

DTU Genomic Proficiency Test 2025



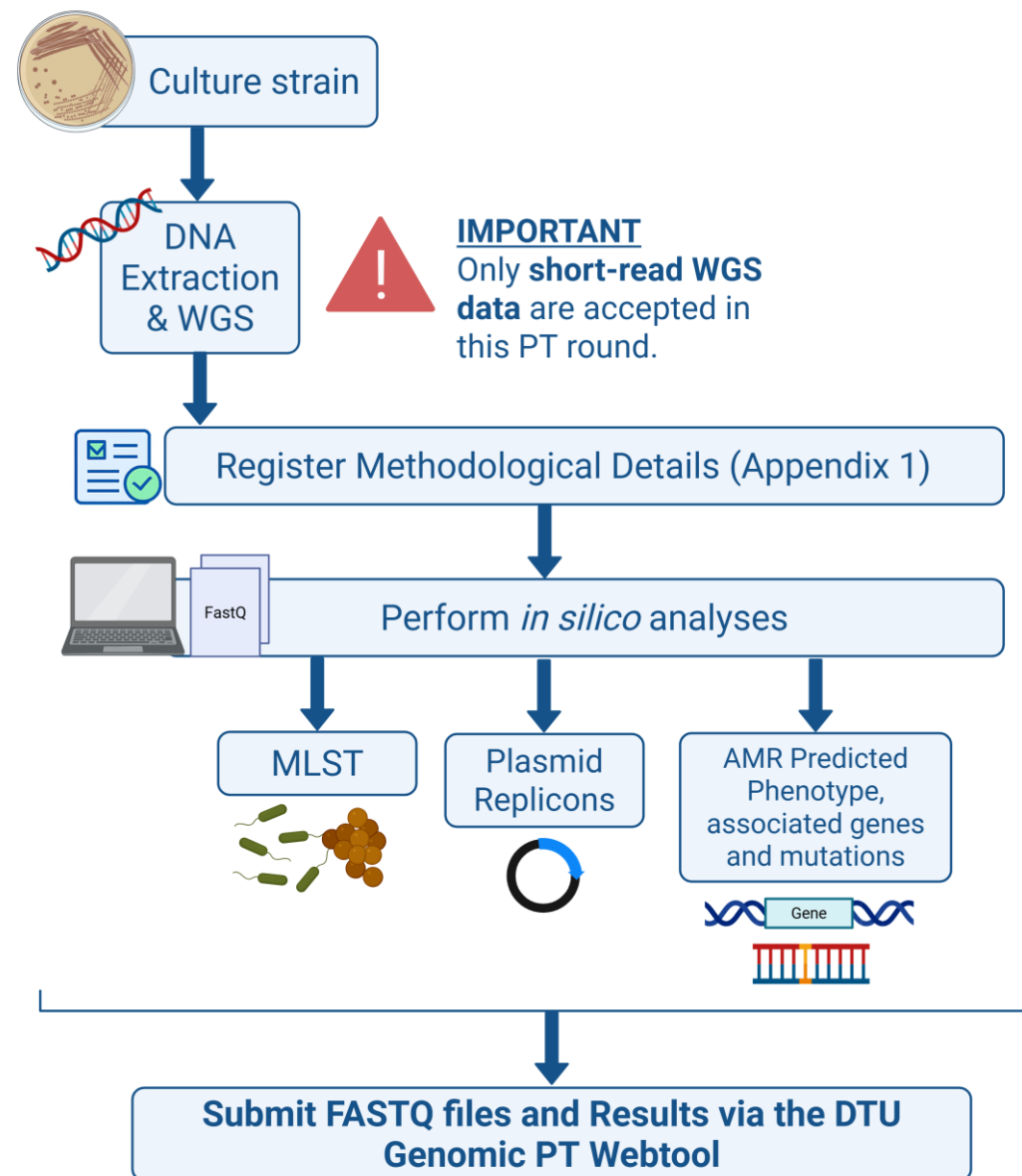
EU Reference Laboratory for Antimicrobial Resistance (EURL-AMR)
National Food Institute (DTU Food), Technical University of Denmark (DTU)

Athina Andrea
EURL-AMR Webinar
Thursday, 18 June 2026

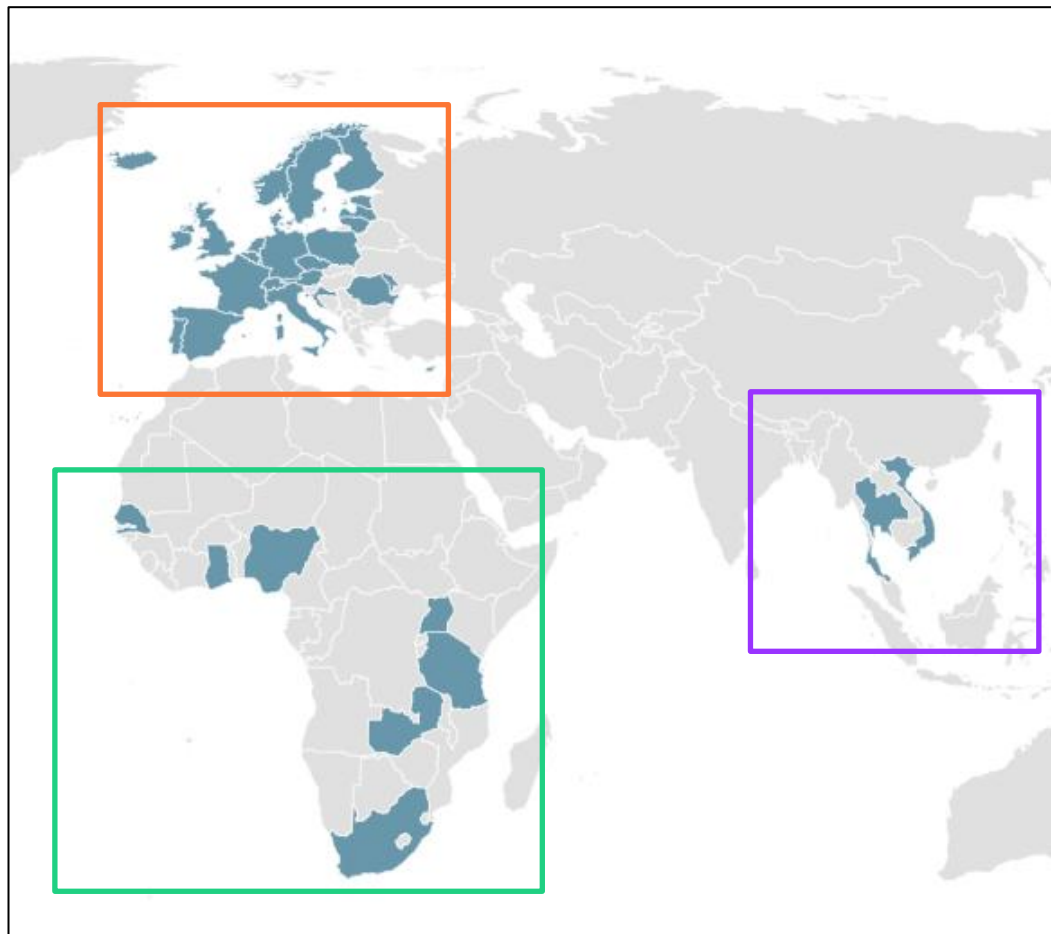


About the DTU Genomic PT

- Organised annually by the DTU National Food Institute
- Strengthen capacity of WGS and bioinformatic analyses within international laboratory networks
- Participants receive 6 bacterial strains representing 3 bacterial species and required to perform DNA extraction, WGS (short-read), and *in silico* analyses.
- Laboratories may choose to participate in one or more species



GPT2025: Results from 40 Laboratories (36 Countries)



Geographic region	Laboratories submitting results	Countries submitting results
Africa	7	7
Europe	28	27
Asia	5	2
Total	40	36

Genomic PT 2025 Strains

Organism	Strain	Molecule type	Size (bp)	GC%
<i>Klebsiella pneumoniae</i>	GPT25-01	Chromosome	5,652,062	57.3
		Plasmid_1	191,042	51.6
		Plasmid_2	45,876	54.9
		Plasmid_3	5,225	49.8
		Plasmid_4	3,574	43.8
		Plasmid_5	4,232	44.6
		Plasmid_6	3,789	41.8
		Plasmid_7	3,674	46.4
		Plasmid_8	2,927	46.5
	GPT25-02	Chromosome	5,380,266	57.4
		Plasmid_1	207,546	52.9
		Plasmid_2	113,639	53.9
		Plasmid_3	43,380	46.8
		Plasmid_4	15,100	53.5
		Plasmid_5	5,339	42.0
<i>Campylobacter coli</i>	GPT25-03	Chromosome	1,780,433	31.3
		Plasmid_1	31,330	29.2
<i>Campylobacter jejuni</i>	GPT25-04	Chromosome	1,847,776	30.1
<i>Staphylococcus aureus</i>	GPT25-05	Chromosome	2,835,714	33.0
		Plasmid_1	3,263	30.1
		Plasmid_2	2,649	30.4
		Plasmid_3	2,407	31.0
	GPT25-06	Chromosome	2,842,304	32.9

Antimicrobials in the scope of Genomic PT 2025

Class	Antimicrobial	Abbreviation	<i>K. pneumoniae</i>	<i>Campylobacter</i>	<i>S. aureus</i>
AMINOGLYCOSIDES	Amikacin	AMI	✓	-	-
	Gentamicin	GEN	✓	✓	✓
BETA-LACTAMS	Cefepime	FEP	✓	-	-
	Cefotaxime	FOT	✓	-	-
	Cefoxitin	FOX	✓	-	✓
	Ceftazidime	TAZ	✓	-	-
	Ertapenem	ETP	✓	✓	-
	Imipenem	IMI	✓	-	-
	Meropenem	MERO	✓	-	-
	Temocillin	TRM	✓	-	-
GLYCOPEPTIDES	Vancomycin	VAN	-	-	✓
LINCOSAMIDES	Clindamycin	CLI	-	-	✓
MACROLIDES	Azithromycin	AZI	✓	-	-
	Erythromycin	ERY	-	✓	✓
OXAZOLIDINONES	Linezolid	LZD	-	-	✓
PHENICOLS	Chloramphenicol	CHL	✓	✓	✓
PLEUROMUTILINS	Tiamulin	TIA	-	-	✓
POLYMYXINS	Colistin	COL	✓	-	-
PSEUDOMONIC ACIDS	Mupirocin	MUP	-	-	✓
QUINOLONES	Ciprofloxacin	CIP	✓	✓	✓
	Nalidixic acid	NAL	✓	-	-
STREPTOGRAMINS	Quinupristin/dalfopristin	SYN	-	-	✓
SULFONAMIDES	Sulfamethoxazole	SMX	✓	-	✓
TETRACYCLINES	Tetracycline	TET	✓	✓	✓
	Tigecycline	TGC	✓	-	-
TRIMETHOPRIM	Trimethoprim	TMP	✓	-	✓

- ***S. aureus***: Commission Implementing Decision (EU) 2023/1017 monitoring of MRSA in fattening pigs
- ***K. pneumoniae* & *Campylobacter***: Commission Implementing Decision (EU) 2020/1729 monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria
- **AMR Data on the specific antimicrobials for each organism to be reported**

Expected data generation

Type of analysis	Tool Name, platform	Thresholds Used (COV, coverage; ID, Identity)
MLST	MLST, CGE	100% ID, 100% COV
AMR	ResFinder, command line	95% ID, 95% COV
	NCBI AMRFinderPlus, command line	95% ID, 95% COV
Plasmid typing	PlasmidFinder, command line	95% ID , 90% COV
	MOB-suite, command line	95% ID, 90% COV

Tools run on the **reference genomes**
 Additionally run with lower thresholds on
 Illumina raw reads

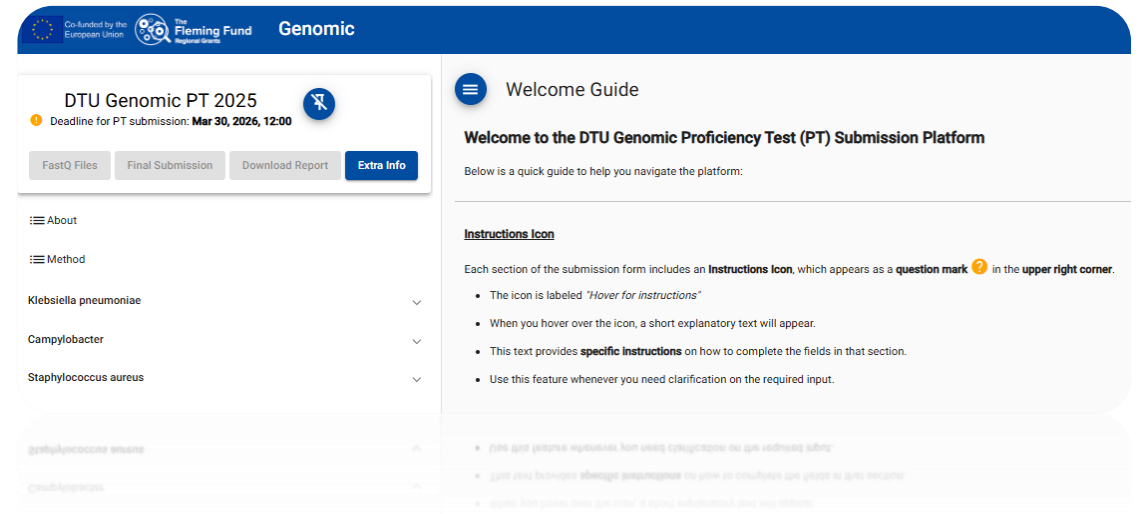
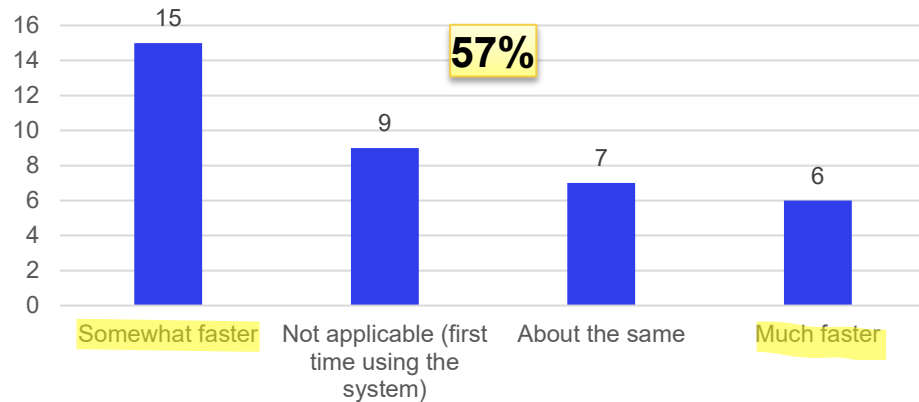
New Genomic PT Webtool for data submission introduced in 2025 scheme

Main challenges with the old webtool:

- Slow speed
- Partial lack of build-in drop-down menus (AMR mutations)
- Lack of copy-paste functionality between fields (Method questions)
- No possibility for uploading the raw data (FASTQ files)

Survey results n=37

Overall, how would you rate the speed/response time of the new webtool compared to the previous platform?



User Interface Feedback

68-87% reported "Very easy" or "Easy to use" for:

- Upload FASTQ files
- Method information
- MLST data
- Plasmid replicon data

New GPT Webtool User Interface Feedback AMR part (n=37)

- **46%** reported “Very easy” or “Easy to use”
- **22%** reported difficulties
- First year each AMR determinant reported under a specific AMR phenotype

Benefits of Phenotype-Linked AMR Reporting

- ✓ Evaluates biological understanding, not only AMR determinant detection
- ✓ Distinguishes analytical from interpretative errors:
 - AMR determinant detection errors
 - AMR Genotype – Phenotype interpretation errors

Genomic PT 2025 reports (*in silico* analyses)

Laboratory evaluation report

- Download from the GPT webtool <https://genomic-pt.dtu.dk>
- Submitted and Expected results as well as scores



LABORATORY EVALUATION REPORT for the Genomic Proficiency Test 'DTU Genomic PT 2025' provided by the National Food Institute, Technical University of Denmark (DTU Food)

Scoring of results was performed automatically on 6/17/2026 at 16:31
The report was downloaded from the web tool on 6/17/2026 at 15:18

Laboratory :

Uniq Id:

Comment from the proficiency test organizer :

Preliminary report

DTU Genomic Proficiency Test 2025 Report:

Interpretation of Submitted Data and Scoring System for
Klebsiella pneumoniae, *Campylobacter* spp. &
Staphylococcus aureus

- A detailed description of the scoring system
- The expected AMR, MLST and plasmid replicon data for each strain
- Explanations of scoring with scientific justifications

Preliminary evaluation

Please send your feedback by Friday 3 July

Expected data tables per strain, for MLST, Replicon and AMR

DTU Genomic Proficiency Test 2025 Report:

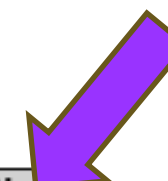
Interpretation of Submitted Data and Scoring System for
Klebsiella pneumoniae, *Campylobacter* spp. &
Staphylococcus aureus

3.1. Expected AMR data for *K. pneumoniae* strain GPT25-01

Class (A-Z)	Antimicrobial	Predicted AMR Phenotype	AMR <u>Gene Mutation</u>	Protein name	Location
AMINOGLYCOSIDES	Amikacin	Susceptible	None detected	-	-
	Gentamicin	Resistant	<u>aac(3)-IV</u> or <u>aac(3)-Iva</u>	aminoglycoside N-acetyltransferase AAC(3)-IVa	Plasmid 2
BETA-LACTAMS	Cefotaxime	Resistant	<i>bla</i> _{CTX-M-15}	extended-spectrum class A beta-lactamase CTX-M-15	Plasmid 1
	Ceftazidime	Resistant	<i>bla</i> _{CTX-M-15}	extended-spectrum class A beta-lactamase CTX-M-15	Plasmid 1

Participants' Data Evaluation - AMR

Class (A-Z)	PREDICTED AMR PHENOTYPE				AMR GENE_MUTATION				No of Labs
	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	
AMINOGLYCOSIDES	Gentamicin	1	0	EXP	<i>aac(3)-IV</i> or <i>aac(3)-IVa</i>	1	0	EXP	32
					<i>aph(4)-Ia</i>	0	-	N-EXP ³	1
					<i>aadA2</i>	0	-	N-EXP ⁴	1
					<i>aadA1</i>	0	-	N-EXP ⁴	1
	Streptomycin	-	-	OOS	<i>aadA1</i>	-	-	OOS	6
					<i>aph(6)-Id</i>	-	-	OOS	5
					<i>aadA2</i>	-	-	OOS	4
					<i>aph(3'')-Ib</i>	-	-	OOS	3
					<i>aadA2b</i>	-	-	OOS	3
					<i>aph(3')-Ib</i>	-	-	OOS	2



Footnotes

Scoring categories AMR: Expected (EXP) & Not-expected (N-EXP)

Expected result (EXP):

- Score if submitted => **1**
- Score if not submitted => **0**

AMR Phenotype / AMR Determinant part of the expected results

Example – *K. pneumoniae* GPT25-01

Class (A-Z)	PREDICTED AMR PHENOTYPE				AMR GENE_MUTATION				No of Labs
	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	
S	Gentamicin	1	0	EXP	<i>aac(3)-IV</i> or <i>aac(3)-IVa</i>	1	0	EXP	32
					<i>aph(4)-Ia</i>	0	-	N-EXP ³	1
					<i>aadA2</i>	0	-	N-EXP ⁴	1
					<i>aadA1</i>	0	-	N-EXP ⁴	1



- Gene *aph(4)-Ia* is detected in the genome but is known to be related to resistance to hygromycin.
- Genes *aadA2* and *aadA1* are detected in the genome but are known to be related to resistance to spectinomycin and streptomycin.

Not-expected (N-EXP)

- Score if submitted => **0**
- Score if not submitted => -

AMR Phenotype: not part of the expected results

AMR Determinant:

- Not present in the reference genome
- Non-functional
- Incorrect genotype-phenotype association

Scoring categories AMR: Accepted (ACC)

Example – *K. pneumoniae* GPT25-01

Class (A-Z)	PREDICTED AMR PHENOTYPE				AMR GENE_MUTATION				No of Labs
	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	
	Cefotaxime	1	0	EXP	<i>bla</i> CTX-M-15	1	0	EXP	30
					<i>ompK36_A217S</i>	1	-	ACC ^B	1
					<i>ompK36_D223G</i>	1	-	ACC ^B	2
					<i>ompK36_E232R</i>	1	-	ACC ^B	1
					<i>ompK36_F198Y</i>	1	-	ACC ^B	2
					<i>ompK36_F207Y</i>	1	-	ACC ^B	2
					<i>ompK36_G189T</i>	1	-	ACC ^B	2
					<i>ompK36_L228K</i>	1	-	ACC ^B	1
					<i>ompK36_L59V</i>	1	-	ACC ^B	2
					<i>ompK36_N304E</i>	1	-	ACC ^B	1
					<i>ompK36_Q227S</i>	1	-	ACC ^B	1
					<i>ompK36_T222L</i>	1	-	ACC ^B	2



Based on current evidence, alterations in OmpK36 are considered secondary resistance mechanisms that may contribute to elevated cephalosporin MICs in *K. pneumoniae*. OmpK36 alterations alone are generally not considered sufficient to predict a resistant phenotype.

Accepted (ACC)

- Score if submitted => **1**
- Score if not submitted => -

AMR Phenotype: not part of the expected results due to uncertainties in the AMR genetic background interpretation

AMR Determinant:

- Present in the reference genome but detected by some AMR prediction tools
- Current scientific evidence does not support that it is a stand alone AMR determinant

ACC results not counted in the GPT certificate scores

Scoring categories AMR: Out of scope (OOS)

Example – *K. pneumoniae* GPT25-01

Class (A-Z)	PREDICTED AMR PHENOTYPE				AMR GENE_MUTATION				No of Labs
	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	
IDES	Gentamicin	1	0	EXP	<u>aac(3)-IV</u> or <u>aac(3)-IVa</u>	1	0	EXP	32
					<u>aph(4)-Ia</u>	0	-	N-EXP ³	1
					<u>aadA2</u>	0	-	N-EXP ⁴	1
					<u>aadA1</u>	0	-	N-EXP ⁴	1
	Streptomycin	-	-	OOS	<u>aadA1</u>	-	-	OOS	6

Out of scope (OOS)

- Score if submitted => -
- Score if not submitted => -

AMR Phenotype: correct but not in panel antimicrobials

AMR Determinant:

- Present in the reference genome but linked to AMR phenotype out of scope

The same gene can fall into different scoring categories, depending under which predicted AMR phenotype it is submitted.

E.g., gene *aadA1* is:

- N-EXP under AMR phenotype gentamicin
- OOS under AMR phenotype streptomycin (as STR is not in the panel antimicrobials)

Scoring categories AMR: Not acquired resistance (NAR)

Rule	Organisms	Ampicillin/Amoxicillin	Amoxicillin-clavulanic acid	Ampicillin-sulbactam	Ticarcillin	Cefazolin, Cephalothin, Cefalexin, Cefadroxil	Cefoxitin ²	Cefuroxime	Tetracyclines	Tigecycline	Polymyxin B, Colistin	Fosfomycin	Nitrofurantoin
1.7	<i>Klebsiella pneumoniae</i> complex	R			R								



Expected Resistant Phenotypes
Version 1.2 January 2023

https://www.eucast.org/expert_rules_and_expected_phenotypes/expected_phenotypes

Rule	Organisms	Fusidic acid	Streptogramins	Trimethoprim	Nalidixic acid
3.5	<i>Campylobacter jejuni</i> , <i>Campylobacter coli</i>	R	R	R	

Rule	Organisms	Fusidic acid	Ceftazidime	Cephalosporins (except ceftazidime)	Aminoglycosides	Macrolides	Clindamycin	Quinupristin-dalfopristin	Vancomycin	Teicoplanin	Fosfomycin	Novobiocin	Sulfonamides
4.5	Other coagulase-negative staphylococci and <i>S. aureus</i>		R										

NAR

- Score if submitted => -
- Score if not submitted => -

AMR Phenotype: expected AMR phenotype based on EUCAST expect rules

AMR Determinant:

- Core genome component expected to be present in virtually all strains of the species
- Not acquired AMR gene

Scoring categories AMR: Not acquired resistance (NAR)

Example – *K. pneumoniae* GPT25-01

Class (A-Z)	PREDICTED AMR PHENOTYPE				AMR GENE_MUTATION				No of Labs
	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	Submitted Result	Score if Submitted	Score if not Submitted	Scoring category	
BETA-LACTAM	Ampicillin	-	-	NAR	<i>bla</i> _{OXA-1}	-	-	00S ⁵	8
					<i>bla</i> _{CTX-M-15}	-	-	00S ⁵	6
					<i>bla</i> _{TEM-1R}	-	-	00S ⁵	5
					<i>bla</i> _{SHV-11}	-	-	NAR ⁶	4

*bla*_{SHV-11} : species' intrinsic chromosomal β-lactamase contributing only to the expected ampicillin resistance EUCAST lists for *K. pneumoniae*

Genes *bla*_{OXA-1}, *bla*_{CTX-M-15} and *bla*_{TEM-1} are acquired AMR genes present in the genome of this strain.

When submitted under the AMR phenotype ampicillin, they were considered out of scope because *K. pneumoniae* is intrinsically resistant to aminopenicillins due to its chromosomal SHV β-lactamase.

Thank you for your attention !

Athina Andrea

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