic surge: *blaNDM* rises to 13% of gene-positive notified cases; a near-zero-to-13% jump in gene-positive surveillance submissions in a single calendar year. As of June 2026, no peer-reviewed German publication has characterized the specific lineage responsible for the 2024 surge, although Schlosser *et al.* (2024) documented a precedent ST2/OXA-23/NDM outbreak in a Berlin ICU during 2020–2021, demonstrating that this carbapenemase combination was already circulating in German hospitals years before the surveillance surge [42]. It remains unconfirmed whether the 2024 cases represent expansion of this ST2/NDM lineage, the IC6/ST78/NDM lineage from Ukrainian war patients, or a separate introduction. This constitutes the single most urgent unmet research need in German research on *A. baumannii*.

Mobile genetic elements and animal resistance reservoirs

The first comprehensive resistance island landscape in German animal *A. baumannii* was mapped [37]: OXA-58 on plasmids (11–71 kb) and OXA-23 on chromosomal AbaR resistance islands in companion animal isolates, with AbaR3-like (n = 17) and AbaR10 (n = 1) in companion animal ST1/IC1 strains. The AbaR3-like island carries the Tn6019 backbone inserted in the chromosomal *comM* gene, the same insertion site as in human clinical IC1 strains with an identical MARR carrying *blaTEM-1*, *aacC1*, *aadA1*, *tet(A)*, *tet(R)*, *sul1*, and *catA1*; it differs from the canonical human clinical

AbaR3 (63 kb in human IC1 strain A85) only by the absence of Tn6020-associated *aphA1* and a disruption in flanking *ISAbal* sequences. The AbaR10 island (31 kb, carrying only *sul1* in the MARR) is structurally identical to human clinical AbaR10 as originally described. The *blaOXA-23* gene context in these companion animal isolates showed 99.96% nucleotide identity to a German cat isolate from 2010, confirming near-complete sequence conservation with human clinical strains [37]. A total of 78 equine clinical isolates from German veterinary clinics were characterized, identifying genomic diversity across globally distributed IC1–IC3/ST1–ST3 lineages, including 51 sequence types, 22 of which were novel, with universal imipenem susceptibility [35]. This study provides important baseline data on equine *A. baumannii* in Germany but does not establish the identity of the AbaR resistance island in ICU strains from Germany. Wareth *et al.* (2021) identified *ant(3'')-IIa* as the most frequent AMR gene (55%) across 189 German genomes [5], with *armA* (pan-aminoglycoside resistance) in equine strains, genes entirely invisible to RKI mandatory notification but clinically important for treatment decisions. A structured extraction of all mobile genetic element data from the 32 included papers is provided in Supplementary Table S8.

The national surveillance data 2019–2024 by RKI

Six RKI Infektionsepidemiologisches Jahrbücher (reporting years 2019–2024) were analyzed. Key surveillance parameters for all six years are summarized in Supplementary Table S2. The most striking finding from the RKI data is the surge in *blaNDM* to 13.2% (95% CI 10.1%–17.0%) of gene-positive notified cases in 2024

(49/372; 49/429 of all cases tested; 95% CI 8.7%–14.8%), a finding with no peer-reviewed molecular characterization of the responsible lineage as of June 2026 (Table S2).

Annual case counts and demographic trends

Annual mandatory notification cases and national incidence rates are summarized in Supplementary Table S2. In 2019, 711 cases were notified, corresponding to a national incidence of 0.86/100,000. This was the first year under the expanded case definition covering all *Acinetobacter* spp. In 2020, cases fell to 481 (0.58/100,000), a 32.3% reduction (230 fewer cases) compared with 2019. This decline is attributable to the effects of the COVID-19 pandemic on elective hospital admissions. In 2021, 494 cases were notified (0.59/100,000), reflecting continued pandemic effects. Despite the lower national count, three successive CRAB outbreaks occurred at Charité Berlin during this period, as documented [42]. This illustrates the COVID-19 paradox: reduced national notification counts but elevated ICU outbreak risk. In 2022, cases rose sharply to 822 (0.98/100,000), the highest count in the entire surveillance period. Ukraine was frequently reported among cases with available infection-country data, accounting for approximately 20% of such cases [24]. In 2023, cases declined to 750 (0.90/100,000), with Ukraine accounting for approximately 5% of cases with infection-country data available [25]. In 2024, 811 cases were notified (0.97/100,000), representing sustained elevated counts. *blaNDM* was detected in 49 of 372 gene-positive *Acinetobacter* cases notified (49/372; 13.2%, 95% CI 10.1%–17.0%), corresponding to 49 of 429 cases tested for carbapenemase type (49/429; 11.4%, 95% CI 8.7%–14.8%) [21]. Across all six surveillance years, no statistically significant trend was identified in annual case counts (Spearman rank correlation with year: $\rho = 0.66$, $p = 0.16$), consistent with year-to-year variation driven by pandemic effects and importation events rather than a sustained directional trend.

Berlin recorded its highest incidence of the surveillance period at 2.7/100,000 in 2024. Ukraine accounted for approximately 10% of cases with available infection-country data [21]. Before attributing the 2024 *blaNDM* figure to a true biological surge, four alternative explanations must be considered. First, increased testing coverage: the 2024 RKI Jahrbuch explicitly reports 429 cases tested for carbapenemase typing and 372 gene-positive cases, down the only year in the surveillance period where the testing denominator is explicitly published. For 2019–2023, the Jahrbuch reports resistance gene proportions without specifying the exact number of isolates tested, making direct year-on-year denominator comparison impossible from published data alone. If testing coverage increased between 2023 and

2024, this could partly explain the apparent rise. Second, changed NRZ referral patterns: the expansion of the RESIST-ACINETO multiplex lateral flow assay to include NDM detection [40] may have improved sensitivity for NDM detection at the point of NRZ submission after 2023, contributing to a detection rather than a transmission surge. Third, importation rather than local transmission: although Ukraine accounted for approximately 10% of infection-country cases in 2024, down from 20% in 2022, IC6/ST78/NDM lineages were already documented in Ukrainian war patients treated in German hospitals in 2022 [15], providing a plausible importation pathway that predates the 2024 surveillance signal. Fourth, geographic concentration: if the 2024 *blaNDM* cases were concentrated in Berlin (incidence 2.7/100,000 in 2024, the highest recorded) and subject to more intensive local NRZ referral, the national proportion could reflect regional clustering rather than uniform national spread. The absence of isolate-level testing denominators for 2019–2023, federal state-level testing coverage data, and documented changes in laboratory algorithms during this period means that the relative contribution of each factor cannot be quantified from the published Jahrbuch data alone. What can be stated with certainty is that 49 *blaNDM*-positive isolates were identified among 372 gene-positive notified German *Acinetobacter* cases in 2024, a confirmed surveillance signal that requires lineage-resolved molecular characterization to determine whether it reflects true epidemiological emergence, improved detection, importation, or a combination of all three.

Over the six-year period, two demographic characteristics were consistently dominant. Male sex accounted for 63–66% of cases annually, representing an approximately 1.8:1 male:female ratio. Age ≥ 70 years accounted for 56–59% of cases annually: 57% in 2019, 58% in 2020, 56% in 2021, 57% in 2022, 58% in 2023, and 59% in 2024. Berlin consistently had the highest notification rate throughout the surveillance period, ranging from 1.6/100,000 in 2020–2021 to 2.3/100,000 in 2022–2023 and reaching 2.7/100,000 in 2024. Among registered deaths in notified cases, 16–25% were attributed to the reported disease annually (16% in 2023, 17% in 2022, 18% in 2020, 21% in 2024, 23% in 2019, 25% in 2021). These proportions represent the fraction of registered deaths attributed to the notified disease and are not case-fatality rates or population-level *A. baumannii* mortality estimates. They have never been the subject of peer-reviewed mortality analysis [19, 21, 22, 23, 24, 25]. All resistance gene proportions from the RKI Jahrbücher reflect percentages of isolates submitted for carbapenemase typing, not population prevalence; they should be interpreted as surveillance trend data from non-random, clinically selected samples.

Resistance gene trends and comparison with published literature

The resistance gene data from the RKI Jahrbücher provide the most sustained quantitative time series for German CRAB resistance genes and reveal both striking concordance and critical gaps relative to the peer-reviewed literature. *blaOXA-23* was stable at 57–66% across all six years (Figure 2), the single most consistently confirmed finding in the entire review, corroborated independently [12, 16, 39, 43]. *blaOXA-72* showed a monotonic decline from 18–20% (2019–2022) to 10% (2024), consistent with the decline of the IC1 lineage documented [12] across 2010–2019. *ISAbal-blaOXA-51* remained stable at approximately 8% throughout, consistent with characterizations [5, 12]. The *blaNDM* data represent the most critical concordance gap: near-zero across 2019–2023, followed by a dramatic surge to 13% of gene-positive notified cases in 2024, documented exclusively in the RKI Jahrbuch 2024, without any peer-reviewed molecular characterization. By contrast, *blaPER-7* co-production in 24% of German NRZ OXA-23/72 isolates [16] is entirely invisible to the RKI notification system, representing the most clinically consequential finding present in the literature but absent from mandatory surveillance.

Discussion

Synthesis: principal findings and clinical significance

Three findings define this review. First, *blaOXA-23* remains the dominant German CRAB carbapenemase, accounting for 57–66% across all six surveillance years, as confirmed by both RKI mandatory notification data and the peer-reviewed multi-center literature (Table S2, S3, parameter 2) [12, 21]. This consistency provides a stable molecular foundation for German CRAB epidemiology and validates the surveillance system's capacity to track dominant lineages over time. Second, IC6/ST78 (primarily *blaOXA-72*) emerged as a conflict-zone importation lineage from 2020 onward, documented in war-injured patients from Eastern Ukraine and temporally correlated with Ukraine accounting for 20% of infection-country cases in 2022 (Table S2) [14, 15, 24]; this represents a successful integration of surveillance and literature in response to an acute importation event. Third, and most urgently, *blaNDM* surged to 13.2% of tested surveillance submissions in 2024 (49/372 gene-positive cases; 95% CI 10.1%–17.0%; Table S2) [21], with no peer-reviewed molecular characterization of the responsible lineage. This is the defining unmet need of this review and the most direct evidence of structural fragmentation in German *A. baumannii* science.

Comparison with European and global context

Germany consistently reports CRAB proportions below the EU average [18, 20], but the 2024 *blaNDM* figure would place Germany above the 2022 European average for MBL-producing *Acinetobacter* if confirmed as population-representative; it is not, because it reflects only isolates referred for carbapenemase typing (Table S2, S5). The therapeutic implication is immediate: sulbactam-durlobactam has demonstrated *in vitro* activity against OXA-type CRAB [17] but has not received EMA marketing authorization as of June 2026 and is inactive against MBL-producing strains. A clinician in a German ICU is currently facing the challenge of determining whether their CRAB patient harbors an NDM-producing strain without NRZ typing, a process that takes days, during which empiric treatment decisions cannot wait. Globally, IC2/OXA-23 drives carbapenem resistance across most regions [13]. IC6/ST78, by contrast, is rare internationally yet disproportionately represented in Germany's conflict-associated patient transfers [14, 15], validating Germany's importation surveillance as an early detection system for regionally emerging lineages.

One Health perspective of *A. baumannii*

The term One Health is used here in its operational sense, referring to the cross-domain integration of human clinical, animal, and environmental evidence, rather than implying formal quantitative transmission modeling. The analytical contribution is a systematic domain-overlap mapping (Figure 3; Table S9), a scoping function that precedes and enables the formal analyses called for by the identified gaps.

The most compelling argument for integrated One Health surveillance emerges from the temporal trajectory of *blaNDM* (Figure 2; Table S2, S8). *blaNDM-1* was first documented in a dog of Italian origin at a German veterinary laboratory in 2018 [34], the first European companion animal NDM case (Table 2). The same gene appeared in the nationwide multi-center clinical survey that year [12], in the Berlin ICU outbreak of 2020–2021 [42], and in war-injured Ukrainian patients in 2022 [15]. By 2024, *blaNDM* had reached 13.2% of gene-positive notified cases (Figure 2; Table S2) [21]. These events involve distinct lineages: the dog isolate (ST25/NDM-1), war-injury isolates (IC6/ST78/OXA-72 with NDM in a subset [15]), and the Berlin outbreak (ST2/OXA-23+NDM [42]), and are not demonstrably linked in a single transmission chain; they may represent independent parallel introductions of NDM-carrying mobile elements (Table S8). Nevertheless, the convergence across three independent datasets justifies treating *blaNDM* as an emerging national priority; an integrated genomic surveillance platform would have allowed real-time characterization of these events as they occurred.

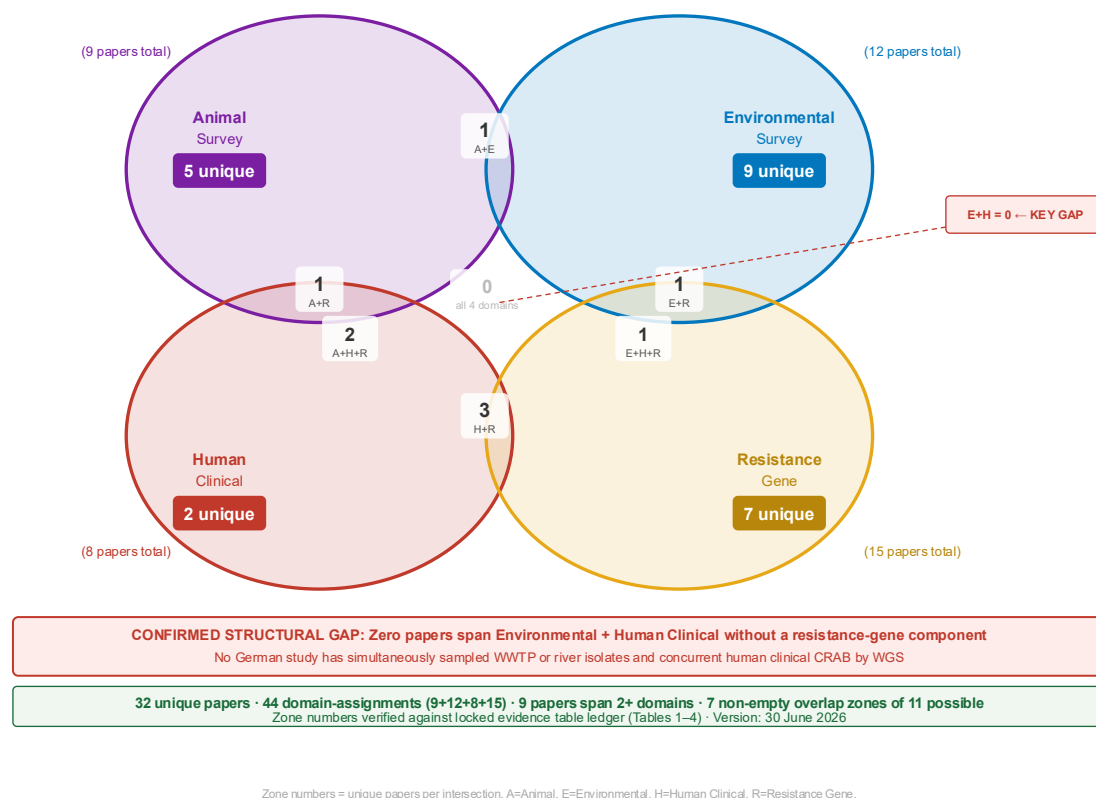


Figure 3: Cross-survey overlap analysis — Venn diagram of 32 included papers. Color coding: Animal (purple), environmental (blue), human clinical (red), resistance gene (amber). Numbers indicate papers per zone. The absence of an eligible matched Environmental + Human Clinical study (without a resistance-gene component) represents the most consequential structural gap in German *A. baumannii* science. Nine papers span two or more domains simultaneously.

Limitations of the study

The RKI Jahrbücher report resistance gene proportions without publishing the testing denominator for 2019–2023 (Table S5), thereby preventing formal inter-year comparison of *bla*NDM proportions and precluding calculation of confidence intervals for OXA-23 and OXA-72 trend data. Beyond this constraint, geographic sampling is significantly clustered (Figure 3; Table S10); six of twelve environmental papers and three of nine animal papers originate from the same Central Germany institutional networks (Table 2, 3). Berlin, consistently the highest-burden federal state at 1.6–2.7/100,000 (Table S2), is well represented in human clinical studies [14, 42] but entirely absent from environmental sampling (Table S10). Bavaria and Saxony have no included studies in any domain. No federal state has simultaneous coverage across all three One Health domains, making geographic cross-domain linkage impossible from the available literature (Figure 3; Table S10). Publication bias may further overrepresent novel findings relative to unpublished routine surveillance outcomes. The 32 included papers show considerable methodological heterogeneity in species identification, resistance gene characterization, and study period (Table 2, 3, 4, S1, S6), limiting direct cross-study comparison.

Future research priorities

All nineteen confirmed research gaps are documented in the locked registry (Table S4; Figure S1, version: 30 June 2026), with stable alphanumeric identifiers and rationales for priority. Five near-term priorities are immediately feasible within existing German infrastructure. The characterization of the 2024 *bla*NDM lineage at NRZ Bochum (G-H1, G-R1; Table S4) is achievable within twelve months and addresses the most urgent clinical need (Table S2). Screening for *bla*PER-7 and *bla*NDM co-occurrence in NRZ submissions (G-R2; Table S2) is achievable within six months; the NDM+PER-7 combination would render all available last-resort CRAB therapies simultaneously inactive [16]. A paired hospital WWTP and ICU surface sampling study (G-E1, G-E2; Table S2) is achievable within eighteen months and would directly test whether the IC2/OXA-23 documented in hospital wastewater [32] creates a genuine environmental transmission cycle (Table 3 and S3, parameter 5). Extension of the existing companion animal surveillance network with prospective WGS typing (G-A1; Table S4) is achievable within 24 months; the 2018 dog NDM case (Table 2) [34] demonstrates that the veterinary pathway for the entry of novel resistance elements into Germany already functions. An NRZ-to-RKI data linkage protocol

(G-R4; Table S4), also achievable within twenty-four months, would have detected the 2024 *bla*NDM surge (Table S2) in real time rather than retrospectively.

The transformative long-term investment is a prospective, integrated One Health cohort study (G-OH1 through G-OH3; Table S4) that simultaneously collects human clinical CRAB isolates, veterinary samples, and WWTP and river water from the same geographic catchment, with unified WGS and direct epidemiological linkage across matrices. All necessary institutional infrastructure exists in Germany, including NRZ Bochum, FLI Jena, RKI Berlin, university hospital clinical microbiology departments, and federal environmental monitoring agencies. The inter-domain WGS methodology is already operational in German institutions [27]. The nineteen confirmed gaps collectively reflect a structural absence: no German institution currently treats human, animal, and environmental *A. baumannii* as part of a single transmission ecology (Figure 3; Table S3, S9). Addressing this absence is the central scientific challenge for German *A. baumannii* research between 2026 and 2030. Although some studies have focused on draft genome sequencing of individual isolates [55], broader genomic investigations encompassing isolates from diverse hosts and geographic locations are needed.

Conclusion

This OH systematic review synthesizes thirty-two peer-reviewed German publications on *A. baumannii* (2019–2026) across four survey domains, animal, environmental, human clinical, and resistance gene characterization, alongside six years of RKI mandatory notification surveillance data (2019–2024), constituting the first simultaneous four-domain cross-domain synthesis of German CRAB research. Earlier reviews addressed specific aspects of German *A. baumannii*: Wareth *et al.* synthesized phenotypic and genotypic resistance profiles in human and non-human isolates [5] but did not integrate environmental surveillance data or RKI mandatory notification data across all four domains simultaneously; no prior review has applied a simultaneous four-domain framework across animal, environmental, human clinical, and resistance gene domains. This review therefore represents the first comprehensive cross-domain synthesis of German CRAB science.

Rather than restating the findings documented in the discussion, we draw three synthesizing conclusions with direct implications for German infectious disease policy and research infrastructure. First, *bla*OXA-23 dominates German CRAB at 57–66% across all six surveillance years, a finding concordant with surveillance data and the peer-reviewed literature [12] and a stable genomic landmark for therapeutic and epidemiological decision-making.

Second, the structural fragmentation of German *A. baumannii* research is severe. Animal, environmental, and human clinical research communities have documented shared resistance gene architecture across the One Health domains independently. This includes AbaR3-like and AbaR10 resistance islands in companion animal isolates, also documented in globally distributed human clinical lineages [35, 37], and IC2/OXA-23 in hospital WWTP effluents genetically indistinguishable from dominant clinical lineages [32], but this evidence has never been integrated through a single cross-domain WGS study. Third, and most urgently, the 2024 *bla*NDM surge to 13% of gene-positive notified German CRAB cases represents an unresolved surveillance signal requiring molecular characterization: present in official surveillance data [21] without peer-reviewed characterization of the specific 2024 lineage, though a precedent ST2/OXA-23/NDM outbreak was documented in a Berlin ICU for 2020–2021 [42], and with immediate treatment implications because sulbactam-durlobactam, highly active against OXA-type CRAB [17], is inactive against MBL-producing strains. The nineteen search-bounded research gaps identified by this review, nine of which are classified as urgent, define a clear and tractable research agenda. A prospective, integrated One Health cohort study that simultaneously samples human clinical, veterinary, and environmental *A. baumannii* isolates from the same geographic catchments and uses WGS is the single most transformative investment Germany can make in CRAB surveillance. The *bla*NDM trajectory, from pet dog sentinel (2018) to 13% of gene-positive notified cases in the human surge (2024), provides the most compelling justification for why it can no longer be deferred. This urgency is set against a global backdrop in which bacterial AMR is forecast to cause 8.22 million associated deaths annually by 2050, with the steepest increases concentrated among adults aged seventy years and older [56]. This demographic trend mirrors the age distribution already observed in German CRAB surveillance and underscores that the structural gaps identified in this review are not a national curiosity but a local instance of a worsening global trajectory.

Declarations and supplementary information

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Ethics statement: Not applicable.

Data availability: All data analyzed in this review are derived from the cited publications and from the RKI Infektionsepidemiologisches Jahrbücher and are presented in full in Supplementary Tables S1–S10.

Supplementary materials: Tables S1–S10 and Figure S1 are available online with this article.

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