Clinical prediction models for multidrug-resistant organism colonisation or infection in critically ill patients: a systematic review protocol

Yi Wang, Yanyan Xiao, Qidi Yang, Fang Wang, Ying Wang, Cui Yuan

ABSTRACT

Introduction Multidrug-resistant organisms (MDROs) are pathogenic bacteria that are the leading cause of hospital-acquired infection which is associated with high morbidity and mortality rates in intensive care units, increasing hospitalisation duration and cost. Predicting the risk of MDRO colonisation or infection for critically ill patients supports clinical decision-making. Several models predicting MDRO colonisation or infection have been developed; however, owing to different disease scenarios, bacterial species and few externally validated cohorts in different prediction models; the stability and applicability of these models for MDRO colonisation or infection in critically ill patients are controversial. In addition, there are currently no standardised risk scoring systems to predict MDRO colonisation or infection in critically ill patients. The aim of this systematic review is to summarise and assess models predicting MDRO colonisation or infection in critically ill patients and to compare their predictive performance.

Methods and analysis We will perform a systematic search of PubMed, Cochrane Library, CINAHL, Embase, Web of science, China National Knowledge Infrastructure and Wanfang databases to identify all studies describing the development and/or external validation of models predicting MDRO colonisation or infection in critically ill patients. Two reviewers will independently extract and review the data using the Data Extraction for Systematic Reviews of Prediction Modelling Studies checklist; they will also assess the risk of bias using the Prediction Model Risk of Bias Assessment Tool. Quantitative data on model predictive performance will be synthesised in meta-analyses, as applicable.

Ethics and dissemination Ethical permissions will not be required because all data will be extracted from published studies. We intend to publish our results in peer-reviewed scientific journals and to present them at international conferences on critical care.

PROSPERO registration number CRD42022274175.

INTRODUCTION

Multidrug-resistant organisms (MDROs) increase the risk of poor outcomes worldwide.1 MDROs, including methicillin-resistant Staphylococcus aureus (MRSA), carbapenem-resistant Enterobacteriaceae (CRE), vancomycin-resistant Enterococcus (VRE) and extended-spectrum β-lactamase-producing Enterobacteriaceae (ESBL-EKP), etc, among others, are the leading causes of hospital-acquired infections.2 A recent study, based on data from patients treated across 890 hospitals in the USA from 2012 to 2017, reported 622 390 cases of infection; MRSA and ESBL infections accounted for most of these cases.3 In China, the national report on bacterial resistance in 2020 found that the detection rates of erythromycin-resistant Streptococcus pneumoniae (ERSP), methicillin-resistant coagulase-negative Staphylococci (MRCNS) and carbapenem-resistant Acinetobacter baumannii (CRAB) were highest at tertiary hospitals.4 The intensive care unit (ICU) has the highest incidence of MDROs across all hospital departments. Even in developed countries, where infection control is well-organised, approximately 25% of ICU
Review objectives

The aim of this systematic review is to evaluate the reporting and methodology of studies on models predicting MDRO colonisation or infection in critically ill patients. We will apply the Prediction Model Risk of Bias Assessment Tool (PROBAST) to assess the risk of bias in studies on model development and validation. The specific objectives of this review are to:

1. Summarise models predicting MDRO colonisation or infection in critically ill patients.
2. Critically assess the methodology of these models.
3. Qualitatively describe the relevant models.
4. Conduct meta-analyses, as suitable, to estimate the overall performance of each risk model for predicting MDRO colonisation or infection.

METHODS AND ANALYSIS

This protocol is presented according to the Preferred Reporting Items for Systematic reviews and Meta-Analyses Protocols (PRISMA-P) guidelines (online supplemental file 1).22 This systematic review is scheduled to be performed from April to December 2022.

Literature search

PubMed, CINAHL, Embase, Web of Science, Cochrane Library, China National Knowledge Infrastructure and Wanfang databases will be searched from inception until April 2022. Relevant unpublished studies and grey literature will be identified using Google, conference articles, shortlisted study reference lists, index-related articles on PubMed and existing relevant reviews.

The following search strategy with related key words was developed: (extended-spectrum beta-lactamase OR multidrug-resistant* OR extensively drug-resistant* OR antimicrobial-resistant* OR antibiotic-resistant* OR antibiotic-resistant* OR carbapenem-resistant* OR colistin-resistant* OR polymyxin-resistant* OR methicillin-resistant* OR vancomycin-resistant*) AND (Acinetobacter baumannii OR Pseudomonas aeruginosa OR Escherichia coli OR Klebsiella pneumoniae OR Enterobacteriaceae OR Staphylococcus OR Enterococcus* OR microorganism* OR bacteria) AND ((prediction model* OR predicted model* OR predictive model* OR risk model* OR risk prediction OR predicted factor* OR predictive factor* OR prognostic model* OR prognosis model* OR prognostic factor* OR scoring model*) AND (critical care OR intensive care unit* OR critical illness OR ICU OR intensive care OR critically ill) in English and (耐药性OR抗生素OR耐药OR耐药菌OR耐药性菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌) AND (絆病原菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌 OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌OR耐药菌) AND (预测模型OR预测模型OR预测模型OR预测模型OR预测模型OR预测模型OR预测模型OR预测模型OR预测模型) AND (风险模型OR风险模型OR风险模型OR风险模型OR风险模型OR风险模型OR风险模型OR风险模型OR风险模型) AND (预测因素OR预测因素OR预测因素OR预测因素OR预测因素OR预测因素OR预测因素OR预测因素OR预测因素) AND (ICU OR 重度监护 OR 监护室) in Chinese. We will use medical subject headings and...
free-text to identify prediction model studies. The search methods for databases are included in online supplemental file 2).

Eligibility criteria
Studies will be included in this review if they are primary experimental or observational studies on the development and/or validation of a multivariable prediction model for MDRO colonisation or infection in critically ill patients and were published any time before April 2022. Population, intervention, comparator, outcomes, timing and setting characteristics are as follows: (1) ICU duration less than 24 hours; (2) MDROs detected before the patient entered the ICU or within the first 48 hours in the ICU.

Outcome Any prediction model which predicts the risk of MDRO colonisation or infection in patients with critical illness, to distinguish critically ill patients with poor outcomes (who will develop multidrug-resistant bacterial infection), with reporting of at least two predictors will be included. Any disease caused by MDRO will be included. All types of MDROs, including MRSA, CRE, VRE, ESBL-EKP or others will be included.

Comparator Not applicable.

Outcomes The outcome (to be predicted) is MDRO cultured from any of the clinical specimens after 48 hours of admission to the ICU. MDRO infection is defined as the invasion of the body tissues by MDROs resulting in disease. Infectious diseases included but are not limited to bacteremia, pneumonia and infections of the skin and soft issue, urinary tract, bloodstream or abdomen. The legal communicable disease diagnostic criteria approved by countries or international organisations were applied to diagnose these infectious diseases. MDRO colonisation is defined as any patient who had MDRO positive culture results and with no symptoms of clinical infection found.

Timing Predictive variables measured at any time point during the course of the MDRO colonisation or infection while patients were being treated in the ICU.

Setting Any type of ICU.

<table>
<thead>
<tr>
<th>Item</th>
<th>Definition</th>
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<tbody>
<tr>
<td>Population</td>
<td>Both male and female adult critically ill patients (aged ≥18 years) will be considered. The exclusion criteria are as follows: (1) ICU duration less than 24 hours; (2) MDROs detected before the patient entered the ICU or within the first 48 hours in the ICU.</td>
</tr>
<tr>
<td>Intervention</td>
<td>Any prediction model which predicts the risk of MDRO colonisation or infection in patients with critical illness, to distinguish critically ill patients with poor outcomes (who will develop multidrug-resistant bacterial infection), with reporting of at least two predictors will be included. Any disease caused by MDRO will be included. All types of MDROs, including MRSA, CRE, VRE, ESBL-EKP or others will be included.</td>
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<td>Comparator</td>
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</tr>
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<tr>
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<td>Any type of ICU.</td>
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</table>

CRE, carbapenem-resistant *Enterobacteriaceae*; ESBL-EKP, extended-spectrum β-lactamase-producing *Enterobacteriaceae*; ICU, intensive care unit; MDROs, multidrug-resistant organisms; MRSA, methicillin-resistant *Staphylococcus aureus*; PICOTS, population intervention, comparator, outcomes, timing of prediction and of outcomes and setting; VRE, vancomycin-resistant *Enterococcus*.

**Table 1** Eligibility criteria for the systematic review framed using the PICOTS* system

**Data abstraction**
At least two trained reviewers (Yi W and QY) will independently extract data from included studies. A standardised data extraction form will be created based on the Checklist for Critical Appraisal and Data Extraction for Systematic Reviews of Prediction Modelling Studies (the CHARMS checklist). This data extraction form will be piloted on five papers and amended by at least three reviewers (Yi W, FW and YX). Any revisions will be implemented based on group consensus. Data on the following study characteristics will be extracted: first author, year of publication, study design and characteristics, source of data, participant eligibility, recruitment, description and sample size, type of ICU, the number and/or incidence of predicted outcomes, the type of MDRO, infectious diseases, candidate predictors, missing data, modelling method and evaluation, risk ratios or ORs for the predictors (both overall and stratified), model performance and calibration (eg, calibration plot and Hosmer-Lemeshow test), discriminating capacity (eg, area under the receiver operating characteristic curve and Concordance Index) and model evaluation (eg, sensitivity, specificity, positive and negative predictive values), as well as relevant studies using NoteExpress software. Full-text manuscripts will be retrieved and independently evaluated for inclusion. Disagreements will be resolved by consensus or a third-researcher (CY or FW) arbitration. The selection process will be presented in a PRISMA flow diagram (figure 1).
Critical appraisal

Two reviewers (Ying W and YX) will independently appraise each included prediction model using the PROBAST instrument, a tool for assessing the risk of bias and applicability of diagnostic and prognostic prediction model studies, which was published in 2019.25,26 As well as serving clinical medical personnel who are considering using a prediction model, it is also used to help researchers develop a model or include models in a systematic review or meta-analysis.27 In recent years, PROBAST has been used in systematic reviews of infection prediction models, like COVID-19 infection,28 but unfortunately, it has not been fully applied in prediction models of MDRO colonisation or infection. PROBAST is widely used for quality evaluation of prediction models, therefore, this study will use this tool for critical appraisal. PROBAST includes four steps, which are described in detail to support assessment completion. The four domains are as follows: participants, predictors, outcome and analysis, and are divided into a total of 20 questions to support structured risk of bias assessments. Each domain is rated as at a ‘high’, ‘low’ or ‘unclear’ risk of bias. Any disagreement will be resolved by consensus and consultation with a third reviewer (CY/Yi W).

Statistical analysis

We will also produce a narrative summary of the included studies. A summary of the characteristics (eg, study design, population size, national location, year, participants’ characteristics, species of bacteria and statistical method) will be included. Counts and percentages will be used to describe categorical outcome data and risk of bias assessment findings. Continuous data, including sample size and predictor count, will be presented using means and SD, and medians and IQRs, for normally and non-normally distributed variables, respectively.

Meta-analytical methods will be used where data pooling is suitable. We will follow the recently published framework for the meta analysis of prediction models.23,29 We will group study results according to the species of bacteria (eg, MDRO, CRE and CRKP). To pool prediction findings from models developed for different strains of drug-resistant bacteria, a random-effects model will be used to obtain a summary estimate of model performance.
and calibration. As validation studies per model are likely to be few, they will be analysed using the C-statistic and 95% CIs in a random-effect models based on the restricted maximum likelihood estimation method. Finally, 95% prediction intervals, which account for heterogeneity, will be assessed to provide a predicted range of C-statistic values to be used for reference by future validation studies. Heterogeneity will be calculated with the $\chi^2$ test and I² test (<25%, low heterogeneity; 25%–50%, moderate heterogeneity and >50%, strong heterogeneity). A funnel plot will be generated to assess publication bias if more than 10 studies are included in a meta-analysis. All statistical analyses will be performed using R Statistical Software V.3.2.3 (R Core Team, R Foundation for Statistical Computing, Vienna, Austria) and Stata V.15.0 (Stata Corporation, College Station, TX, USA). We will use the R package ‘metamisc’ for the meta-analysis of prediction models, which is available from https://CRAN.R-project.org/package=metamisc.

**Patient and public involvement**

No patient or member of the public will be involved in the design, conduct, or reporting of this systematic review.

**ETHICS AND DISSEMINATION**

Ethical approval will not be required because this systematic review will be based on data extracted from previous studies. We plan to publish our findings in peer-reviewed journals dedicated to critical care medicine or nursing research. We also plan to present our results at the International Council of Nurses and at other conferences relevant to critical care.

**Amendments**

This systematic review protocol will be amended during the peer-review process.

**DISCUSSION**

The rates of infections caused by MDROs (eg, MRSA, CRE, VRE and ESBL-EKP) are increasing. These infections lead to poor outcomes in critically ill patients. Several models predicting MDRO infection have been developed, potentially supporting infection control and prevention measures. To the best of our knowledge, one systematic review has evaluated the evidence on models predicting ESBL colonisation or infection. This previous systematic review included studies published before April 2018 and focused on ESBL-EKP infection or colonisation. In contrast, this proposed systematic review has a broader scope, including all MDRO colonisation or infections acquired in the ICU, and will interrogate five English-language and three Chinese-language databases, as well as grey literature to ensure comprehensive coverage. There is a strong research team and sufficient time to ensure literature screening, quality evaluation and data extraction. Owing to the complex and scattered influencing factors, we will package the similarity factors, and conduct a meta-analysis to draw valuable conclusions, which will be completed with the help of a statistician and an evidence-based expert. This review will contribute to the understanding of the risk of MDRO colonisation or infection among critically ill patients. This review may also support evidence-based approaches to infection control and prevention that do not involve antibiotic use, helping improve outcomes.

**Contributors**

The study concept and design were conceived by all authors. All authors drafted and revised the manuscript and agree to its content. YW, YX, QY, FW and YingW will conduct article screening and data extraction. YW, YX and YingW will evaluate the risk of bias and applicability of each included prediction model. YW and QY will perform data analysis. CY, the corresponding author, is the guarantor of the review.

**Funding**

The authors have not declared a specific grant for this research from any funding agency in the public, commercial or not-for-profit sectors.

**Competing interests**

None declared.

**Patient and public involvement**

Patients and/or the public were not involved in the design, or conduct, or reporting or dissemination plans of this research.

**Patient consent for publication**

Not required.

**Provenance and peer review**

Not commissioned; externally peer reviewed.

**Supplemental material**

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**REFERENCES**

### ADMINISTRATIVE INFORMATION

<table>
<thead>
<tr>
<th>Section and topic</th>
<th>Item No</th>
<th>Checklist item</th>
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</thead>
<tbody>
<tr>
<td>Title: Identification</td>
<td>1a</td>
<td>Identify the report as a protocol of a systematic review</td>
</tr>
<tr>
<td>Update</td>
<td>1b</td>
<td>If the protocol is for an update of a previous systematic review, identify as such</td>
</tr>
<tr>
<td>Registration</td>
<td>2</td>
<td>If registered, provide the name of the registry (such as PROSPERO) and registration number</td>
</tr>
<tr>
<td>Authors: Contact</td>
<td>3a</td>
<td>Provide name, institutional affiliation, e-mail address of all protocol authors; provide physical mailing address of corresponding author</td>
</tr>
<tr>
<td>Contributions</td>
<td>3b</td>
<td>Describe contributions of protocol authors and identify the guarantor of the review</td>
</tr>
<tr>
<td>Amendments</td>
<td>4</td>
<td>If the protocol represents an amendment of a previously completed or published protocol, identify as such and list changes; otherwise, state plan for documenting important protocol amendments</td>
</tr>
<tr>
<td>Support: Sources</td>
<td>5a</td>
<td>Indicate sources of financial or other support for the review</td>
</tr>
<tr>
<td>Sponsor</td>
<td>5b</td>
<td>Provide name for the review funder and/or sponsor</td>
</tr>
<tr>
<td>Role of sponsor or funder</td>
<td>5c</td>
<td>Describe roles of funder(s), sponsor(s), and/or institution(s), if any, in developing the protocol</td>
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### INTRODUCTION

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<th>Checklist item</th>
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<tbody>
<tr>
<td>Rationale</td>
<td>6</td>
<td>Describe the rationale for the review in the context of what is already known</td>
</tr>
<tr>
<td>Objectives</td>
<td>7</td>
<td>Provide an explicit statement of the question(s) the review will address with reference to participants, interventions, comparators, and outcomes (PICO)</td>
</tr>
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</table>

### METHODS

<table>
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<tr>
<th>Section and topic</th>
<th>Item No</th>
<th>Checklist item</th>
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<tr>
<td>Eligibility criteria</td>
<td>8</td>
<td>Specify the study characteristics (such as PICO, study design, setting, time frame) and report characteristics (such as years considered, language, publication status) to be used as criteria for eligibility for the review</td>
</tr>
<tr>
<td>Information sources</td>
<td>9</td>
<td>Describe all intended information sources (such as electronic databases, contact with study authors, trial registers or other grey literature sources) with planned dates of coverage</td>
</tr>
<tr>
<td>Search strategy</td>
<td>10</td>
<td>Present draft of search strategy to be used for at least one electronic database, including planned limits, such that it could be repeated</td>
</tr>
<tr>
<td>Study records: Data management</td>
<td>11a</td>
<td>Describe the mechanism(s) that will be used to manage records and data throughout the review</td>
</tr>
<tr>
<td>Selection process</td>
<td>11b</td>
<td>State the process that will be used for selecting studies (such as two independent reviewers) through each phase of the review (that is, screening, eligibility and inclusion in meta-analysis)</td>
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<tr>
<td>Data collection process</td>
<td>11c</td>
<td>Describe planned method of extracting data from reports (such as piloting forms, done independently, in duplicate), any processes for obtaining and confirming data from investigators</td>
</tr>
<tr>
<td>Data items</td>
<td>12</td>
<td>List and define all variables for which data will be sought (such as PICO items, funding sources), any pre-planned data assumptions and simplifications</td>
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<tr>
<td>Outcomes and prioritization</td>
<td>13</td>
<td>List and define all outcomes for which data will be sought, including prioritization of main and additional outcomes, with rationale</td>
</tr>
<tr>
<td>Risk of bias in individual studies</td>
<td>14</td>
<td>Describe anticipated methods for assessing risk of bias of individual studies, including whether this will be done at the outcome or study level, or both; state how this information will be used in data synthesis</td>
</tr>
<tr>
<td>Data synthesis</td>
<td>15a</td>
<td>Describe criteria under which study data will be quantitatively synthesised</td>
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<td></td>
<td>15b</td>
<td>If data are appropriate for quantitative synthesis, describe planned summary measures, methods of handling data and methods of combining data from studies, including any planned exploration of consistency (such as $I^2$, Kendall’s τ)</td>
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<td></td>
<td>15c</td>
<td>Describe any proposed additional analyses (such as sensitivity or subgroup analyses, meta-regression)</td>
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<td></td>
<td>15d</td>
<td>If quantitative synthesis is not appropriate, describe the type of summary planned</td>
</tr>
<tr>
<td>Meta-bias(es)</td>
<td>16</td>
<td>Specify any planned assessment of meta-bias(es) (such as publication bias across studies, selective reporting within studies)</td>
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<tr>
<td>Confidence in cumulative evidence</td>
<td>17</td>
<td>Describe how the strength of the body of evidence will be assessed (such as GRADE)</td>
</tr>
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</table>

* It is strongly recommended that this checklist be read in conjunction with the PRISMA-P Explanation and Elaboration (cite when available) for important clarification on the items. Amendments to a review protocol should be tracked and dated. The copyright for PRISMA-P (including checklist) is held by the PRISMA-P Group and is distributed under a Creative Commons Attribution Licence 4.0.

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<td>#1: 'extended spectrum beta lactamase':ti,ab,kw OR 'multidrug resistant':ti,ab,kw OR 'extensively drug resistant':ti,ab,kw OR 'antimicrobial resistant':ti,ab,kw OR 'antibiotic resistant':ti,ab,kw OR 'antibacterial resistant':ti,ab,kw OR 'pandrug resistant':ti,ab,kw OR 'carbapenem resistant':ti,ab,kw OR 'colistin resistant':ti,ab,kw OR 'polymyxin resistant':ti,ab,kw</td>
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<td>Filters applied: Chinese, English.</td>
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</table>
#1: SU "extended spectrum beta lactamase" OR SU "multidrug resistant" OR SU "extensively drug resistant" OR SU "antimicrobial resistant" OR SU "antibiotic resistant" OR SU "antibacterial resistant" OR SU "pandrug resistant" OR SU "carbapenem resistant" OR SU "colistin resistant" OR SU "polymyxin resistant" OR SU "methicillin resistant" OR SU "vancomycin resistant"

#2: SU "acinetobacter baumannii" OR SU "pseudomonas aeruginosa" OR SU "escherichia coli" OR SU "klebsiella pneumoniae" OR SU Enterobacteriaceae OR SU staphylococcus OR SU enterococcus OR SU microorganism OR SU bacteria

#3: (MH "Pseudomonas Infections") OR (MM "Acinetobacter Infections") OR (MH "Escherichia Coli") OR (MH "Escherichia Coli Infections") OR (MH Enterobacteriaceae) OR (MH Enterobacteriaceae Infections) OR (MH Staphylococcus) OR (MH Enterococcus) OR (MH Bacteria)

#4: #1 AND (#2 OR #3)

#5: (MH "Methicillin-Resistant Staphylococcus Aureus") OR (MH "Carbapenem-Resistant Enterobacteriaceae") OR (MH "Vancomycin Resistant Enterococci") OR (MH "Vancomycin-Resistant Staphylococcus Aureus") OR (MH "Drug Resistance, Microbial") OR (MH "Drug Resistance, Multiple") OR (MH "Drug Resistance, Neoplasm")

#6: #4 OR #5

#7: SU "prediction model" OR SU "predicted model" OR SU "predictive model" OR SU "risk model" OR SU "risk prediction" OR SU "risk calculat" OR SU "risk assessment" OR SU "predicted factor" OR SU "prognostic model" OR SU "prognosis model" OR SU "prognostic factor" OR SU "scoring model" OR SU "scoring system"

#8: (MH "Risk Assessment") OR (MH "Survival Analysis") OR (MH "Predictive Value of Tests") OR (MH "Prediction Models")

#9: #7 OR #8

#10: SU "critical care" OR SU "intensive care unit" OR SU "critical illness" OR SU "ICU" OR SU "intensive care" OR SU "critically ill"

**Search Strategy in CINAHL**

| #1 | SU "extended spectrum beta lactamase" OR SU "multidrug resistant" OR SU "extensively drug resistant" OR SU "antimicrobial resistant" OR SU "antibiotic resistant" OR SU "antibacterial resistant" OR SU "pandrug resistant" OR SU "carbapenem resistant" OR SU "colistin resistant" OR SU "polymyxin resistant" OR SU "methicillin resistant" OR SU "vancomycin resistant"
| #2 | SU "acinetobacter baumannii" OR SU "pseudomonas aeruginosa" OR SU "escherichia coli" OR SU "klebsiella pneumoniae" OR SU Enterobacteriaceae OR SU staphylococcus OR SU enterococcus OR SU microorganism OR SU bacteria
| #3 | (MH "Pseudomonas Infections") OR (MM "Acinetobacter Infections") OR (MH "Escherichia Coli") OR (MH "Escherichia Coli Infections") OR (MH Enterobacteriaceae) OR (MH Enterobacteriaceae Infections) OR (MH Staphylococcus) OR (MH Enterococcus) OR (MH Bacteria)
| #4 | #1 AND (#2 OR #3)
| #5 | (MH "Methicillin-Resistant Staphylococcus Aureus") OR (MH "Carbapenem-Resistant Enterobacteriaceae") OR (MH "Vancomycin Resistant Enterococci") OR (MH "Vancomycin-Resistant Staphylococcus Aureus") OR (MH "Drug Resistance, Microbial") OR (MH "Drug Resistance, Multiple") OR (MH "Drug Resistance, Neoplasm")
| #6 | #4 OR #5
| #7 | SU "prediction model" OR SU "predicted model" OR SU "predictive model" OR SU "risk model" OR SU "risk prediction" OR SU "risk calculat" OR SU "risk assessment" OR SU "predicted factor" OR SU "prognostic model" OR SU "prognosis model" OR SU "prognostic factor" OR SU "scoring model" OR SU "scoring system"
| #8 | (MH "Risk Assessment") OR (MH "Survival Analysis") OR (MH "Predictive Value of Tests") OR (MH "Prediction Models")
| #9 | #7 OR #8
| #10 | SU "critical care" OR SU "intensive care unit" OR SU "critical illness" OR SU "ICU" OR SU "intensive care" OR SU "critically ill"
#1: extended spectrum beta lactamase (Topic) or multidrug resistant* (Topic) or extensively drug resistant* (Topic) or antimicrobial resistant* (Topic) or antibiotic resistant* (Topic) or antibacterial resistant* (Topic) or pandrug resistant* (Topic) or carbapenem resistant* (Topic) or colistin resistant* (Topic) or polymyxin resistant* (Topic) or methicillin resistant* (Topic) or vancomycin resistant* (Topic)
#2: acinetobacter baumannii (Topic) or pseudomonas aeruginosa (Topic) or escherichia coli (Topic) or klebsiella pneumoniae (Topic) or enterobacteriaceae (Topic) or staphylococce (Topic) or enterococcus (Topic) or microorganism* (Topic) or bacteria (Topic)
#3: #1 and #2
#4: prediction model* (Topic) or predicted model* (Topic) or predictive model* (Topic) or risk model* (Topic) or risk prediction (Topic) or risk calculator* (Topic) or risk assessment (Topic) or predicted factor* (Topic) or 'predictive factor*' (Topic) or prognostic model* (Topic) or prognosis model* (Topic) or prognostic factor* (Topic) or scoring model* (Topic) or scoring system (Topic)
#5: critical care (Topic) or intensive care unit* (Topic) or critical illness (Topic) or icu (Topic) or intensive care (Topic) or critically ill (Topic)
#6: #3 and #4 and #5

Search Strategy in Cochrane Library
#1: ("extended spectrum beta lactamase"):ti,ab,kw OR ("multidrug resistant"):ti,ab,kw OR ("multidrug resistant"):ti,ab,kw OR ("extensively drug resistant"):ti,ab,kw OR ("antimicrobial resistant"):ti,ab,kw OR ("antibiotic resistant"):ti,ab,kw OR ("antibacterial resistant"):ti,ab,kw OR ("pandrug resistant"):ti,ab,kw OR ("carbapenem resistant"):ti,ab,kw OR ("colistin resistant"):ti,ab,kw OR ("polymyxin resistant"):ti,ab,kw OR ("methicillin resistant"):ti,ab,kw OR ("vancomycin resistant"):ti,ab,kw
#2: ("acinetobacter baumannii"):ti,ab,kw OR ("pseudomonas aeruginosa"):ti,ab,kw OR ("escherichia coli"):ti,ab,kw OR ("klebsiella pneumoniae"):ti,ab,kw OR ("enterobacteriaceae"):ti,ab,kw OR ("staphylococce"):ti,ab,kw OR ("enterococcus"):ti,ab,kw OR ("microorganism"):ti,ab,kw OR ("bacteria"):ti,ab,kw
#4: #1 AND (#2 OR #3)
#6: #4 OR #5
#7: ("prediction model"):ti,ab,kw OR ("predicted model"):ti,ab,kw OR ("predictive model"):ti,ab,kw OR ("risk model"):ti,ab,kw OR ("risk prediction"):ti,ab,kw OR ("risk calculator"):ti,ab,kw OR ("risk assessment"):ti,ab,kw OR ("predicted factor"):ti,ab,kw OR ("predictive factor"):ti,ab,kw OR ("prognostic model"):ti,ab,kw OR ("prognosis model"):ti,ab,kw OR ("scoring model"):ti,ab,kw OR ("scoring system"):ti,ab,kw
#9: #7 OR #8
#10: ("critical care"):ti,ab,kw OR ("intensive care unit*":ti,ab,kw OR ("critical illness"):ti,ab,kw OR (ICU):ti,ab,kw OR ("intensive care"):ti,ab,kw OR ("critically ill"):ti,ab,kw
#11: "Critical Care"[MeSH descriptor] OR "Critical Illness"[MeSH descriptor] OR "Intensive Care Units"[MeSH descriptor] explode all trees
#12: #10 OR #11
#13: #6 AND #9 AND #12
Filters applied: Chinese, English.

**Search Strategy in CNKI**

#1: SU=(耐药+耐抗生素+耐细菌+耐甲氧西林+耐碳青霉烯+耐万古霉素+超广谱β内酰胺酶+耐粘菌素+耐多粘菌素
#2: SL=细菌+微生物+肠杆菌+肠球菌+鲍曼不动杆菌+铜绿假单胞菌+肺炎克雷伯菌+金黄色葡萄球菌
#3: SU=预测模型+预警模型+判别模型+风险模型+风险预测+风险评估+预测因素+评分模型+评分系统
#4: SU=重症监护+监护室+ICU
#5: #1 and #2 and #3 and #4
Filters applied: academic journals, dissertations, Chinese

**Search Strategy in Wanfang**

#1 主题(耐药 or 耐抗生素 or 耐细菌 or 耐甲氧西林 or 耐碳青霉烯 or 耐万古霉素 or 超广谱β内酰胺酶 or 耐粘菌素 or 耐多粘菌素)
#2: 主题(细菌 or 微生物 or 肠杆菌 or 肠球菌 or 鲍曼不动杆菌 or 铜绿假单胞菌 or 肺炎克雷伯菌 or 金黄色葡萄球菌 or 结核分枝杆菌)
#3: 主题(预测模型 or 预警模型 or 判别模型 or 风险模型 or 风险预测 or 风险评估 or 预测因素 or 评分模型 or 评分系统)
#4: 主题(重症监护 or 监护室 or ICU)
#5: #1 and #2 and #3 and #4
Filters applied: academic journals, dissertations, Chinese