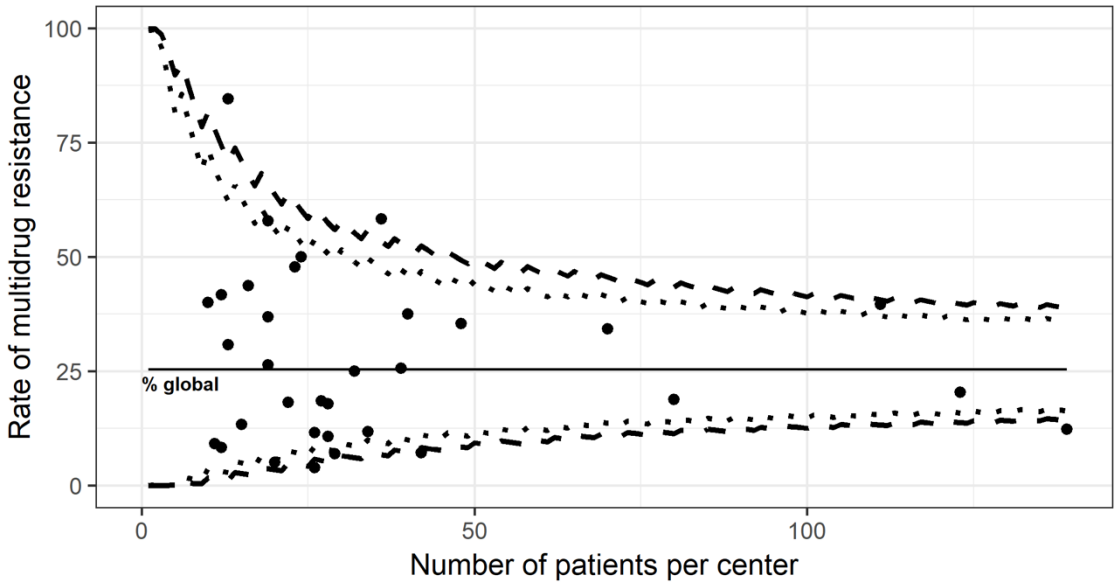
Table S1. Key predictors of multidrug resistance and the percentages in the bootstrap models.

Key predictor	N	%	Selected
Prior use of piperacillin/tazobactam	10000	100	Yes
Prior use of antipseudomonal carbapenems	10000	99.4	Yes
Age	10000	83.1	Yes
Urinary catheter	10000	82.3	Yes
Diabetes mellitus	10000	77.4	No
Underlying disease	10000	74.4	Yes
Sex	10000	71	Yes
Prior fluoroquinolone prophylaxis	10000	70.2	Yes
Prior bloodstream infection during hospitalization	10000	63.8	No
Septic shock	10000	57.7	No
Prior orotraqueal intubation (7 days)	10000	56.9	No
Prior hospital admission (3 months)	10000	56.6	No
Severe mucosity last 3days	10000	55	No
High-risk bloodstream infection	10000	54.4	No
Prior use of ceftriaxone	10000	54.3	No
Cerebral vascular disease	10000	50.5	No
MASCC risk index score (value)	10000	44.9	No
Prior therapy with fluoroquinolones	10000	42.1	No
Comorbidities	10000	42.1	No
Blood pressure <=90 mmHg	10000	38.1	No
Hematopoietic stem cell transplant	10000	36.7	No
Nosocomial acquisition	10000	36.5	No
Pneumonia	10000	32.8	No
Prior use of amoxicillin/clavulanate	10000	29.9	No
Chronic obstructive pulmonary disease	10000	28	No
Solid organ transplant	10000	27.7	No
HIV infection	10000	26.5	No
Chronic heart disease	10000	26.1	No
Asthma	10000	26	No
Prior use of ertapenem	10000	24.7	No
High-risk MASCC index score	10000	24.3	No

Chronic renal disease	10000	24.3	No
Chronic liver disease	10000	22.9	No
Systemic inflamatory disease	10000	22.7	No
Prior intensive care unit admission	10000	22	No
Prior use of antipseudomonal cephalosporins	10000	21.7	No
Thyroid disease	10000	21.5	No
Corticosteroids (30 days)	10000	19.3	No

Figure S1


100
75
50
25
0
Rate of multidrug resistance
% global
0
50
100
Number of patients per center

TRIPOD Checklist: Prediction Model Development and Validation

Section/Topic			Checklist Item	Page
Title and abstract				
Title	1	D;V	Identify the study as developing and/or validating a multivariable prediction model, the target population, and the outcome to be predicted.	1
Abstract	2	D;V	Provide a summary of objectives, study design, setting, participants, sample size, predictors, outcome, statistical analysis, results, and conclusions.	5
Introduction				
Background and objectives	3a	D;V	Explain the medical context (including whether diagnostic or prognostic) and rationale for developing or validating the multivariable prediction model, including references to existing models.	7,8
	3b	D;V	Specify the objectives, including whether the study describes the development or validation of the model or both.	8
Methods				
Source of data	4a	D;V	Describe the study design or source of data (e.g., randomized trial, cohort, or registry data), separately for the development and validation data sets, if applicable.	9
	4b	D;V	Specify the key study dates, including start of accrual; end of accrual; and, if applicable, end of follow-up.	9
Participants	5a	D;V	Specify key elements of the study setting (e.g., primary care, secondary care, general population) including number and location of centres.	9
	5b	D;V	Describe eligibility criteria for participants.	9
	5c	D;V	Give details of treatments received, if relevant.	NA
Outcome	6a	D;V	Clearly define the outcome that is predicted by the prediction model, including how and when assessed.	11
	6b	D;V	Report any actions to blind assessment of the outcome to be predicted.	NA
Predictors	7a	D;V	Clearly define all predictors used in developing or validating the multivariable prediction model, including how and when they were measured.	12
	7b	D;V	Report any actions to blind assessment of predictors for the outcome and other predictors.	NA
Sample size	8	D;V	Explain how the study size was arrived at.	11
Missing data	9	D;V	Describe how missing data were handled (e.g., complete-case analysis, single imputation, multiple imputation) with details of any imputation method.	12
Statistical analysis methods	10a	D	Describe how predictors were handled in the analyses.	12
	10b	D	Specify type of model, all model-building procedures (including any predictor selection), and method for internal validation.	12
	10c	V	For validation, describe how the predictions were calculated.	12
	10d	D;V	Specify all measures used to assess model performance and, if relevant, to compare multiple models.	12
	10e	V	Describe any model updating (e.g., recalibration) arising from the validation, if done.	NA
Risk groups	11	D;V	Provide details on how risk groups were created, if done.	NA
Development vs. validation	12	V	For validation, identify any differences from the development data in setting, eligibility criteria, outcome, and predictors.	NA
Results				
Participants	13a	D;V	Describe the flow of participants through the study, including the number of participants with and without the outcome and, if applicable, a summary of the follow-up time. A diagram may be helpful.	13
	13b	D;V	Describe the characteristics of the participants (basic demographics, clinical features, available predictors), including the number of participants with missing data for predictors and outcome.	12,13
	13c	V	For validation, show a comparison with the development data of the distribution of important variables (demographics, predictors and outcome).	Suppl. Material
Model development	14a	D	Specify the number of participants and outcome events in each analysis.	13,14
	14b	D	If done, report the unadjusted association between each candidate predictor and outcome.	NA
Model specification	15a	D	Present the full prediction model to allow predictions for individuals (i.e., all regression coefficients, and model intercept or baseline survival at a given time point).	
	15b	D	Explain how to the use the prediction model.	Suppl. Material
Model performance	16	D;V	Report performance measures (with CIs) for the prediction model.	Figure 2
Model-updating	17	V	If done, report the results from any model updating (i.e., model specification, model performance).	NA
Discussion				
Limitations	18	D;V	Discuss any limitations of the study (such as nonrepresentative sample, few events per predictor, missing data).	18
Interpretation	19a	V	For validation, discuss the results with reference to performance in the development data, and any other validation data.	16,17
	19b	D;V	Give an overall interpretation of the results, considering objectives, limitations, results from similar studies, and other relevant evidence.	16-19

Implications	20	D;V	Discuss the potential clinical use of the model and implications for future research.	16-19
Other information				
Supplementary information	21	D;V	Provide information about the availability of supplementary resources, such as study protocol, Web calculator, and data sets.	15
Funding	22	D;V	Give the source of funding and the role of the funders for the present study.	22

*Items relevant only to the development of a prediction model are denoted by D, items relating solely to a validation of a prediction model are denoted by V, and items relating to both are denoted D;V. We recommend using the TRIPOD Checklist in conjunction with the TRIPOD Explanation and Elaboration document.

Tool to calculate de risk of multidrug resistance

To estimate the probability of developing multidrug resistance (MDR) of a particular patient:

$$\mathrm{P(MDR)} = \left[\frac{e^{\beta_0+\sum_{j=1}^{k}\beta_j X_j}}{1+e^{\beta_0+\sum_{j=1}^{k}\beta_j X_j}}\right]$$

where β_0 stands for the intercept value and $\sum_{j=1}^{k}\beta_j X_j$ stands for the linear function of model predictors. Each predictor is multiplied by its corresponding β as in the table below.

For illustrative purposes, we calculate the multidrug-resistance risk for a 60-years old patient with prior use of piperacillin/tazobactam, urinary catheter in the previous 48 hours, with an hematologic underlying disease, with no prior use of anti-pseudomonal carbapenems and no prior fluoroquinolone prophylaxis:

Key factor	Beta	Patient	Result
Prior piperacillin/tazobactam	1.24891532	Yes	1.24891532*1=1.24891532
Prior fluoroquinolone prophylaxis	1.0963422	No	1.0963422*0=0
Urinary catheter	0.93336107	Yes	0.93336107 *1=0.93336107
Prior anti-pseudomonal carbapenems	0.92899160	No	0.92899160*0=0
Hematologic underlying disease	0.73714079	Yes	0.73714079*1=0.73714079
Age	-0.01720178	60	-0.01720178*60=-1.032107
$\sum_{j=1}^{k}\beta_j X_j$			1.88731
$\beta_0+\sum_{j=1}^{k}\beta_j X_j$			-1.65226955+1.88731= 0.2350405
$\exp\left(\beta_0+\sum_{j=1}^{k}\beta_j X_j\right)$			exp(0.2350405) = 1.26496
$\frac{\exp\left(\beta_0+\sum_{j=1}^{k}\beta_j X_j\right)}{1+\exp\left(\beta_0+\sum_{j=1}^{k}\beta_j X_j\right)}$			1.26496/(1+1.26496)= 0.5584911
$P(MDR)$			0.5585
Given 100 people with this profile, 56 will develop MDR			

Based on this, the risk of this patient of developing multidrug resistance is **56%**.

To account for the cluster effect of center, a mixed logistic regression model was used. Therefore, for each patient profile we can estimate several probabilities, one per each center. Since a patient can only be attended in one center, we report three probabilities to show three different scenarios. One, where the patient is admitted in a center with a low rate of MDR (lower than 8%: mean rate minus one standard deviation), another where the patient is admitted in a center with an intermediate rate of MDR (between 8% and 46%: mean rate), and finally, another where the patient is admitted in a center with a high rate of MDR (higher than 46%: mean rate plus one standard deviation).

Type of centre	Center MDR incidence	Probability of MDR	Given 100 people with this profile
Low MDR incidence center	<8%	0.3775	38 will develop MDR
Medium MDR incidence center	8%-46%	0.5585	56 will develop MDR
High MDR incidence center	>46%	0.7252	73 will develop MDR

Supplemental Figure Legends

Figure S1. Multidrug resistance rates among *Pseudomonas aeruginosa* isolates by center, according to the number of patients included.