LABQUALITY

External Quality Assessment Scheme

General Bacteriology 1
Round 1, 2023

Specimens
Please find enclosed 4 lyophilized samples S001, S002, S003 and S004 and vials of rehydration fluid, each 0.5 mL.

Caution
The specimens simulate patient samples and should be handled with the same care as patient samples, i.e. as potential transmitters of serious diseases.

Background information
Sample S001
Keratitis in patient using contact lenses.

Sample S002
CSF. Suspected meningitis.

Sample S003
Cardiac valve. Patient with endocarditis.

Sample S004
Tooth abscess, sample taken by puncture.

Examinations
Bacterial culture, aerobes and anaerobes, of S001-S004
Antimicrobial susceptibility testing of S001

Storage and use
After arrival, the samples should be stored at +2…8 °C.

1. Let the samples and the rehydration fluids warm up to room temperature.
2. Cut the foil packet open at the end where you can feel the thicker part of the loop.
3. Remove the plastic sheath from the loop. Break the loop shaft off from handle (appr. 2 cm) directly into the tube containing warm rehydration fluid (blue cap).
4. Incubate the tube for 30 minutes in +35…37 °C incubator.
5. Check that the black film inside the loop (containing the lyophilized sample) has dissolved completely.
6. Mix well the contents of the tube and proceed immediately with the examination similar to a patient sample.

Result reporting
Please enter the results via LabScala (www.labscala.com). Give the final answer to the clinician (findings) for samples S001, S002, S003 and S004. Also report the significance of the finding/s and the possible referring. Merely the results reported in the *Final answer to the clinician* section will be scored. Susceptibility testing results may be reported for sample S001. Identification test results may be reported for samples S003 and S004.

Reporting of antimicrobial susceptibility testing results
Report which guideline is followed in your laboratory for susceptibility testing procedures. As the NORDIC AST breakpoint values are based on the corresponding values published in the EUCAST guideline, the laboratories following NORDIC AST should select EUCAST as their reference group.

2023-03-21

INSTRUCTIONS

Product no. 5080
LQ760123011-014/US
UN3373

Subcontracting: Sample pretesting

If the kit is incomplete or contains damaged specimens, please report immediately to info@labquality.fi

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The results should be reported no later than **April 14, 2023**.

The expected results of the round are published in LabScala in the View reports section by April 18, 2023.

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FINAS
Finnish Accreditation Service
PT02 (EN ISO/IEC 17043)

For the disk diffusion method, report the inhibitory zone diameter (mm). The value should be between 5 and 55 mm for the result to be accepted in the result processing. For MIC method, report the MIC value as mg/L. Note, that a rounded MIC result is to be reported in addition to the actual MIC result. Only the rounded values are included in the report. Guidance for correct rounding can be found in table below and is also available in LabScala (click the *i*-button in column “MIC result, rounded”). The rounded MIC value should always be selected from the list on the result form, also when it is the same as the actual obtained MIC result (see examples below guidance table). In the last column report the corresponding SIR interpretation (Sensitive/Intermediate/Resistant). The interpretation should be reported by taking into consideration possible resistance mechanisms of the microbe.

Guidance for the rounding of MIC values

E-test or other MIC test result (mg/L)	Rounded value (mg/L)
<0.002, <0.003, 0.002	0.002
<0.004, <0.006, 0.003, 0.004	0.004
<0.008, <0.012, 0.006, 0.008	0.008
<0.015, <0.016, <0.023, 0.012, 0.015, 0.016	0.016
<0.03, <0.032, <0.047, 0.023, 0.03, 0.032	0.032
<0.06, <0.064, <0.094, 0.047, 0.06, 0.064	0.064
<0.12, <0.125, <0.19, 0.094, 0.12, 0.125	0.125
<0.25, <0.38, 0.19, 0.25	0.25
<0.5, <0.75, 0.38, 0.5	0.5
<1, <1.5, >0.5, 0.75, 1	1
<2, <3, >1, >1.5, 1.5, 2	2
<4, <6, >2, >3, 3, 4	4
<12, <8, >4, >6, 6, 8	8
<16, <24, >12, >8, 12, 16	16
<32, <48, >16, >24, 24, 32	32
<64, <96, >32, >48, 48, 64	64
<128, <192, >64, >96, 128, 96	128
<256, <384, >128, >192, 192, 256	256
<512, <768, >256, >384, 384, 512	512
<1024, <1536, >512, >768, 1024, 768	1024
<2048, >1024, >1536, 1536, 2048	2048

Example 1: Obtained test result is 0.002 mg/L, rounded value is 0.002 mg/L
Example 2: Obtained test result is 0.003 mg/L, rounded value is 0.004 mg/L
Example 3: Obtained test result is >16 mg/L, rounded value is 32 mg/L

For combination antibiotics note the following:
When the used MIC method gives the result of trimethoprim-sulfamethoxazole (used in ratio 1:19) as a common value of both components and not merely as a value of the trimethoprim component (which is 1/20 of the total), you should divide the result with 20 and thereafter round the value according to the table above. Example: the MIC method gives the result >320 mg/L, which is divided by 20 and yields the result >16 mg/L. After the rounding (see table above) the result is reported as 32 mg/L.

When the result for a combination antibiotic (e.g. piperacillin-tazobactam) includes the value of both components, report the MIC value of the actual antibiotic component (in this case piperacillin) merely. Example: Obtained test result is >128/4 mg/L, the non-rounded MIC value is reported as >128 mg/L and the rounded MIC value is 256 mg/L.

S001
LQ760123011

S003
LQ760123013

S002
LQ760123012

S004
LQ760123014

Sample 001

***Pseudomonas aeruginosa* ATCC 27853**

		DISK							MIC					
Antimicrobial agent	**Guideline**	**Own result (mm)**	**x (mm)**	**sd (mm)**	**S**	**I**	**R**	**n**	**Own result (mg/L)**	**Mo (mg/L)**	**S**	**I**	**R**	**n**
Amikacin	CLSI	-	-	-	-	-	-	-	**4** ◉	4	1 (100%) ◉	0 (0%)	0 (0%)	1
	CA-SFM	-	21	-	2 (100%)	0 (0%)	0 (0%)	2	-	2	1 (100%)	0 (0%)	0 (0%)	1
	EUCAST	-	23	4	31 (100%)	0 (0%)	0 (0%)	31	-	2	45 (100%)	0 (0%)	0 (0%)	45
	All				**33 (100%)**	**0 (0%)**	**0 (0%)**	**33**			**47 (100%)**	**0 (0%)**	**0 (0%)**	**47**
Gentamycin	CLSI	-	-	-	-	-	-	-	**1** ◉	1	1 (100%) ◉	0 (0%)	0 (0%)	1
	EUCAST	-	19	2	11 (100%)	0 (0%)	0 (0%)	11	-	1	15 (83%)	3 (17%)	0 (0%)	18
	All				**11 (100%)**	**0 (0%)**	**0 (0%)**	**11**			**16 (84%)**	**3 (16%)**	**0 (0%)**	**19**
Imipenem	CLSI	-	-	-	-	-	-	-	**2** ◉	-	2 (100%) ◉	0 (0%)	0 (0%)	2
	CA-SFM	-	24	-	1 (50%)	1 (50%)	0 (0%)	2	-	4	0 (0%)	1 (100%)	0 (0%)	1
	EUCAST	-	24	2	4 (13%)	27 (87%)	0 (0%)	31	-	2	3 (9%)	31 (91%)	0 (0%)	34
	All				**5 (15%)**	**28 (85%)**	**0 (0%)**	**33**			**5 (14%)**	**32 (86%)**	**0 (0%)**	**37**

Sample 001 | Additional questions

Report info

Participants

Altogether 94 laboratories from 22 countries participated in this EQA round.

Report info

The antimicrobial susceptibility testing results are shown in laboratory specific summary tables and histograms. Histograms are drawn for each antimicrobial agent if the laboratory’s result is included in a group of at least three results. By “group” is meant results which are obtained and interpreted according to the same standard (EUCAST, CLSI or CA-SFM). Laboratory’s own results are indicated with a black radio button in the table and an orange dot in the histograms. Average (x) is used as a reference value for disk results and mode (Mo) is used for MIC results. According to the experts’ assessment some antimicrobials may be excluded from the final summary tables, e.g., antimicrobial agents to which the microbe is intrinsically resistant or to which only one result has been reported.
If you have not reported antimicrobial susceptibility testing results, or, your results have been excluded, you will get a note: “You have not reported antimicrobial susceptibility results, only global report is available.”
For information on report interpretation and performance evaluation, please see the "EQAS Interpretation guidelines" in LabScala User instructions. In case you have any questions regarding the reports, please contact the EQA Coordinator.

General Bacteriology, March, 1-2023

Report to the clinician

XXXX

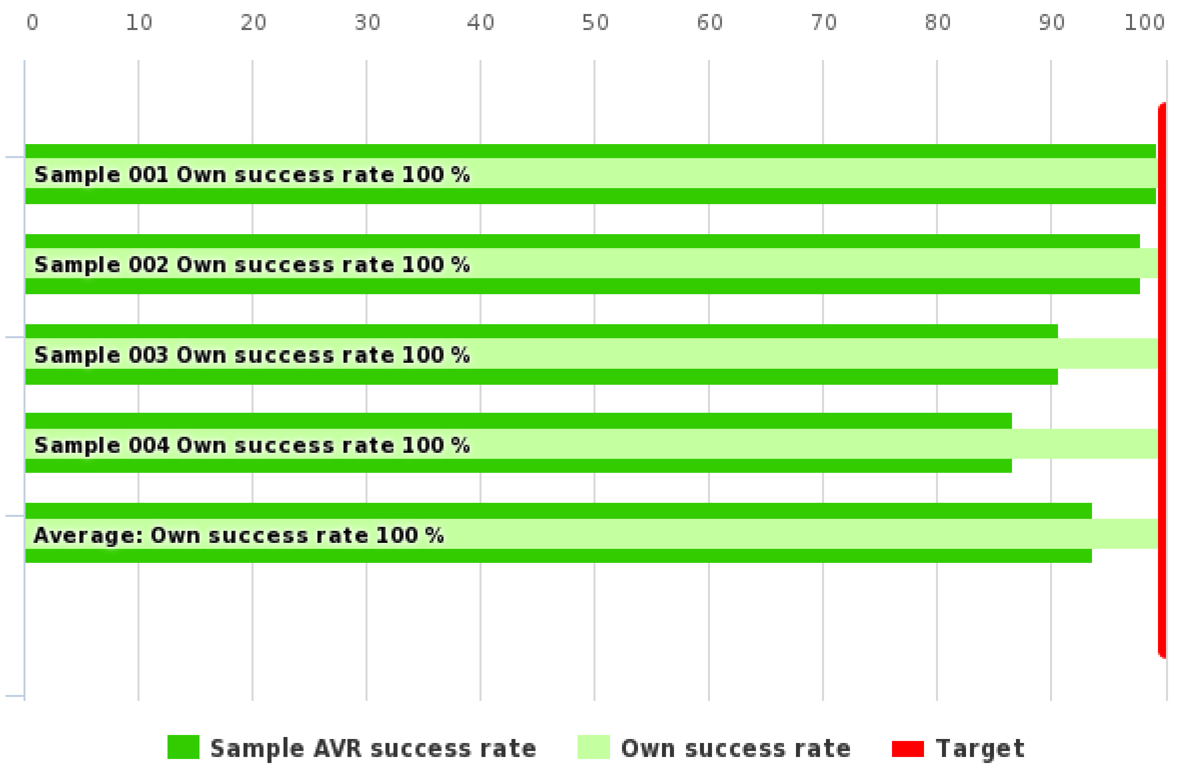
Client report

	No of participants	No of responded participants	Response percentage
General Bacteriology 1 (aerobes and anaerobes), March, 1-2023	59	58	98.3 %

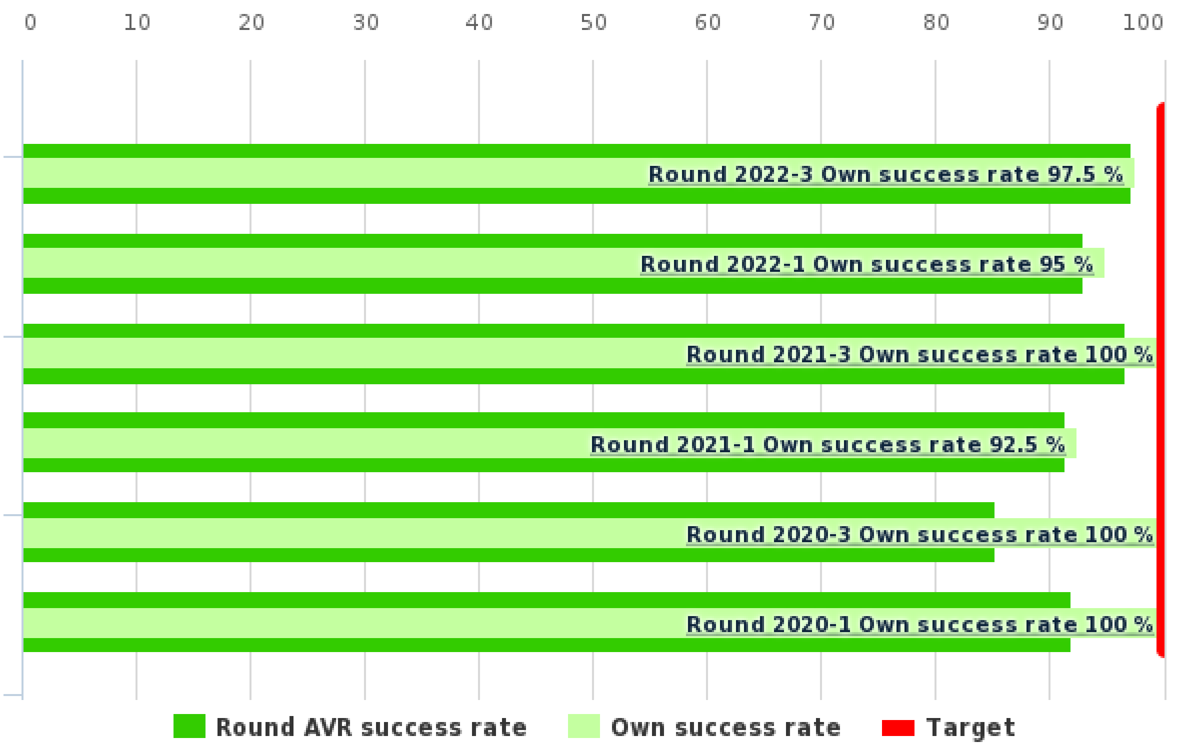
Summary

General Bacteriology 1 (aerobes and anaerobes) (5080)

Overall success rate by samples



Success rate history

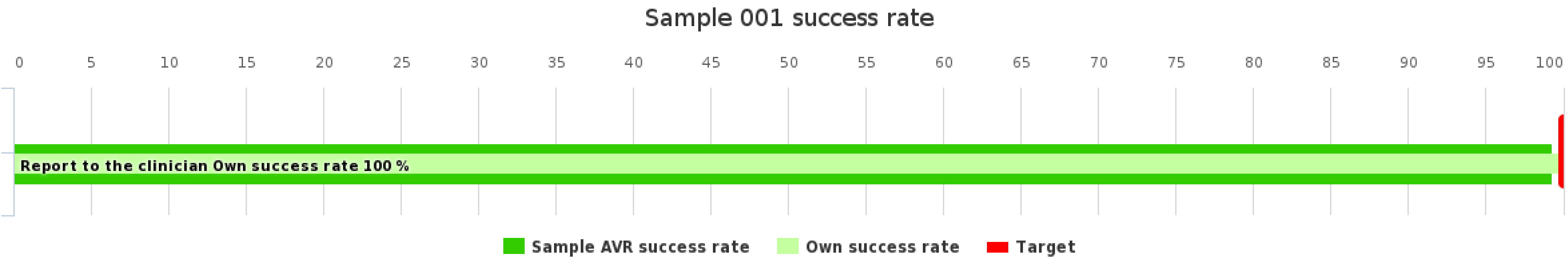


Summary	Own score	Max score	Own success rate	Difference	AVR success rate
Sample 001	5	5	100 %	0.7 %	99.3 %
Sample 002	5	5	100 %	2.1 %	97.9 %
Sample 003	5	5	100 %	9.3 %	90.7 %
Sample 004	5	5	100 %	13.3 %	86.7 %
Average:			100 %	6.4 %	93.6 %

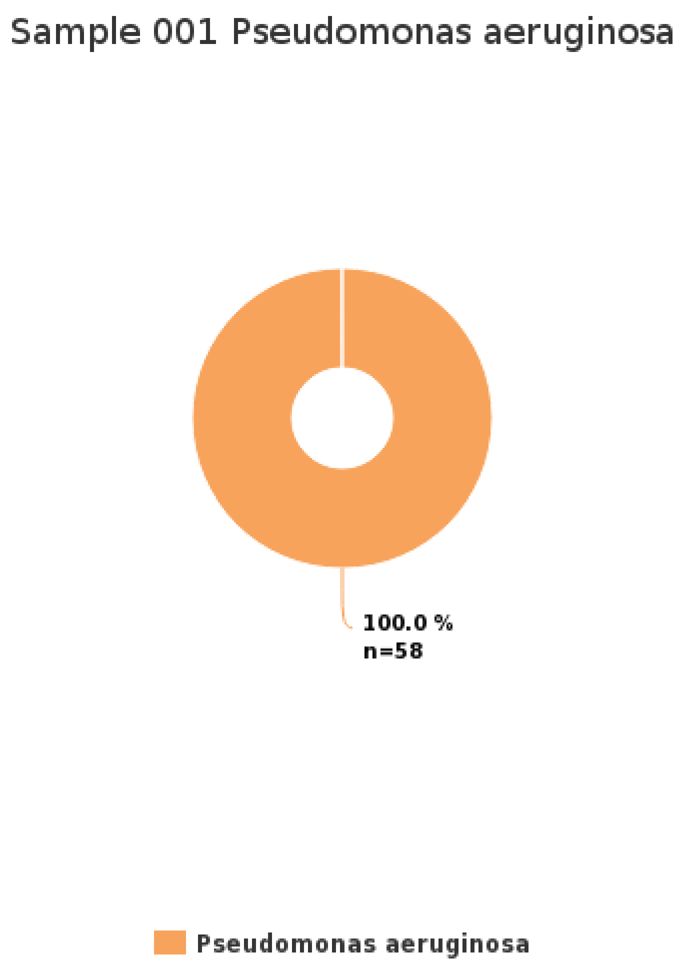
History	Test nr.	Own success rate	Difference	AVR success rate
Round 2022-3	1	97.5 %	0.3 %	97.2 %
Round 2022-1	1	95 %	2 %	93 %
Round 2021-3	1	100 %	3.3 %	96.7 %
Round 2021-1	1	92.5 %	1.1 %	91.4 %
Round 2020-3	1	100 %	14.8 %	85.2 %
Round 2020-1	1	100 %	8 %	92 %

Sample 001 | Pseudomonas aeruginosa

General Bacteriology 1 (aerobes and anaerobes) (5080)



Sample 001 results	Responded	Own score	Max score	Own success rate	Difference	AVR success rate	Count
	Report to the clinician	5	5	100 %	0.7 %	99.3 %	58
Total:		5	5	100 %	0.7 %	99.3 %	58



LABORATORY SPECIFIC SCORING TABLE

Finding group	Finding	Clinical significance	Further action	Own score	Max score	Own success rate	Difference	AVR success rate
Pseudomonas aeruginosa	Pseudomonas aeruginosa	Significant pathogen	Referred	5	5	100 %	0.7 %	99.3 %
Total:				5	5	100 %	0.7 %	99.3 %

REPORT TO THE CLINICIAN

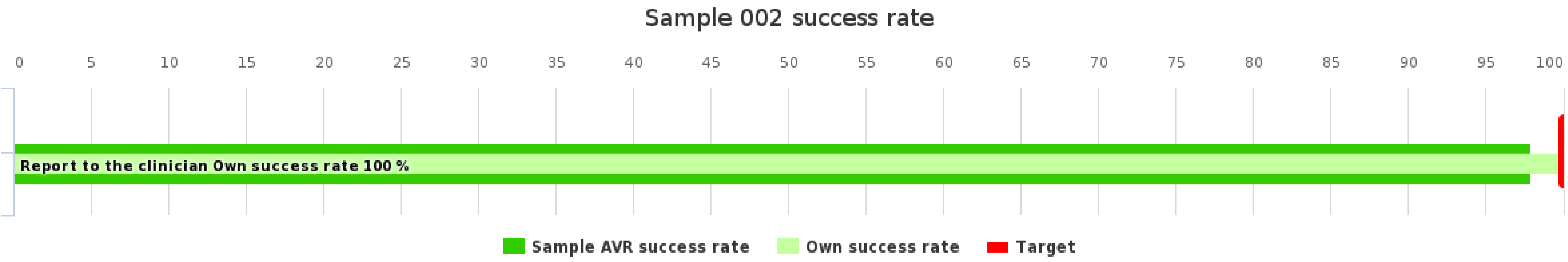
Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Pseudomonas aeruginosa		**58**						**99.3 %**
	◉ Pseudomonas aeruginosa	58	◉ 56	1	1	◉ 2	56	
Total:		58						99.3 %

SCORING SUMMARY

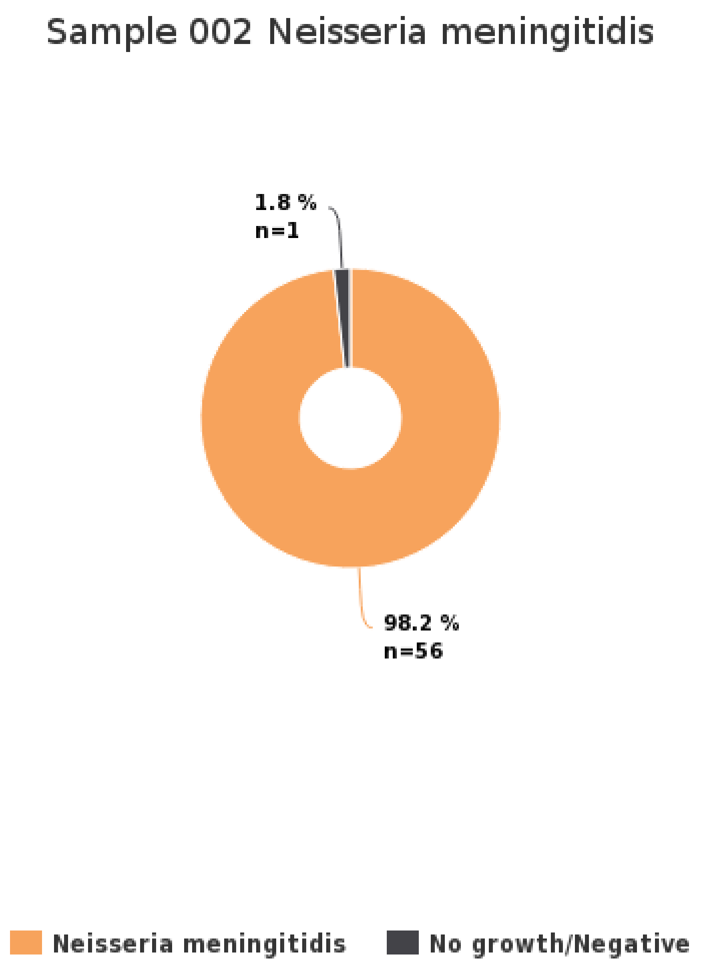
Finding group	Finding	Finding score	Significant pathogen	Max score
Pseudomonas aeruginosa				**5**
	Pseudomonas aeruginosa	4	1	5
Total:				5

Sample 002 | Neisseria meningitidis

General Bacteriology 1 (aerobes and anaerobes) (5080)



Sample 002 results	Responded	Own score	Max score	Own success rate	Difference	AVR success rate	Count
	Report to the clinician	5	5	100 %	2.1 %	97.9 %	57
Total:		5	5	100 %	2.1 %	97.9 %	57



LABORATORY SPECIFIC SCORING TABLE

Finding group	Finding	Clinical significance	Further action	Own score	Max score	Own success rate	Difference	AVR success rate
Neisseria meningitidis	Neisseria meningitidis	Significant pathogen	Not referred	5	5	100 %	2.1 %	97.9 %
Total:				5	5	100 %	2.1 %	97.9 %

REPORT TO THE CLINICIAN

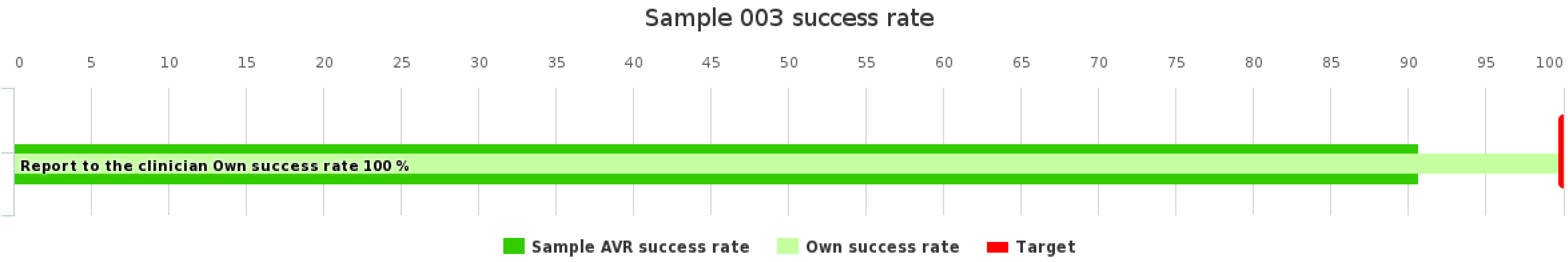
Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Neisseria meningitidis		**57**						**97.9 %**
	◉ Neisseria meningitidis	56	◉ 55	1		38	◉ 18	
	No growth/Negative	1			1		1	
Total:		57						97.9 %

SCORING SUMMARY

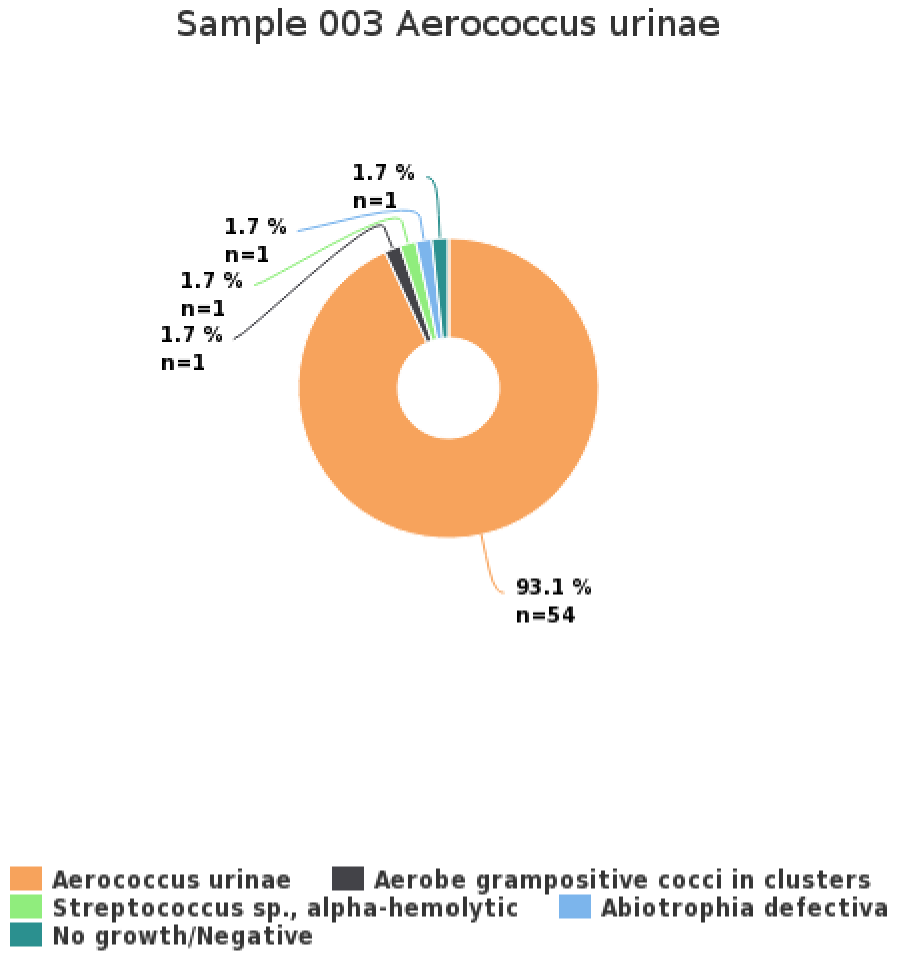
Finding group	Finding	Finding score	Significant pathogen	Max score
Neisseria meningitidis				**5**
	Neisseria meningitidis	4	1	5
	No growth/Negative	0		5
Total:				5

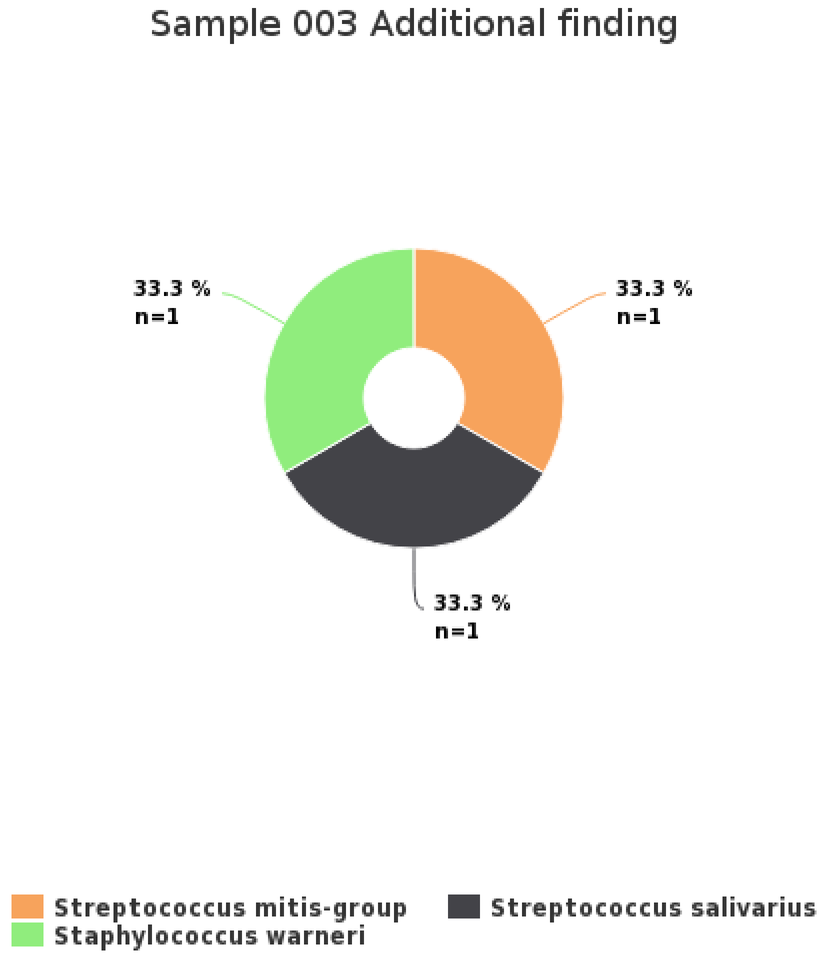
Sample 003 | Aerococcus urinae

General Bacteriology 1 (aerobes and anaerobes) (5080)



Sample 003 results	Responded	Own score	Max score	Own success rate	Difference	AVR success rate	Count
	Report to the clinician	5	5	100 %	9.3 %	90.7 %	61
Total:		5	5	100 %	9.3 %	90.7 %	61





LABORATORY SPECIFIC SCORING TABLE

Finding group	Finding	Clinical significance	Further action	Own score	Max score	Own success rate	Difference	AVR success rate
Aerococcus urinae	Aerococcus urinae	Significant pathogen	Not referred	5	5	100 %	9.3 %	90.7 %
Total:				5	5	100 %	9.3 %	90.7 %

REPORT TO THE CLINICIAN

Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Aerococcus urinae		**58**						**90.7 %**
	◉ Aerococcus urinae	54	◉ 45	9		3	◉ 51	
	Aerobe grampositive cocci in clusters	1	1			1		
	Streptococcus sp., alpha-hemolytic	1	1				1	
	Abiotrophia defectiva	1						
	No growth/Negative	1			1		1	
Additional finding		**3**						**-**
	Streptococcus mitis-group	1			1		1	
	Streptococcus salivarius	1		1			1	
	Staphylococcus warneri	1	1				1	
Total:		61						90.7 %

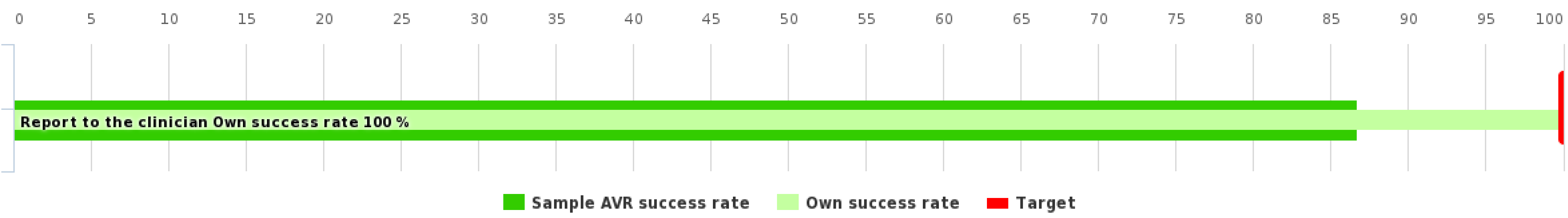
SCORING SUMMARY

Finding group	Finding	Finding score	Significant pathogen	Referred	Max score
Aerococcus urinae					**5**
	Aerococcus urinae	4	1		5
	Aerobe grampositive cocci in clusters	1		1	5
	Streptococcus sp., alpha-hemolytic	0			5
	Abiotrophia defectiva	0			5
	No growth/Negative	0			5
Additional finding					**-**
	Streptococcus mitis-group	-			-
	Streptococcus salivarius	-			-
	Staphylococcus warneri	-			-
Total:					5

Sample 004 | Streptococcus constellatus, Fusobacterium necrophorum

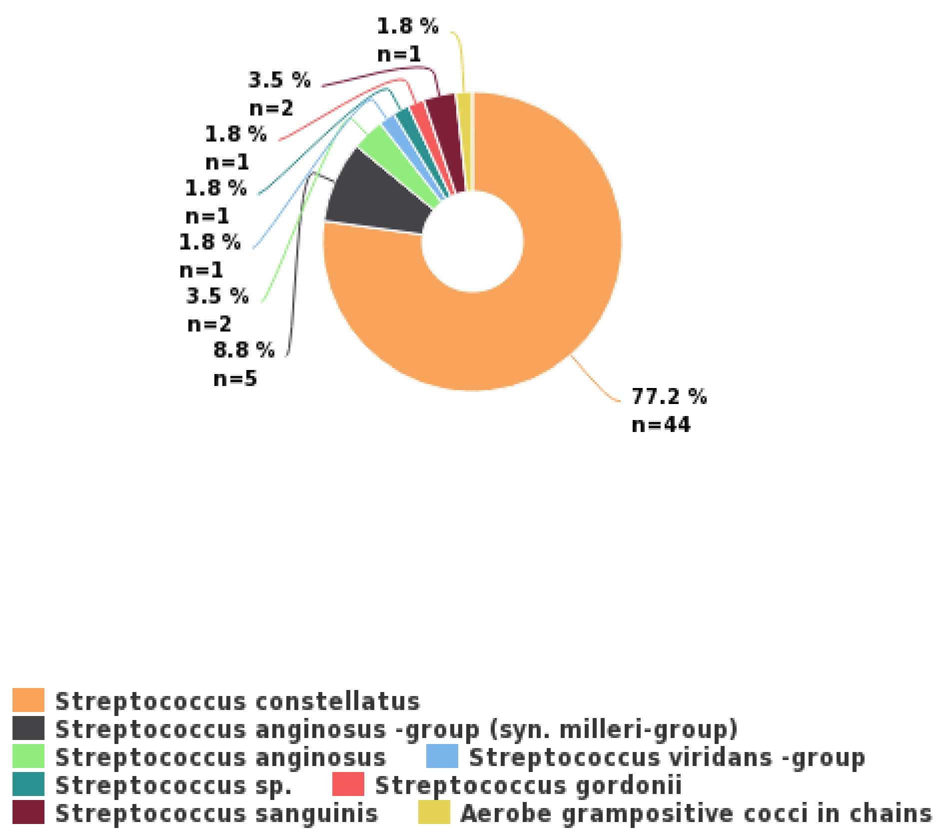
General Bacteriology 1 (aerobes and anaerobes) (5080)

Sample 004 success rate

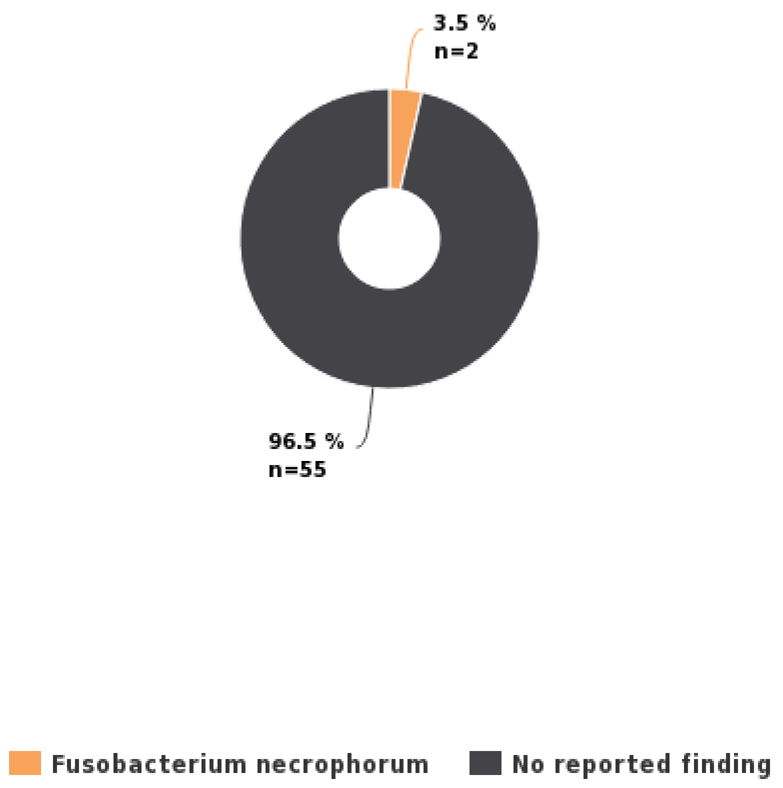


Sample 004 results	Responded	Own score	Max score	Own success rate	Difference	AVR success rate	Count
	Report to the clinician	5	5	100 %	13.3 %	86.7 %	115
Total:		5	5	100 %	13.3 %	86.7 %	115

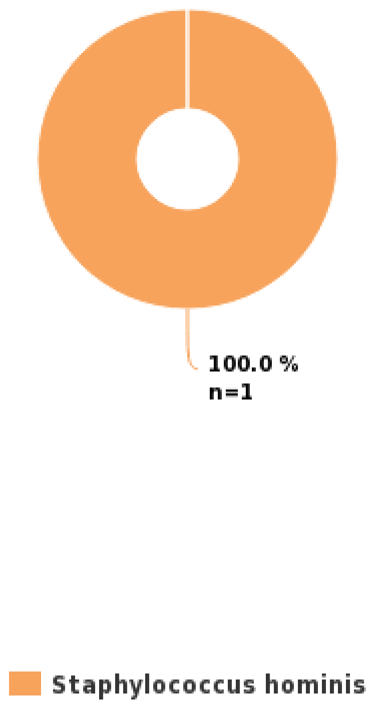
Sample 004 Streptococcus constellatus



Sample 004 Fusobacterium necrophorum



Sample 004 Additional finding



LABORATORY SPECIFIC SCORING TABLE

Finding group	Finding	Clinical significance	Further action	Own score	Max score	Own success rate	Difference	AVR success rate
Streptococcus constellatus	Streptococcus constellatus	Possible pathogen	Not referred	5	5	100 %	13.3 %	86.7 %
Fusobacterium necrophorum	No reported finding			-	-			-
Total:				5	5	100 %	13.3 %	86.7 %

REPORT TO THE CLINICIAN

Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Streptococcus constellatus		**57**						**86.7 %**
	● Streptococcus constellatus	44	28	● 11	5		● 44	
	Streptococcus anginosus -group (syn. milleri-group)	5	5				5	
	Streptococcus anginosus	2	1	1		1	1	
	Streptococcus viridans -group	1	1				1	
	Streptococcus sp.	1		1			1	
	Streptococcus gordonii	1		1			1	
	Streptococcus sanguinis	2	1	1			2	
	Aerobe grampositive cocci in chains	1		1			1	
Fusobacterium necrophorum		**57**						**-**
	Fusobacterium necrophorum	2	2				2	
	● No reported finding	55						
Additional finding		**1**						**-**
	Staphylococcus hominis	1			1		1	
Total:		115						86.7 %

SCORING SUMMARY

Finding group	Finding	Finding score	Significant pathogen	Possible pathogen	Max score
Streptococcus constellatus					**5**
	Streptococcus constellatus	4	1	1	5
	Streptococcus anginosus -group (syn. milleri-group)	4	1		5
	Streptococcus anginosus	2			5
	Streptococcus viridans -group	1			5
	Streptococcus sp.	1			5
	Streptococcus gordonii	0			5
	Streptococcus sanguinis	0			5
	Aerobe grampositive cocci in chains	1			5
Fusobacterium necrophorum					**-**
	Fusobacterium necrophorum	-			-
	No reported finding	-			-
Additional finding					**-**
	Staphylococcus hominis	-			-
Total:					5

Report Info

PARTICIPANTS

Altogether 94 laboratories from 22 countries participated in this EQA round.

REPORT INFO

On the front page you can see summaries of overall success rate and sample specific success rates which have been calculated from the scores. The reported results and the scores are presented in the same report but in separate tables. The global summary report contains the results of schemes General Bacteriology 1 (5080) and General Bacteriology 2 (5081), but in separate tables. The participant specific summary includes the results of your own reference group (product) merely.
In general, the expected results are marked with green color. Accepted results may also be indicated with yellow color. Laboratory’s own results are indicated with a black radio button If you have not reported results, you will get a note: “You have not responded in time, only global report is available.”
For information on report interpretation and performance evaluation, please see the "EQAS Interpretation guidelines" in LabScala User instructions. In case you have any questions regarding the reports, please contact the EQA Coordinator.

SCORING

The results in the “Report to the clinician” part can be scored when at least 60% of the participants have reported the correct/expected result and when there are at least three reported results. The report includes a sample specific scoring summary. Laboratory’s scores have been converted to percentage (own success rate, % from maximum scores) with a target at 100%. Own success rate is compared with the success rate of all results.

The scoring range/finding is 0-5 points. The scoring comprises the following elements:
species identification, a maximum of 4 points is given (see below)
the interpretation of the significance of the finding, a maximum of 1 point is given
in case of insufficient species identification, an additional score (maximum 1 point) might be given to participants that would have referred the isolate for further identification
The following general rules are applied regarding the scoring of the species identification:
4 points is reached by reporting the expected result
1-3 points is given to results that are partly correct/insufficient regarding the expected finding
0 points is given for an incorrect/false result

General Bacteriology, March, 1-2023

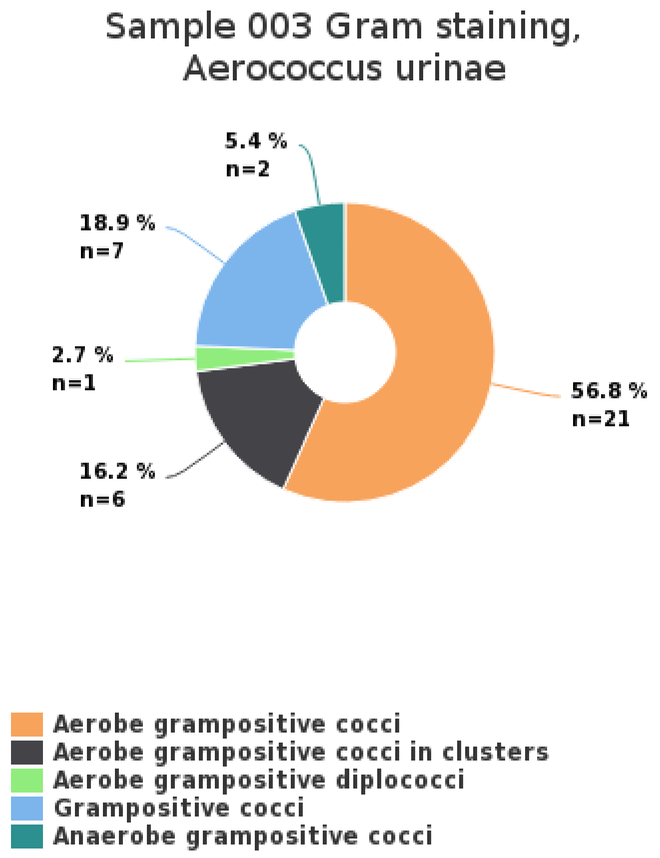
Identification test results

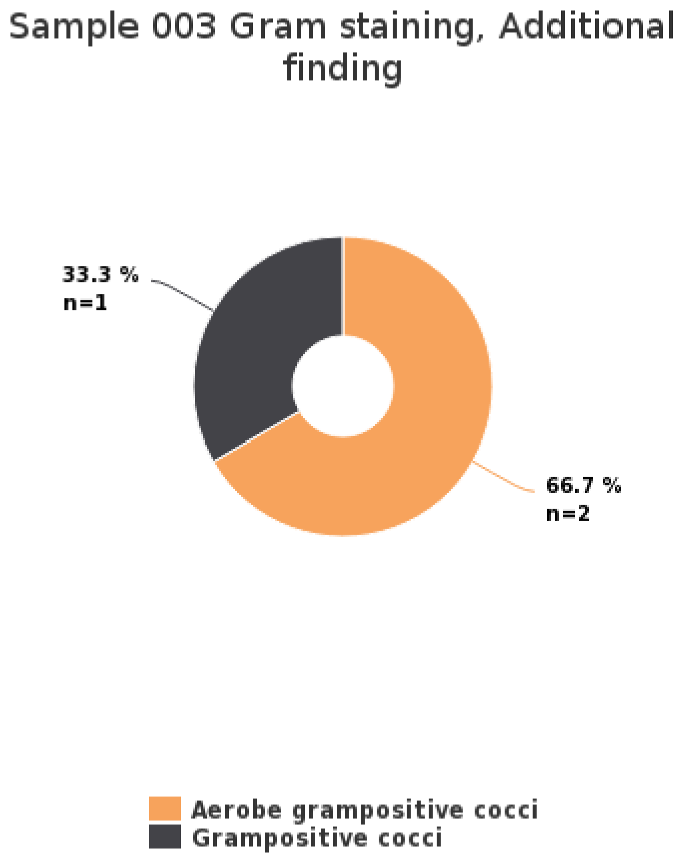
Client report

	No of participants	No of responded participants	Response percentage
General Bacteriology 1 (aerobes and anaerobes), March, 1-2023	59	57	96.6 %

Sample 003 | Aerococcus urinae

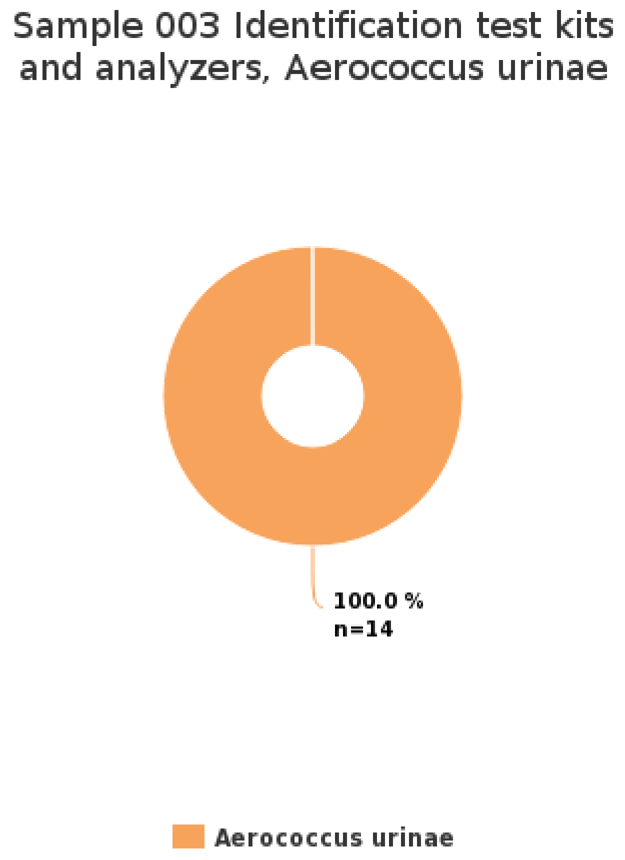
Sample 003 results	Responded	Count
	Gram staining	40
	Identification test kits and analyzers	15
	Identification tests: MALDI-TOF	47
	Identification tests: NAT and DNA-sequencing	1
Total:		103

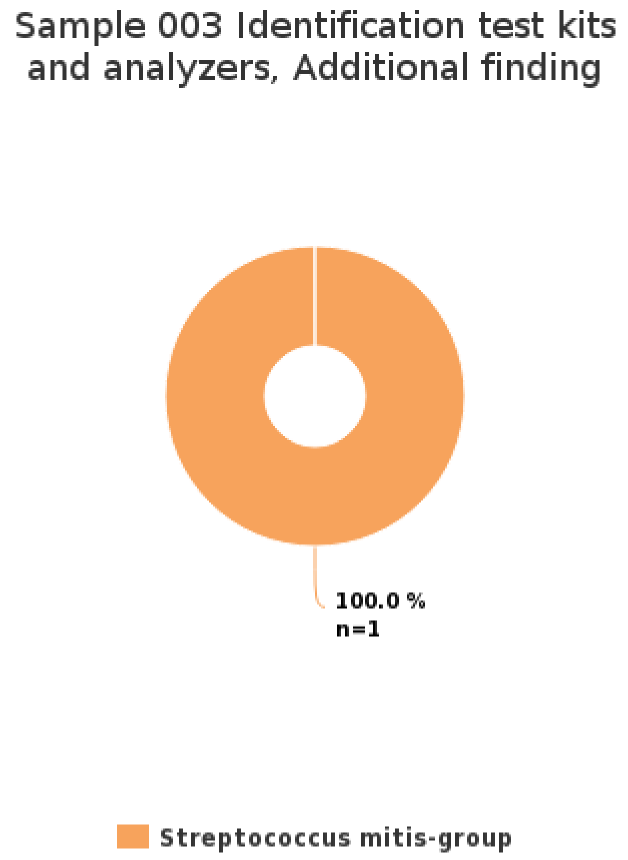


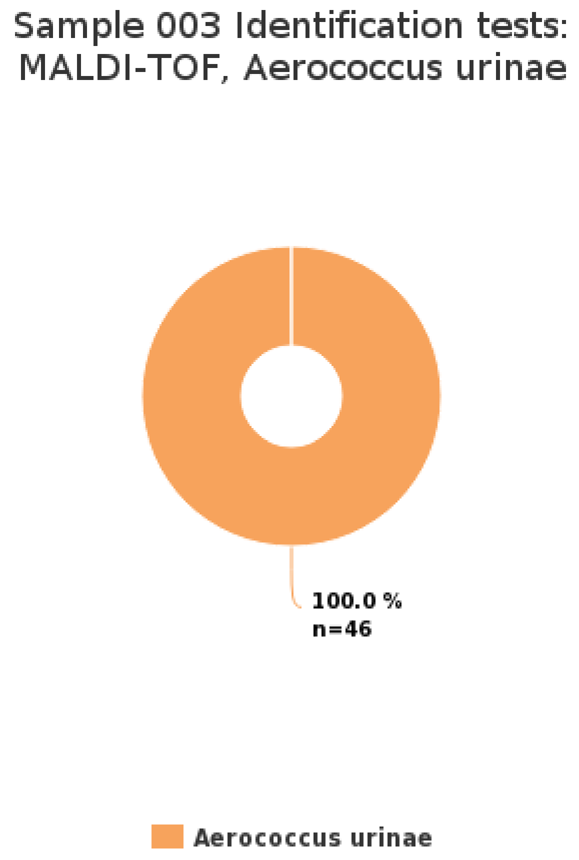


GRAM STAINING

Finding group	Result	Result count
Aerococcus urinae		**37**
	Aerobe grampositive cocci	21
	Aerobe grampositive cocci in clusters	6
	Aerobe grampositive diplococci	1
	Grampositive cocci	7
	Anaerobe grampositive cocci	2
Additional finding		**3**
	Aerobe grampositive cocci	2
	Grampositive cocci	1
Total:		40



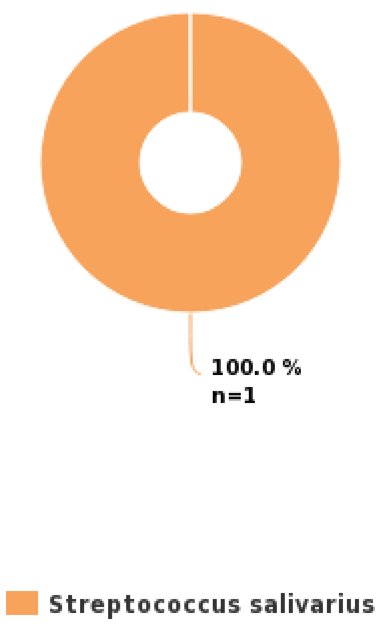




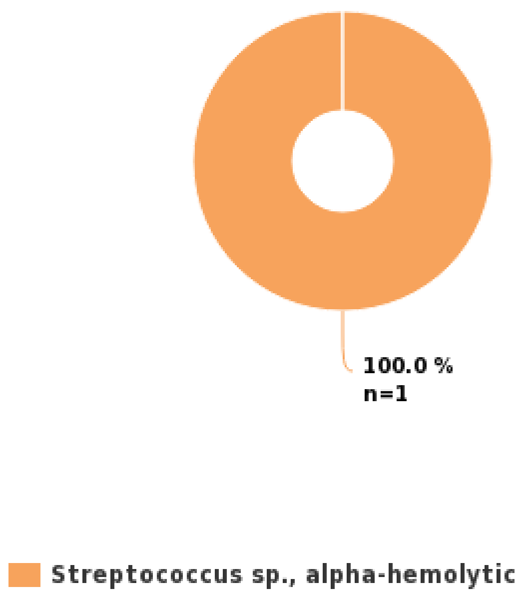
Sample 003 Identification tests:

Sample 003 Identification tests: NAT

MALDI-TOF, Additional finding



and DNA-sequencing, Aerococcus urinae



IDENTIFICATION TEST KITS AND ANALYZERS

Finding group	Method	Result	Profile number	Profile number count
Aerococcus urinae	BD Phoenix PMIC/ID panel (Becton Dickinson)	Aerococcus urinae	N/A	1
	VITEK 2 (bioMerieux)	Aerococcus urinae	000070700040111	1
			000070500050011	1
			000070500040030	1
			000030520040011	1
			000030500050411	1
			000030500040011	1
			000030100040011	1
			N/A	1
	VITEK 2 Compact 15 (bioMerieux)	Aerococcus urinae	000030700040011	1
	VITEK 2 Compact 30 (bioMerieux)	Aerococcus urinae	000030720150111	1
			000030100040010	1
			GP 000030700140011	1
			N/A	1
Additional finding	VITEK 2 Compact 30 (bioMerieux)	Streptococcus mitis-group	021110364305511	1
Total:				15

IDENTIFICATION TESTS: MALDI-TOF

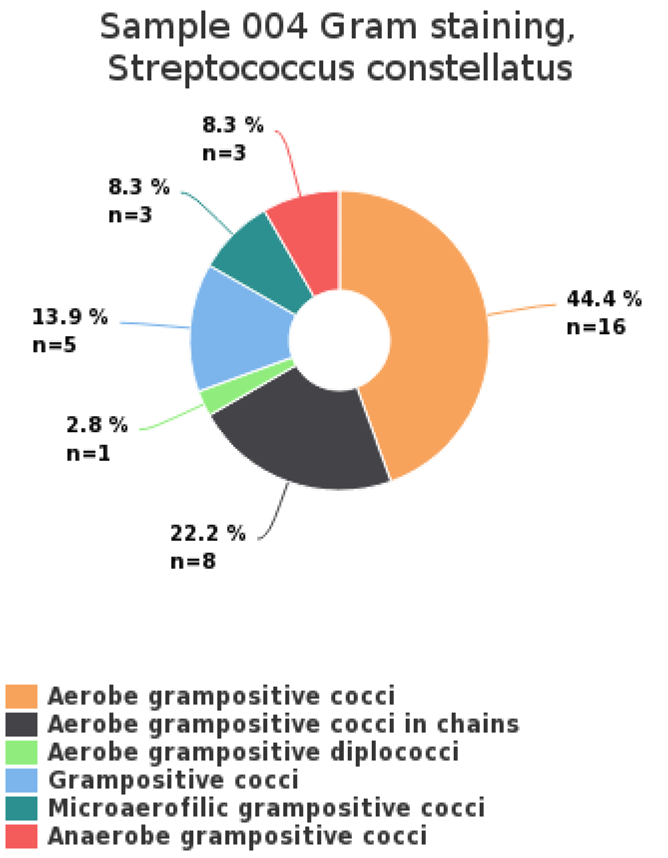
Finding group	Method	Result	Score / Probability %	Score / Probability % count
Aerococcus urinae	MALDI Biotyper (Bruker)	Aerococcus urinae	≥2	25
	VITEK MS (bioMérieux)	Aerococcus urinae	◉ 99,9 %	19
			99 %	2
Additional finding	MALDI Biotyper (Bruker)	Streptococcus salivarius	≥2	1
Total:				47

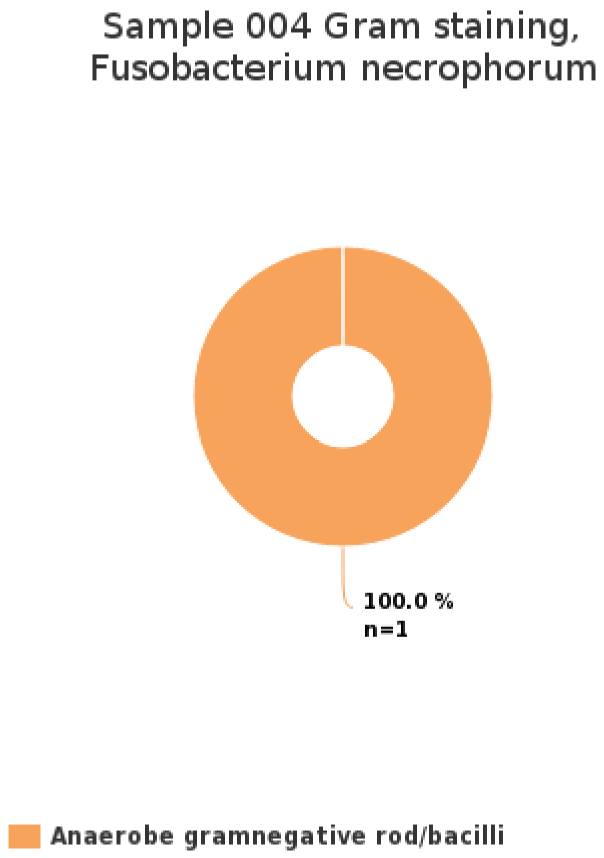
IDENTIFICATION TESTS: NAT AND DNA-SEQUENCING

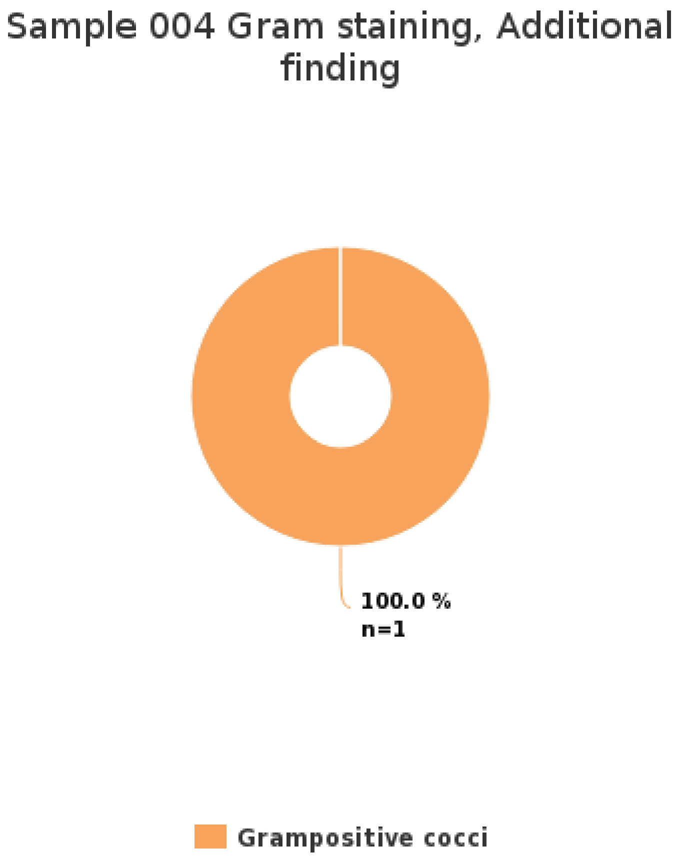
Finding group	Method	Result	Result count
Aerococcus urinae	NAT, In house	Streptococcus sp., alpha-hemolytic	1
Total:			1

Sample 004 | Streptococcus constellatus, Fusobacterium necrophorum

Sample 004 results	Responded	Count
	Gram staining	38
	Identification test kits and analyzers	11
	Identification tests: MALDI-TOF	50
	Identification tests: NAT and DNA-sequencing	1
Total:		100

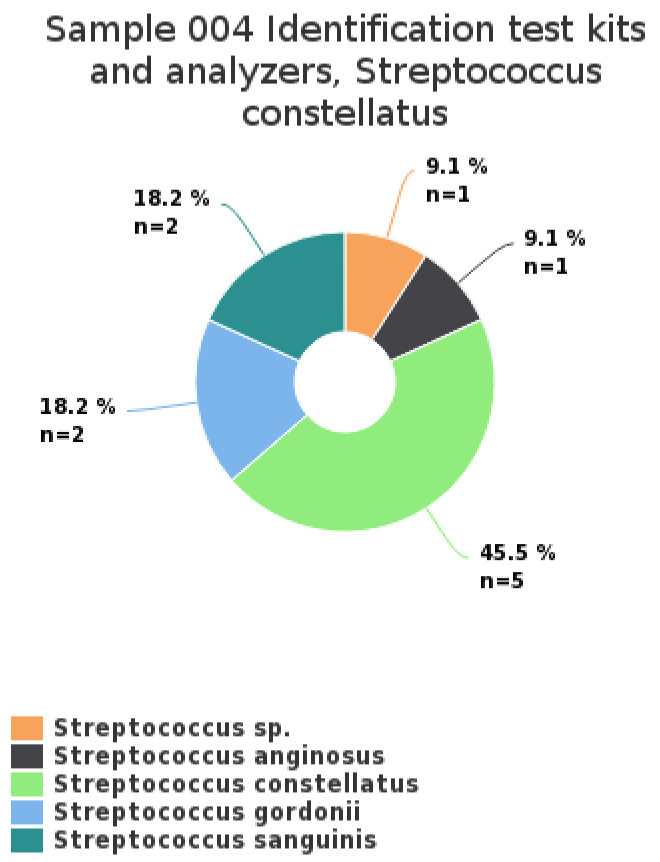

Sample 004 Gram staining, Streptococcus constellatus

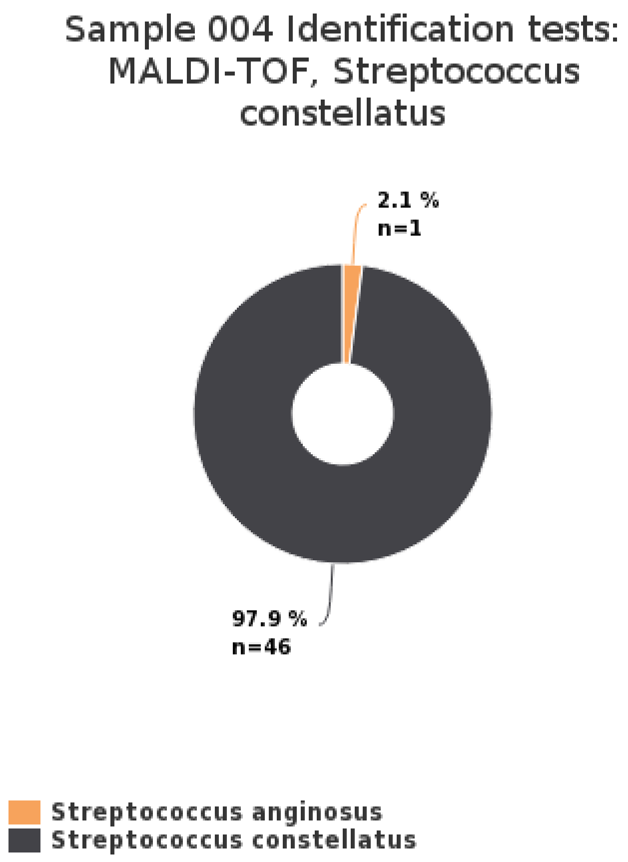

Sample 004 Gram staining, Fusobacterium necrophorum

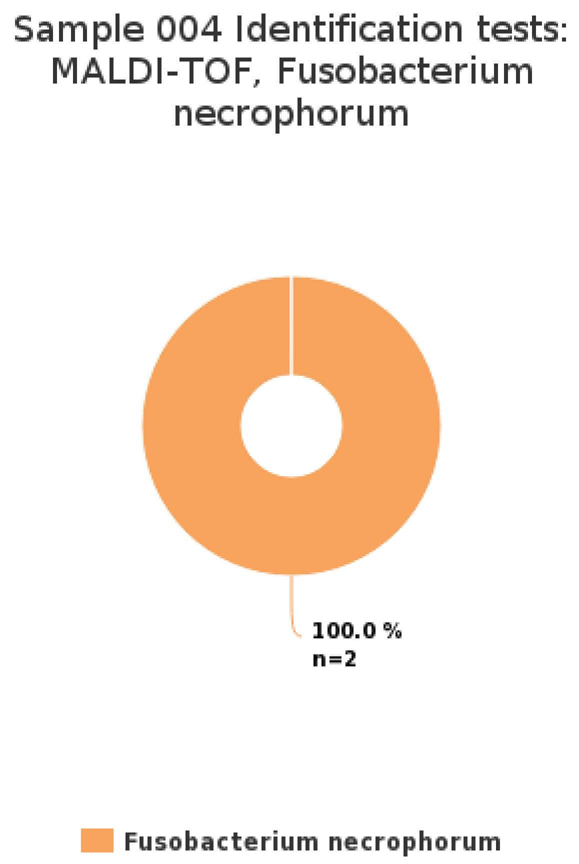

Sample 004 Gram staining, Additional finding

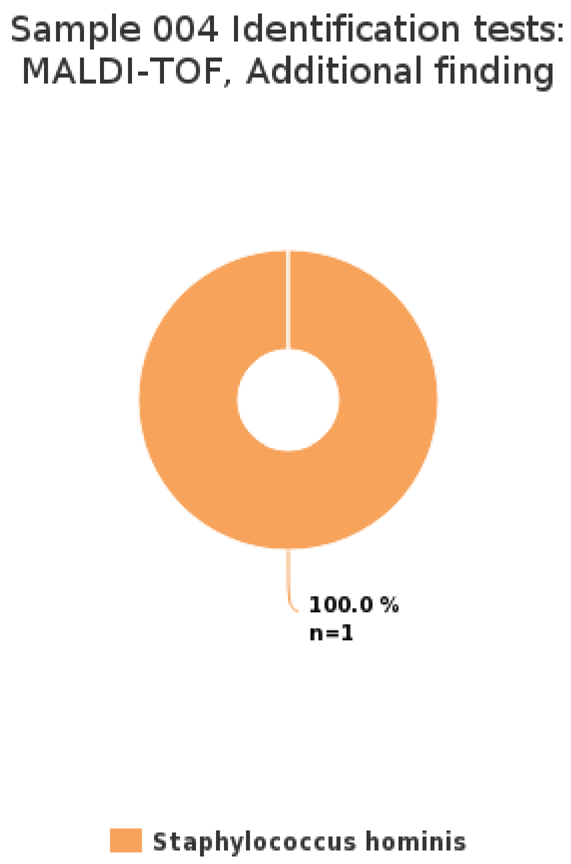
GRAM STAINING

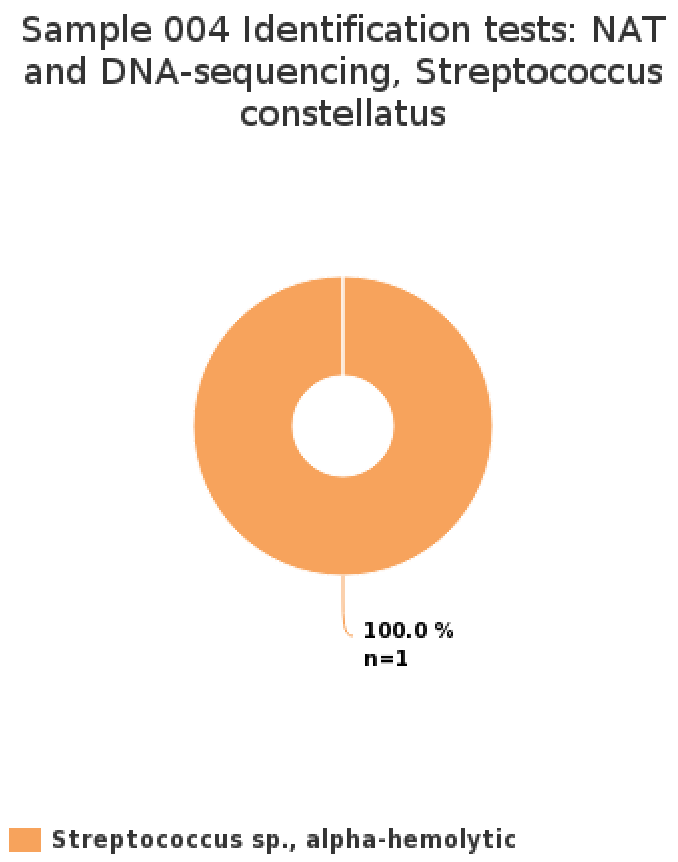
Finding group	Result	Result count
Streptococcus constellatus		**36**
	Aerobe grampositive cocci	16
	Aerobe grampositive cocci in chains	8
	Aerobe grampositive diplococci	1
	Grampositive cocci	5
	Microaerofilic grampositive cocci	3
	Anaerobe grampositive cocci	3
Fusobacterium necrophorum		**1**
	Anaerobe gramnegative rod/bacilli	1
Additional finding		**1**
	Grampositive cocci	1
Total:		38


Sample 004 Identification test kits and analyzers, Streptococcus constellatus


Sample 004 Identification tests: MALDI-TOF, Streptococcus constellatus


Sample 004 Identification tests: MALDI-TOF, Fusobacterium necrophorum


Sample 004 Identification tests: MALDI-TOF, Additional finding


Sample 004 Identification tests: NAT and DNA-sequencing, Streptococcus constellatus

IDENTIFICATION TEST KITS AND ANALYZERS

Finding group	Method	Result	Profile number	Profile number count
Streptococcus constellatus	BD Phoenix SMIC/ID panel (Becton Dickinson)	Streptococcus anginosus	N/A	1
	RapID STR (Thermo Scientific)	Streptococcus constellatus	30211strep	1
	VITEK 2 (bioMerieux)	Streptococcus sp.	N/A	1
		Streptococcus constellatus	051410360713671	1
		Streptococcus gordonii	011410120313471	1
		Streptococcus sanguinis	011010340301431	1
	VITEK 2 Compact 15 (bioMerieux)	Streptococcus sanguinis	001010120203431	1
	VITEK 2 Compact 30 (bioMerieux)	Streptococcus constellatus	051410360713471	1
			011410360713431	1
			N/A	1
		Streptococcus gordonii	N/A	1
Total:				11

IDENTIFICATION TESTS: MALDI-TOF

Finding group	Method	Result	Score / Probability %	Score / Probability % count
Streptococcus constellatus	MALDI Biotyper (Bruker)	Streptococcus constellatus	≥2	22
			≥1.7..<2	3
	VITEK MS (bioMérieux)	Streptococcus anginosus	99,9 %	1
		Streptococcus constellatus	◉ 99,9 %	19
			99 %	1

			98 %	1
Fusobacterium necrophorum	MALDI Biotyper (Bruker)	Fusobacterium necrophorum	≥2	1
	VITEK MS (bioMérieux)	Fusobacterium necrophorum	99,9 %	1
Additional finding	MALDI Biotyper (Bruker)	Staphylococcus hominis	≥1.7..<2	1
Total:				50

IDENTIFICATION TESTS: NAT AND DNA-SEQUENCING

Finding group	Method	Result	Result count
Streptococcus constellatus	NAT, In house	Streptococcus sp., alpha-hemolytic	1
Total:			1

General Bacteriology, March, 1-2023

Antimicrobial susceptibility testing results

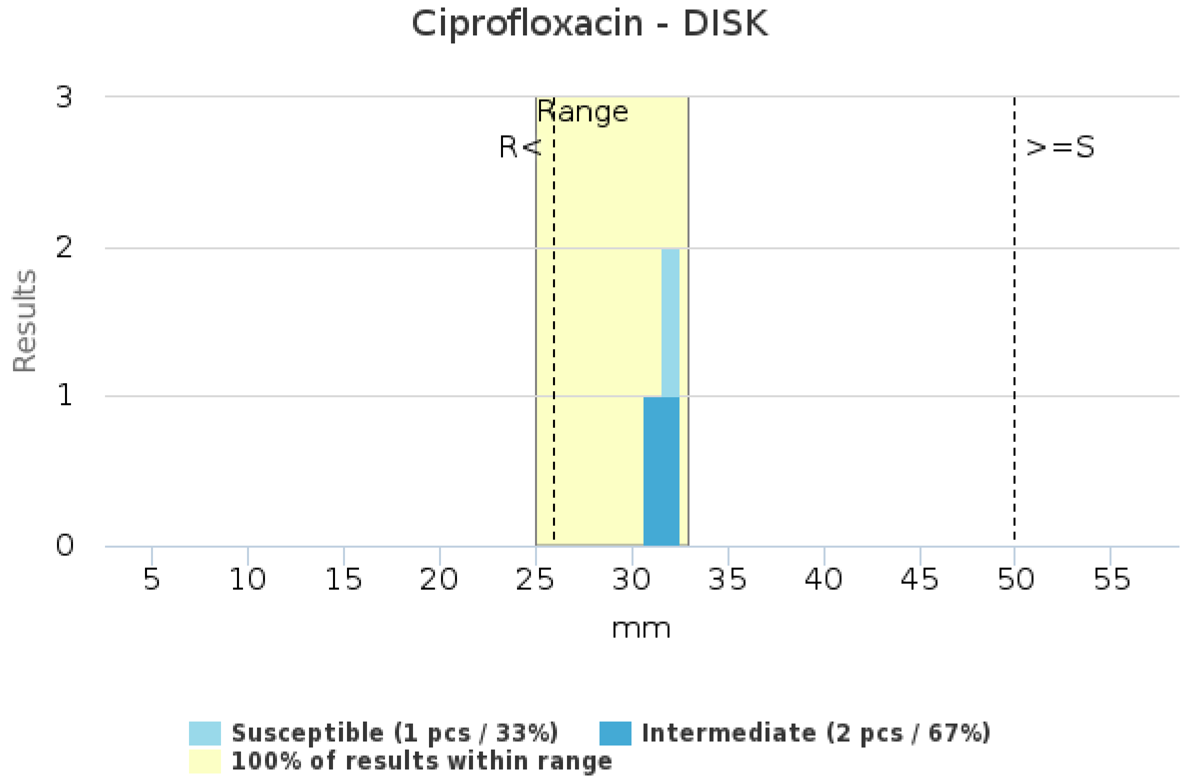
Sample 001

***Pseudomonas aeruginosa* ATCC 27853**

		DISK						MIC				
Antimicrobial agent	**Guideline**	**x (mm)**	**sd (mm)**	**S**	**I**	**R**	**n**	**Mo (mg/L)**	**S**	**I**	**R**	**n**
Amikacin	CA-SFM	21	-	2 (100%)	0 (0%)	0 (0%)	2	2	1 (100%)	0 (0%)	0 (0%)	1
	CLSI	-	-	-	-	-	-	4	1 (100%)	0 (0%)	0 (0%)	1
	EUCAST	23	4	31 (100%)	0 (0%)	0 (0%)	31	2	45 (100%)	0 (0%)	0 (0%)	45
	All			**33 (100%)**	**0 (0%)**	**0 (0%)**	**33**		**47 (100%)**	**0 (0%)**	**0 (0%)**	**47**
Aztreonam	CA-SFM	28	-	1 (50%)	1 (50%)	0 (0%)	2	-	-	-	-	-
	CLSI	-	-	-	-	-	-	4	1 (100%)	0 (0%)	0 (0%)	1
	EUCAST	26	3	2 (15%)	11 (85%)	0 (0%)	13	4	2 (11%)	16 (89%)	0 (0%)	18
	All			**3 (20%)**	**12 (80%)**	**0 (0%)**	**15**		**3 (16%)**	**16 (84%)**	**0 (0%)**	**19**
Cefepime	CA-SFM	28	-	1 (50%)	1 (50%)	0 (0%)	2	2	0 (0%)	1 (100%)	0 (0%)	1
	EUCAST	28	3	2 (10%)	18 (90%)	0 (0%)	20	2	4 (11%)	32 (89%)	0 (0%)	36
	All			**3 (14%)**	**19 (86%)**	**0 (0%)**	**22**		**4 (11%)**	**33 (89%)**	**0 (0%)**	**37**
Ceftazidime	CA-SFM	22	-	1 (50%)	1 (50%)	0 (0%)	2	4	0 (0%)	1 (100%)	0 (0%)	1
	CLSI	-	-	-	-	-	-	1	1 (100%)	0 (0%)	0 (0%)	1
	EUCAST	24	2	5 (11%)	39 (89%)	0 (0%)	44	2	4 (8%)	47 (92%)	0 (0%)	51
	All			**6 (13%)**	**40 (87%)**	**0 (0%)**	**46**		**5 (9%)**	**48 (91%)**	**0 (0%)**	**53**
Ceftazidime-avibactam	EUCAST	25	2	4 (80%)	1 (20%)	0 (0%)	5	2	8 (100%)	0 (0%)	0 (0%)	8
	All			**4 (80%)**	**1 (20%)**	**0 (0%)**	**5**		**8 (100%)**	**0 (0%)**	**0 (0%)**	**8**
Ceftolozane-tazobactam	CA-SFM	25	-	2 (100%)	0 (0%)	0 (0%)	2	-	-	-	-	-
	EUCAST	27	-	2 (100%)	0 (0%)	0 (0%)	2	0.5	13 (100%)	0 (0%)	0 (0%)	13
	All			**4 (100%)**	**0 (0%)**	**0 (0%)**	**4**		**13 (100%)**	**0 (0%)**	**0 (0%)**	**13**
Chloramphenicol	EUCAST	6	0	0 (0%)	0 (0%)	7 (100%)	7	32	0 (0%)	0 (0%)	1 (100%)	1
	All			**0 (0%)**	**0 (0%)**	**7 (100%)**	**7**		**0 (0%)**	**0 (0%)**	**1 (100%)**	**1**
Ciprofloxacin	CA-SFM	32	1	1 (33%)	2 (67%)	0 (0%)	3	-	0 (0%)	2 (100%)	0 (0%)	2
	CLSI	-	-	-	-	-	-	0.5	1 (100%)	0 (0%)	0 (0%)	1
	EUCAST	30	2	7 (15%)	39 (83%)	1 (2%)	47	0.25	6 (13%)	41 (85%)	1 (2%)	48
	All			**8 (16%)**	**41 (82%)**	**1 (2%)**	**50**		**7 (14%)**	**43 (84%)**	**1 (2%)**	**51**
Colistin	EUCAST	16	-	1 (100%)	0 (0%)	0 (0%)	1	2	22 (100%)	0 (0%)	0 (0%)	22
	All			**1 (100%)**	**0 (0%)**	**0 (0%)**	**1**		**22 (100%)**	**0 (0%)**	**0 (0%)**	**22**
Ertapenem	EUCAST	-	-	-	-	-	-	-	0 (0%)	0 (0%)	2 (100%)	2
	All			**0**	**0**	**0**	**0**		**0 (0%)**	**0 (0%)**	**2 (100%)**	**2**
Gentamycin	CLSI	-	-	-	-	-	-	1	1 (100%)	0 (0%)	0 (0%)	1
	EUCAST	19	2	11 (100%)	0 (0%)	0 (0%)	11	1	15 (83%)	3 (17%)	0 (0%)	18
	All			**11 (100%)**	**0 (0%)**	**0 (0%)**	**11**		**16 (84%)**	**3 (16%)**	**0 (0%)**	**19**
Imipenem	CA-SFM	24	-	1 (50%)	1 (50%)	0 (0%)	2	4	0 (0%)	1 (100%)	0 (0%)	1
	CLSI	-	-	-	-	-	-	-	2 (100%)	0 (0%)	0 (0%)	2
	EUCAST	24	2	4 (13%)	27 (87%)	0 (0%)	31	2	3 (9%)	31 (91%)	0 (0%)	34
	All			**5 (15%)**	**28 (85%)**	**0 (0%)**	**33**		**5 (14%)**	**32 (86%)**	**0 (0%)**	**37**
Levofloxacin	CA-SFM	23	-	1 (100%)	0 (0%)	0 (0%)	1	1	0 (0%)	1 (100%)	0 (0%)	1
	EUCAST	24	2	4 (17%)	19 (83%)	0 (0%)	23	1	2 (9%)	21 (91%)	0 (0%)	23
	All			**5 (21%)**	**19 (79%)**	**0 (0%)**	**24**		**2 (8%)**	**22 (92%)**	**0 (0%)**	**24**
Meropenem	CA-SFM	28	-	2 (100%)	0 (0%)	0 (0%)	2	-	-	-	-	-
	EUCAST	29	3	43 (100%)	0 (0%)	0 (0%)	43	0.5	49 (100%)	0 (0%)	0 (0%)	49
	All			**45 (100%)**	**0 (0%)**	**0 (0%)**	**45**		**49 (100%)**	**0 (0%)**	**0 (0%)**	**49**
Piperacillin	CA-SFM	23	-	1 (50%)	1 (50%)	0 (0%)	2	4	0 (0%)	1 (100%)	0 (0%)	1
	EUCAST	25	6	2 (25%)	5 (63%)	1 (13%)	8	4	1 (13%)	7 (88%)	0 (0%)	8
	All			**3 (30%)**	**6 (60%)**	**1 (10%)**	**10**		**1 (11%)**	**8 (89%)**	**0 (0%)**	**9**
Piperacillin-tazobactam	CA-SFM	25	-	1 (50%)	1 (50%)	0 (0%)	2	-	-	-	-	-
	EUCAST	26	2	6 (14%)	37 (86%)	0 (0%)	43	4	7 (15%)	39 (85%)	0 (0%)	46
	All			**7 (16%)**	**38 (84%)**	**0 (0%)**	**45**		**7 (15%)**	**39 (85%)**	**0 (0%)**	**46**
Tetracycline	EUCAST	-	-	-	-	-	-	-	0 (0%)	0 (0%)	2 (100%)	2
	All			**0**	**0**	**0**	**0**		**0 (0%)**	**0 (0%)**	**2 (100%)**	**2**
Ticarcillin	CA-SFM	23	-	1 (50%)	1 (50%)	0 (0%)	2	-	-	-	-	-
	EUCAST	-	-	-	-	-	-	-	0 (0%)	1 (50%)	1 (50%)	2
	All			**1 (50%)**	**1 (50%)**	**0 (0%)**	**2**		**0 (0%)**	**1 (50%)**	**1 (50%)**	**2**

Tikarcillin-clavulanic acid	CA-SFM	23	-	1 (50%)	1 (50%)	0 (0%)	2	16	0 (0%)	1 (100%)	0 (0%)	1
	EUCAST	23	-	0 (0%)	1 (100%)	0 (0%)	1	16	0 (0%)	2 (100%)	0 (0%)	2
	All			**1 (33%)**	**2 (67%)**	**0 (0%)**	**3**		**0 (0%)**	**3 (100%)**	**0 (0%)**	**3**
Tobramycin	CA-SFM	22	-	2 (100%)	0 (0%)	0 (0%)	2	1	1 (100%)	0 (0%)	0 (0%)	1
	EUCAST	23	3	42 (100%)	0 (0%)	0 (0%)	42	1	36 (100%)	0 (0%)	0 (0%)	36
	All			**44 (100%)**	**0 (0%)**	**0 (0%)**	**44**		**37 (100%)**	**0 (0%)**	**0 (0%)**	**37**

Sample 001 | CA-SFM

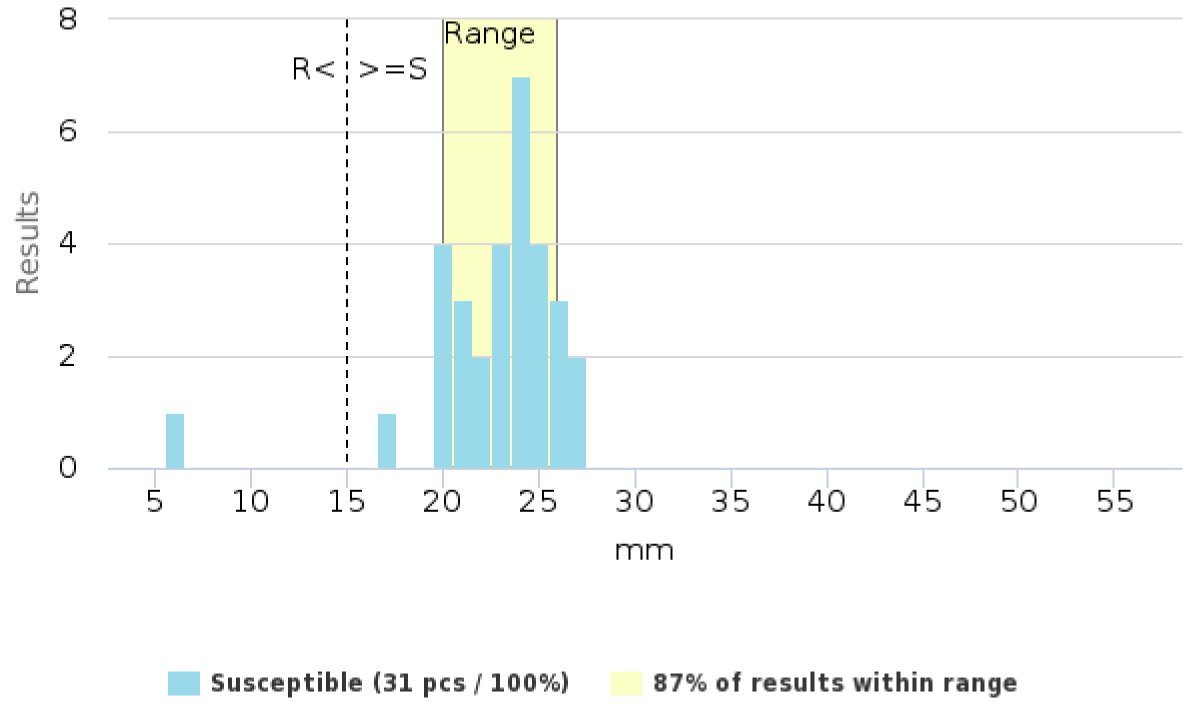


General Bacteriology, March, 1-2023

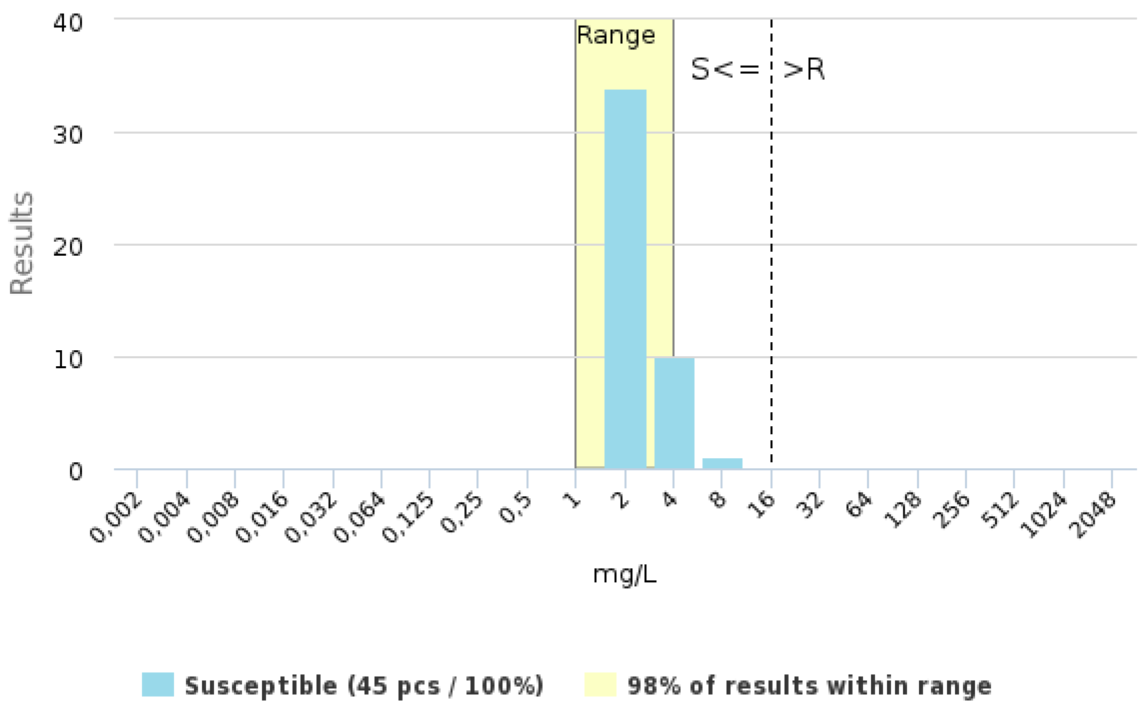
Antimicrobial susceptibility testing results

Sample 001 | EUCAST

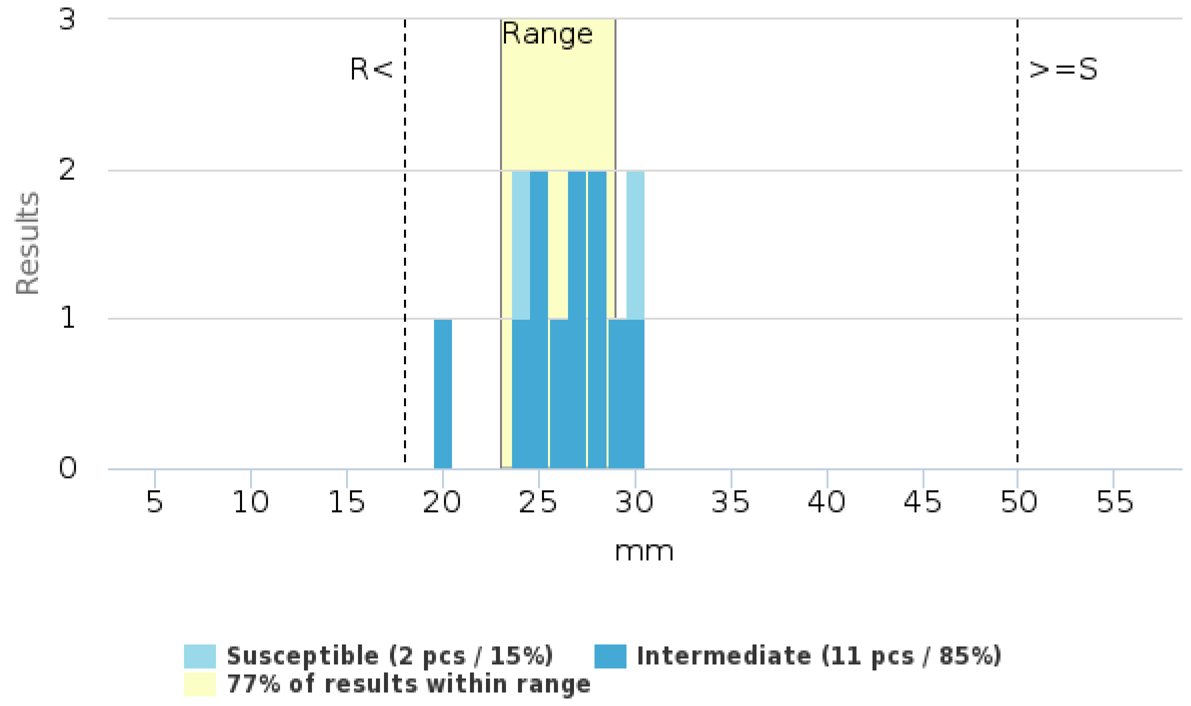
Amikacin - DISK



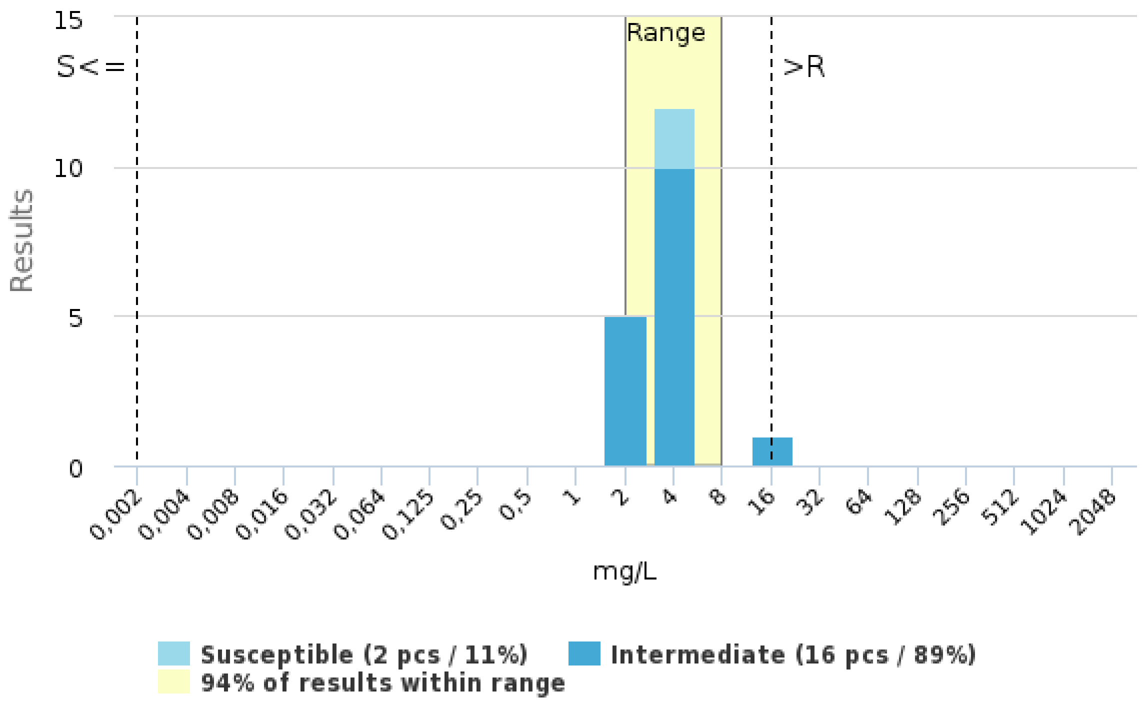
Amikacin - MIC



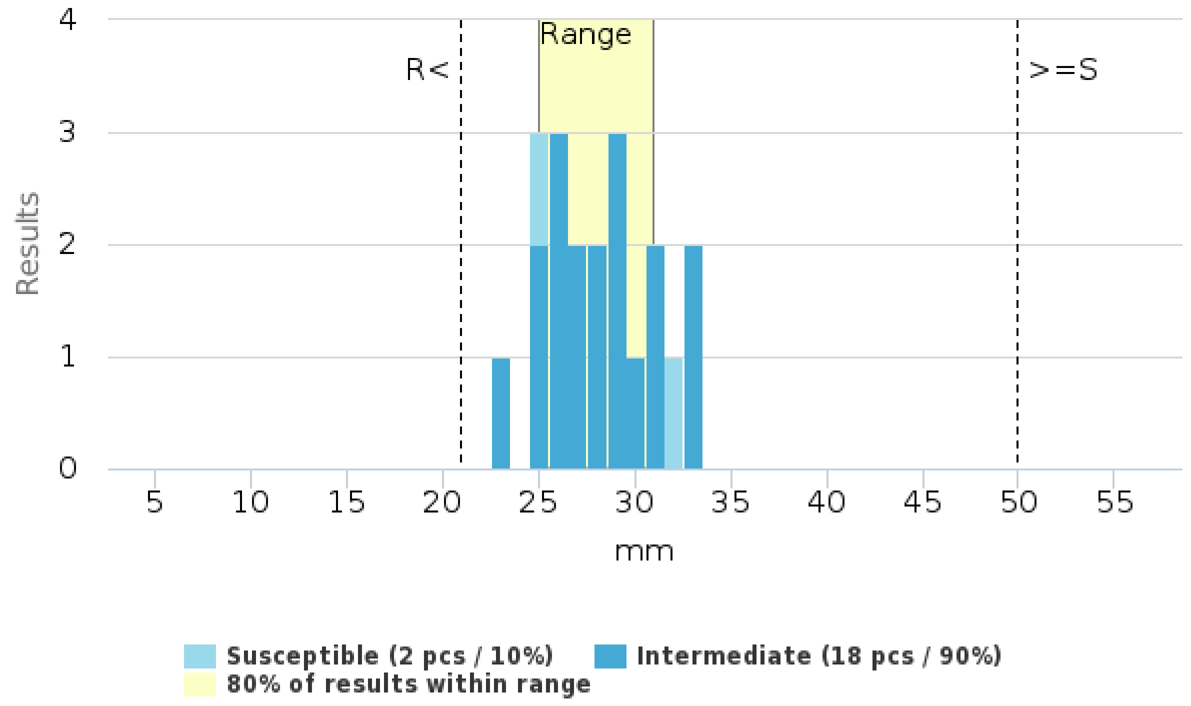
Aztreonam - DISK



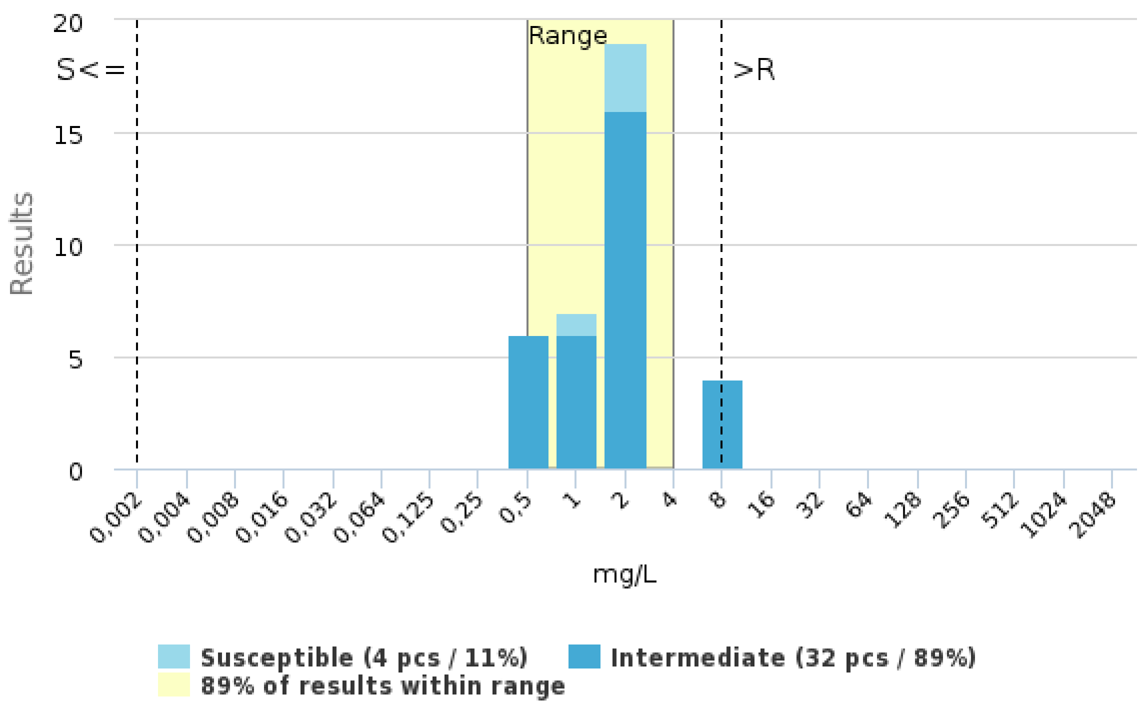
Aztreonam - MIC

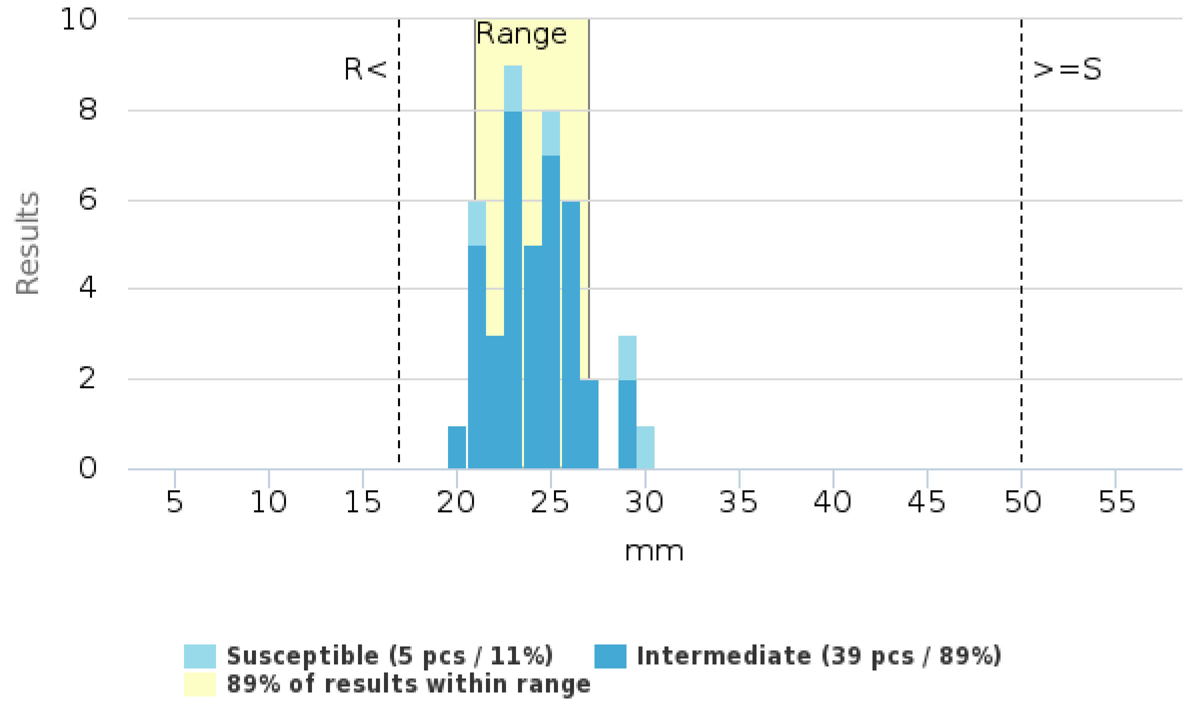


Cefepime - DISK

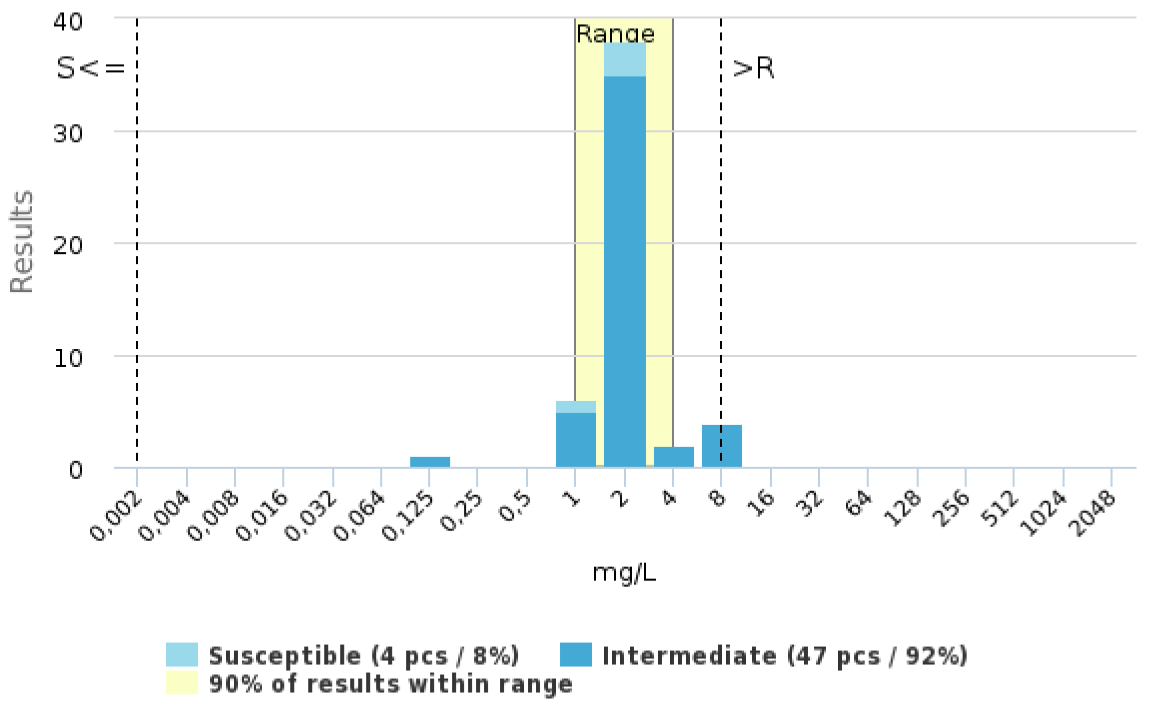


Cefepime - MIC

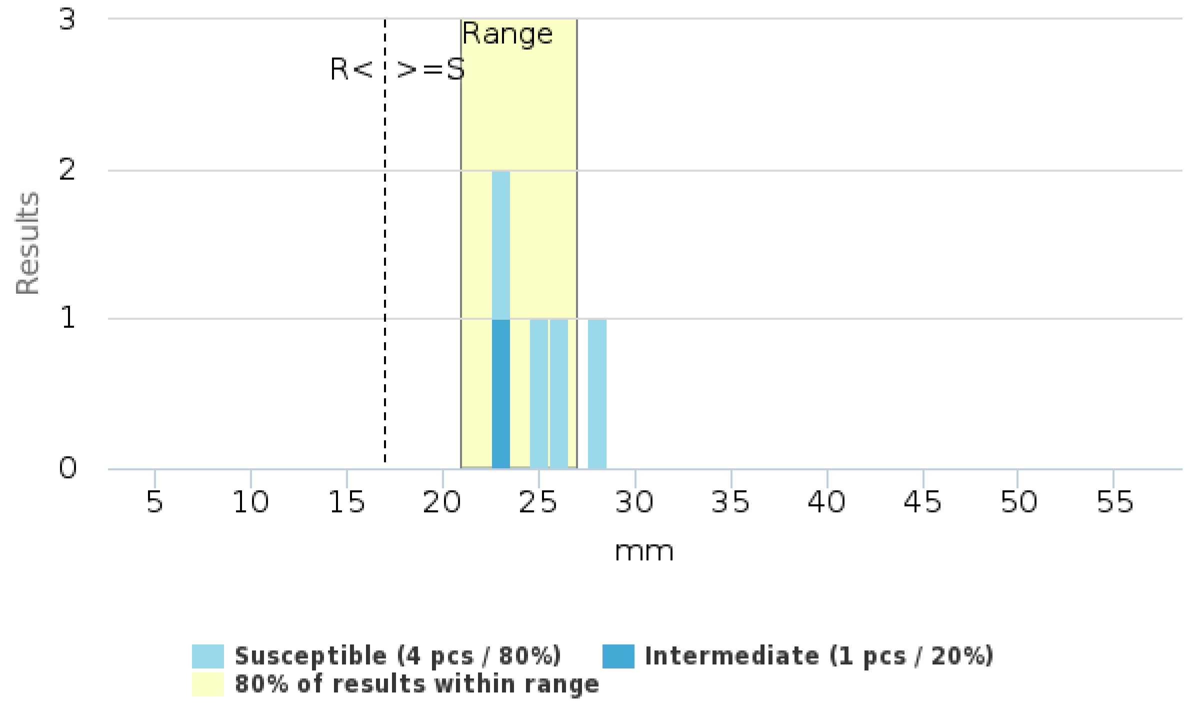




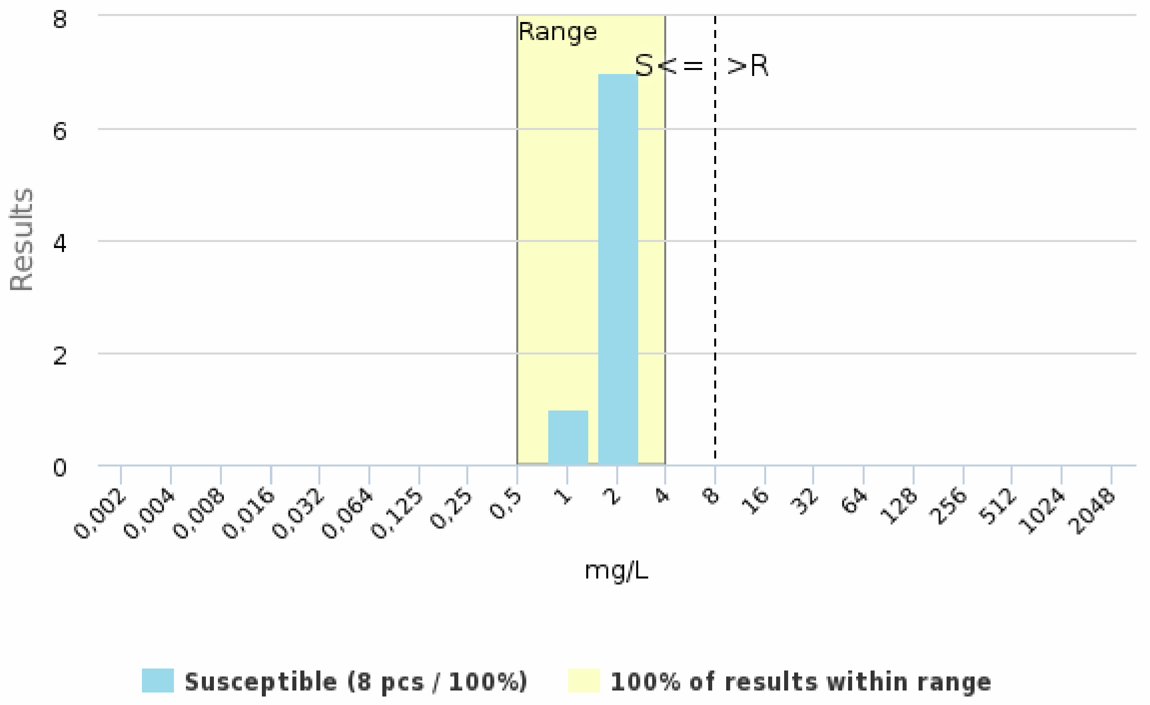
Ceftazidime - DISK



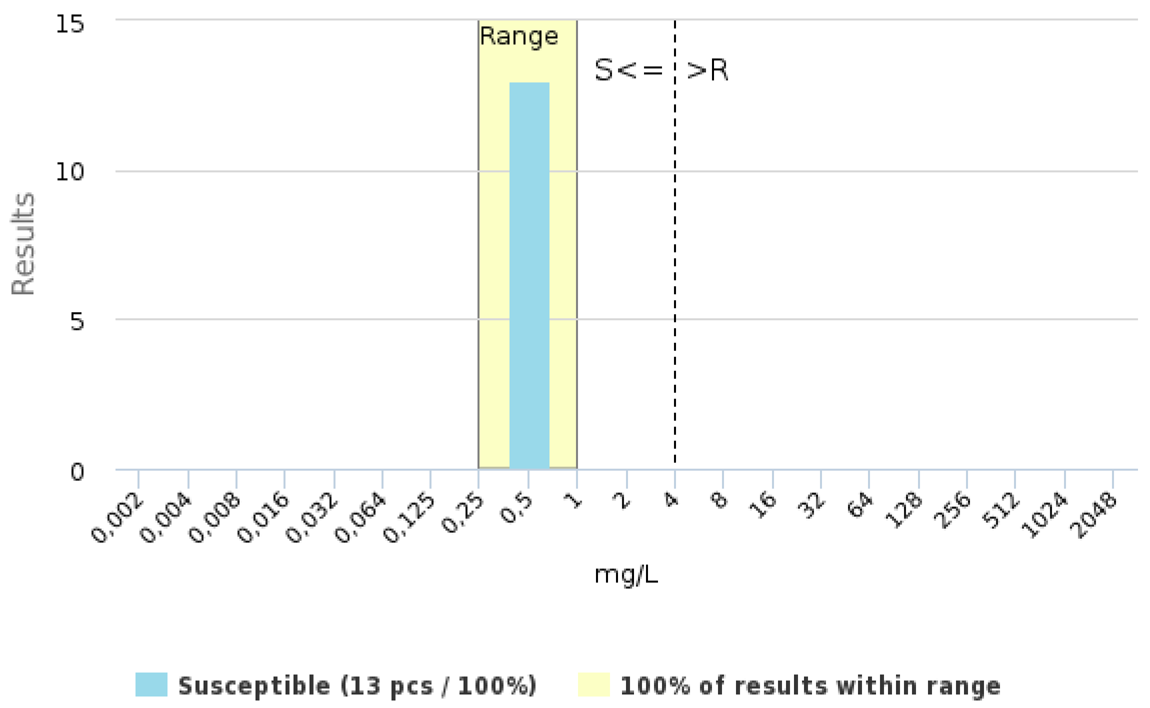
Ceftazidime - MIC



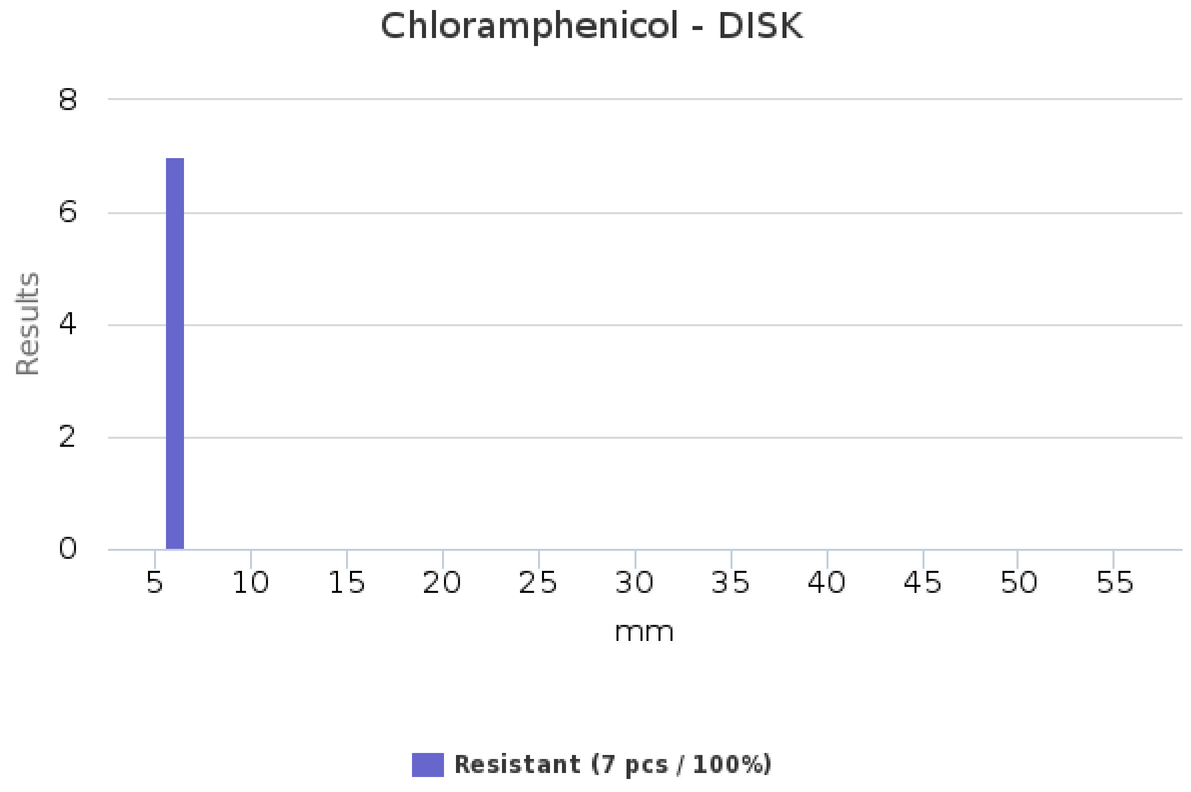
Ceftazidime-avibactam - DISK

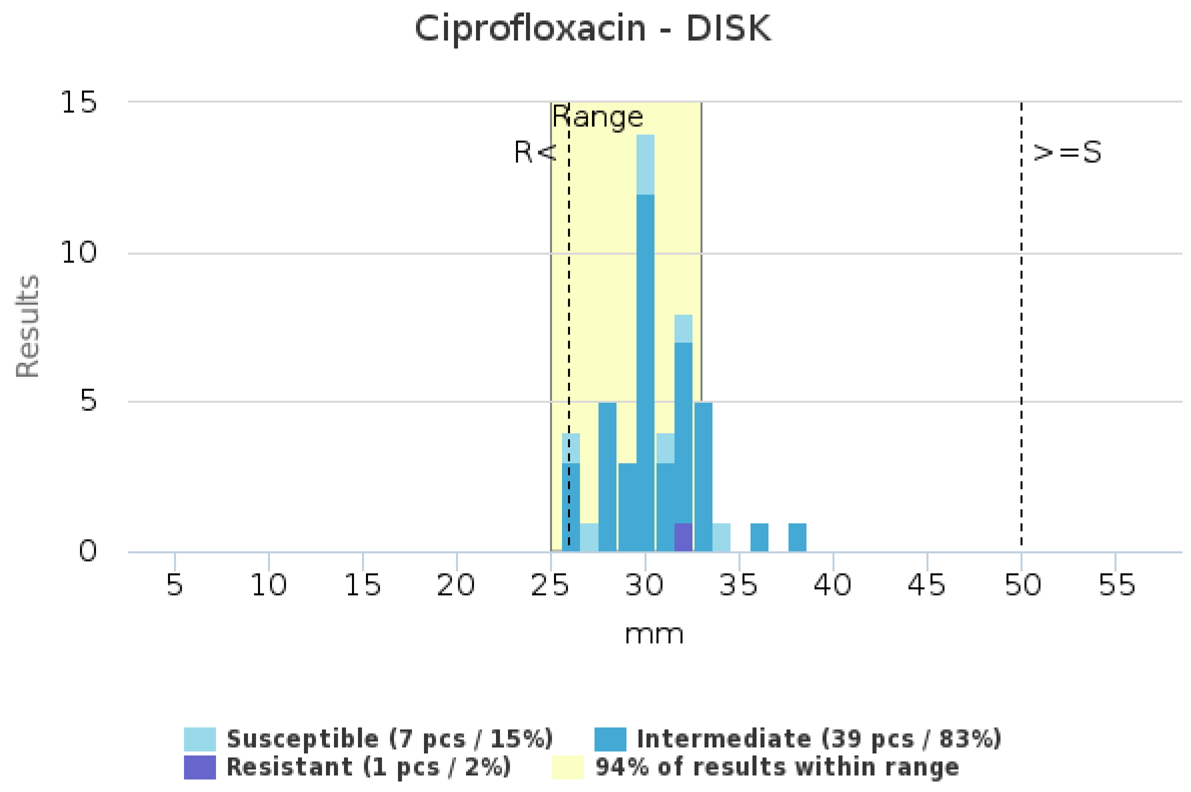


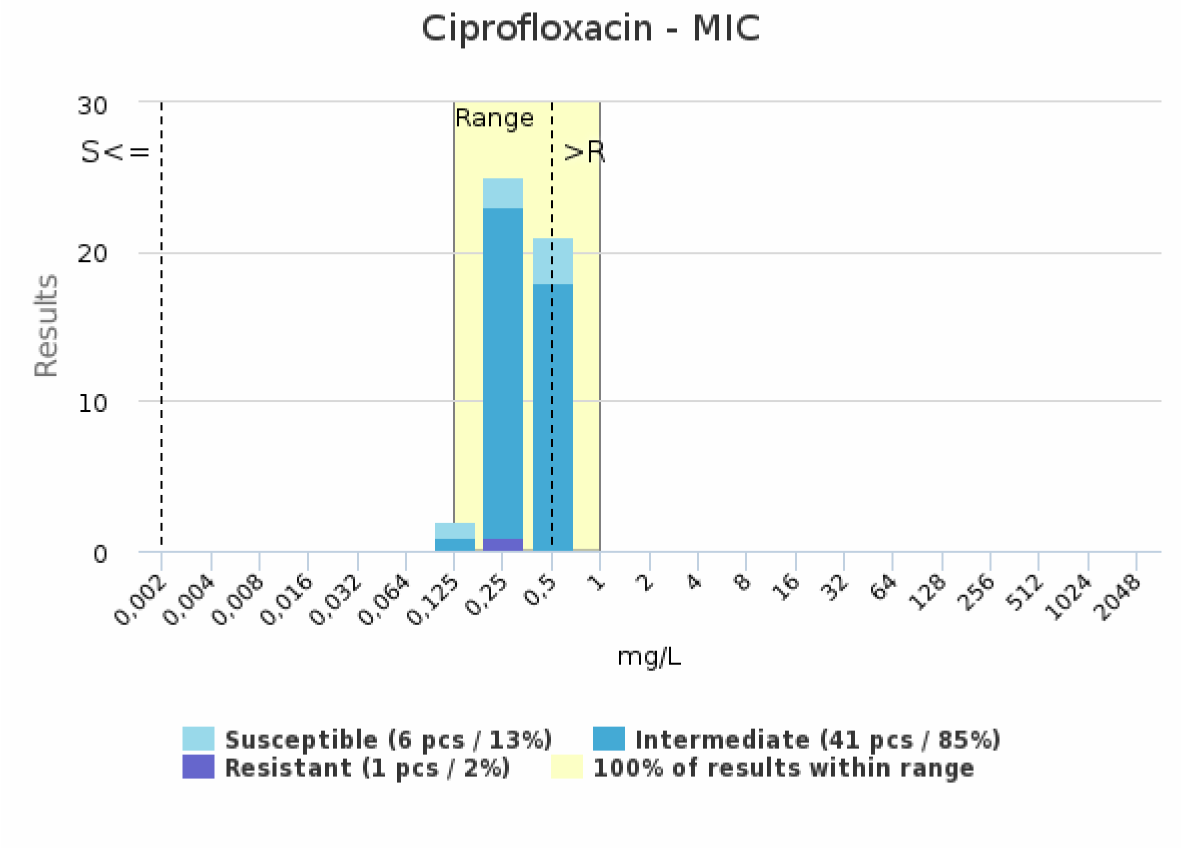
Ceftazidime-avibactam - MIC

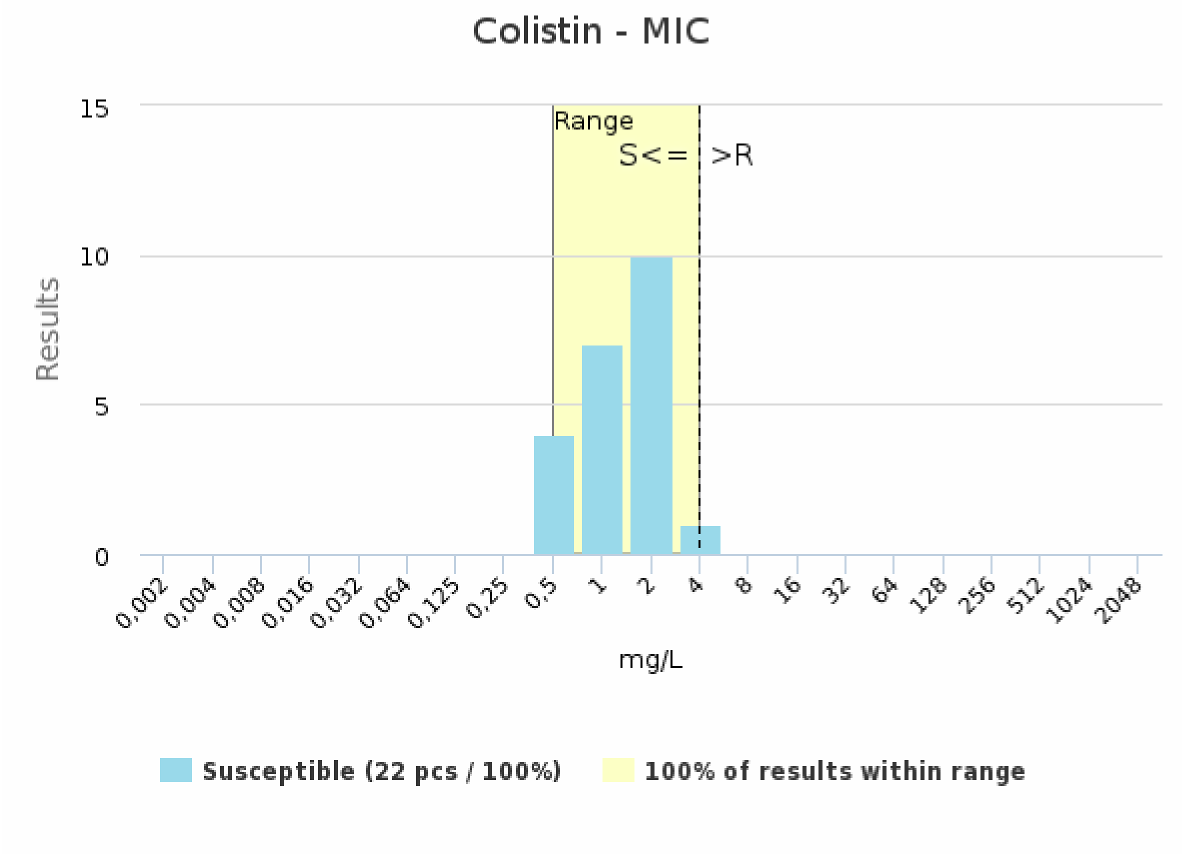


Ceftolozane-tazobactam - MIC


Chloramphenicol - DISK
Results
0
2
4
6
8
5 10 15 20 25 30 35 40 45 50 55
mm
Resistant (7 pcs / 100%)

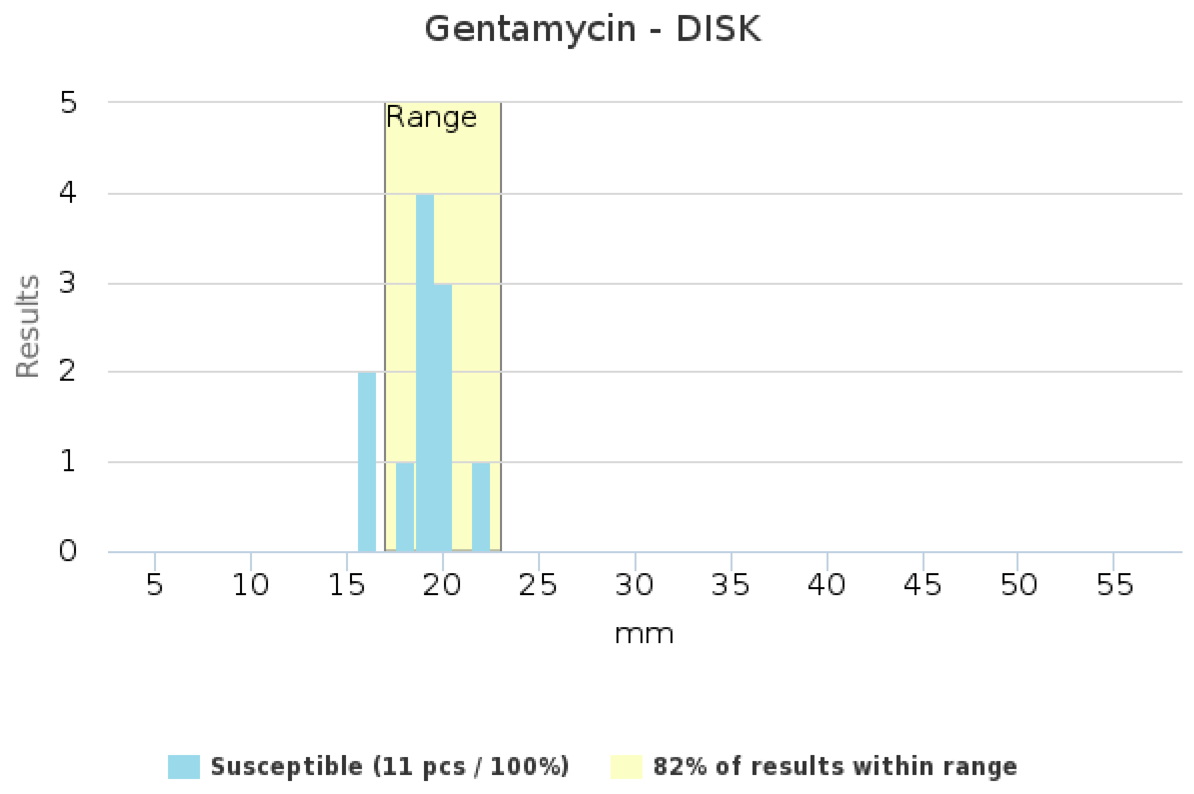

Ciprofloxacin - DISK
Results
0
5
10
15
Range
R<
>=S
5 10 15 20 25 30 35 40 45 50 55
mm
Susceptible (7 pcs / 15%)
Intermediate (39 pcs / 83%)
Resistant (1 pcs / 2%)
94% of results within range

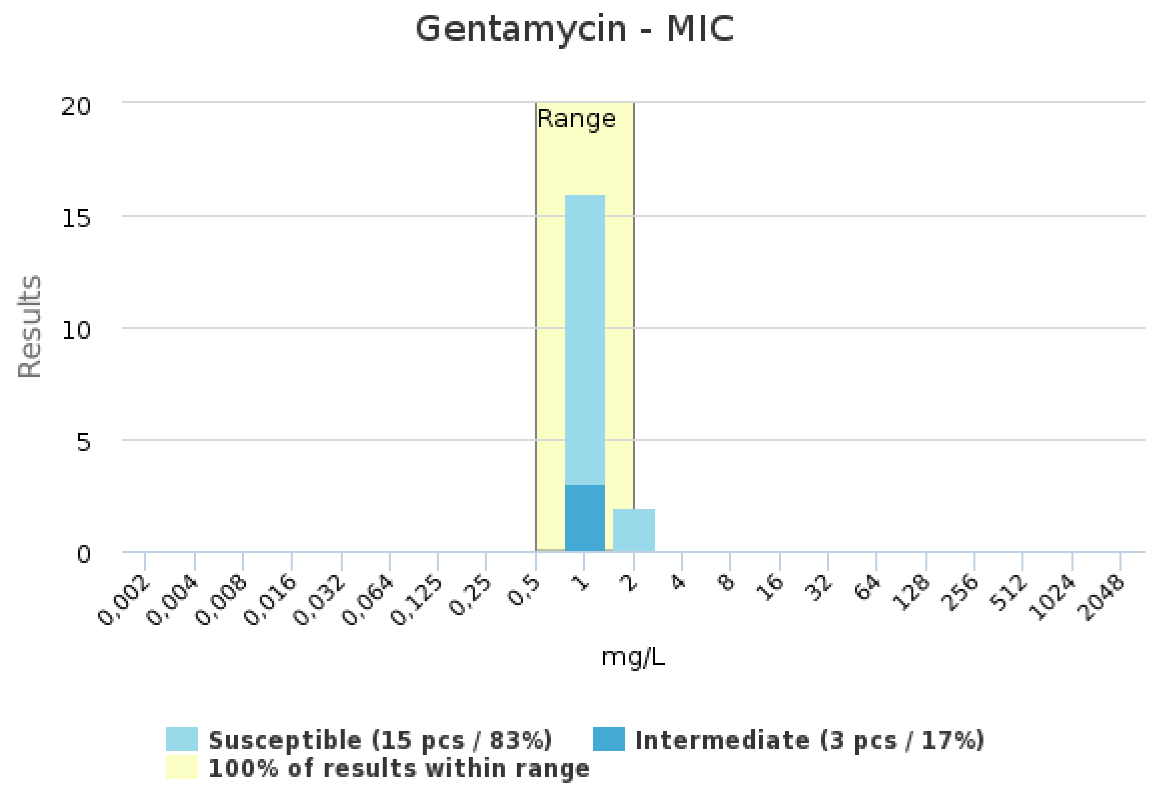

Ciprofloxacin - MIC
Results
0
10
20
30
Range
S<=
>R
0,002 0,004 0,008 0,016 0,032 0,064 0,125 0,25 0,5 1 2 4 8 16 32 64 128 256 512 1024 2048
mg/L
Susceptible (6 pcs / 13%)
Intermediate (41 pcs / 85%)
Resistant (1 pcs / 2%)
100% of results within range

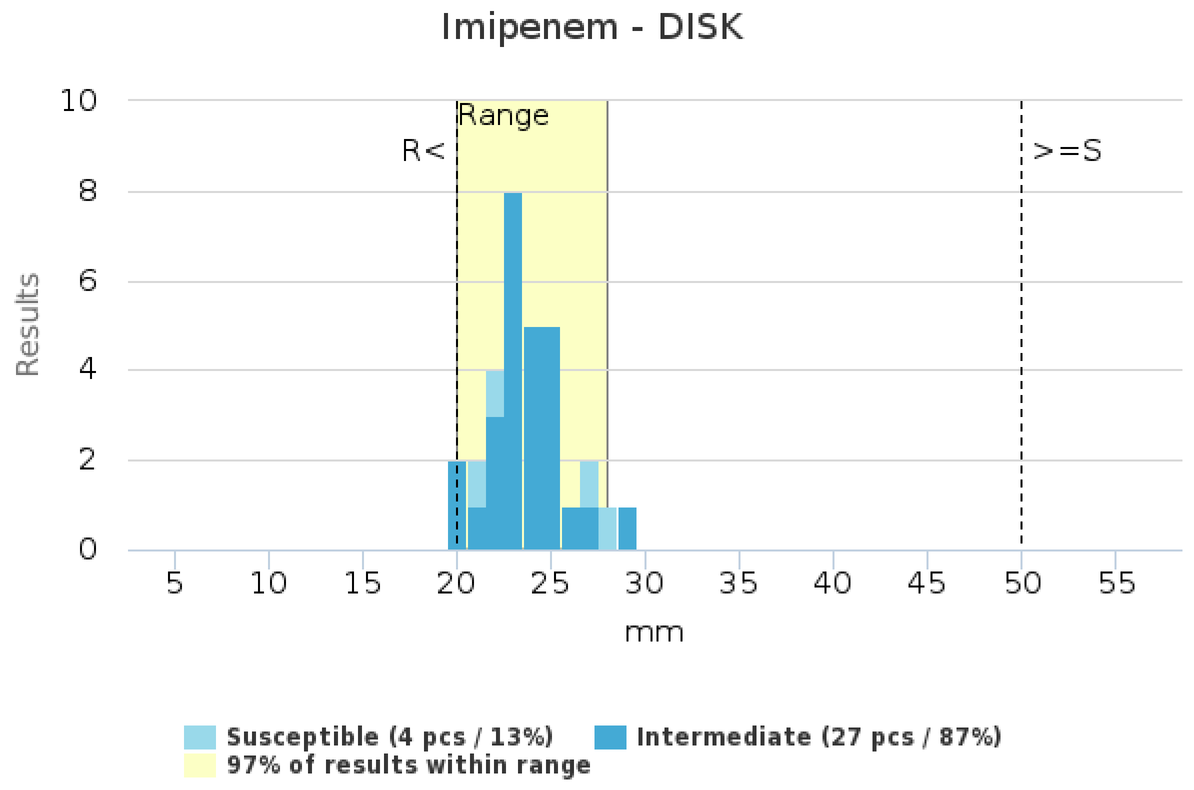

Colistin - MIC
Results
0
5
10
15
Range
S<=
>R
0,002 0,004 0,008 0,016 0,032 0,064 0,125 0,25 0,5 1 2 4 8 16 32 64 128 256 512 1024 2048
mg/L
Susceptible (22 pcs / 100%)
100% of results within range

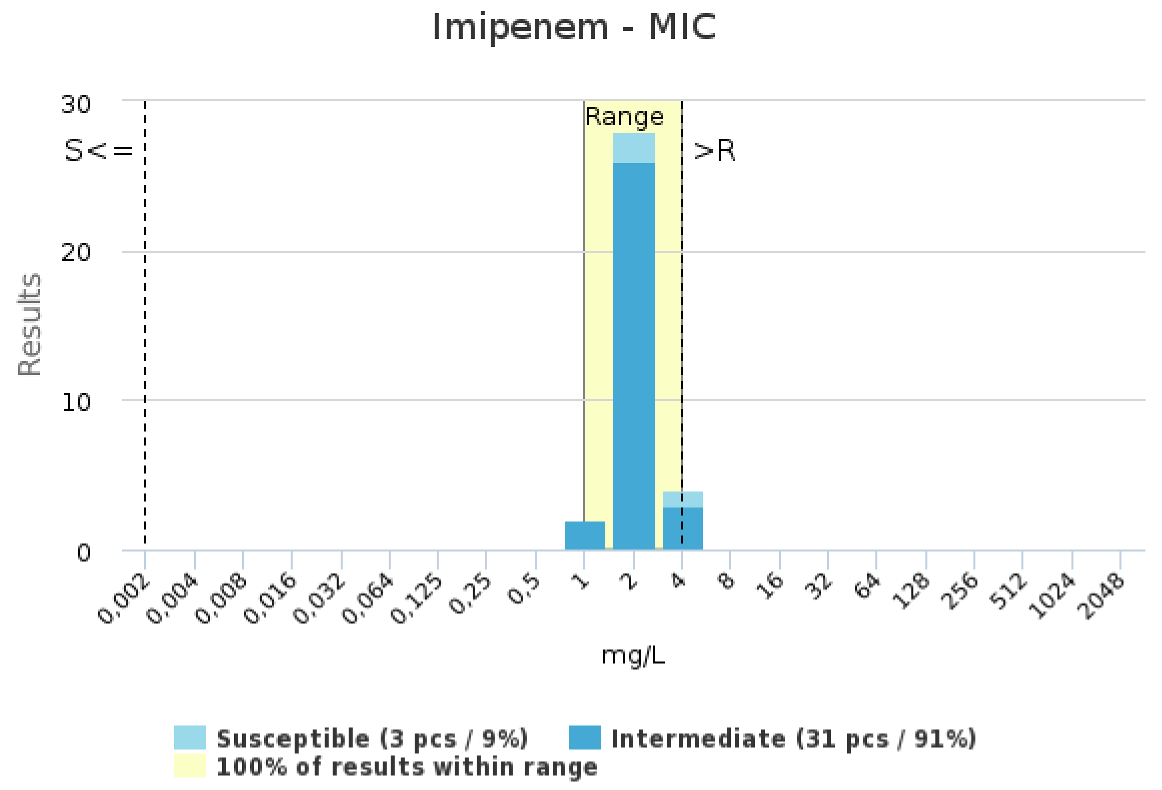
General Bacteriology, March, 1-2023

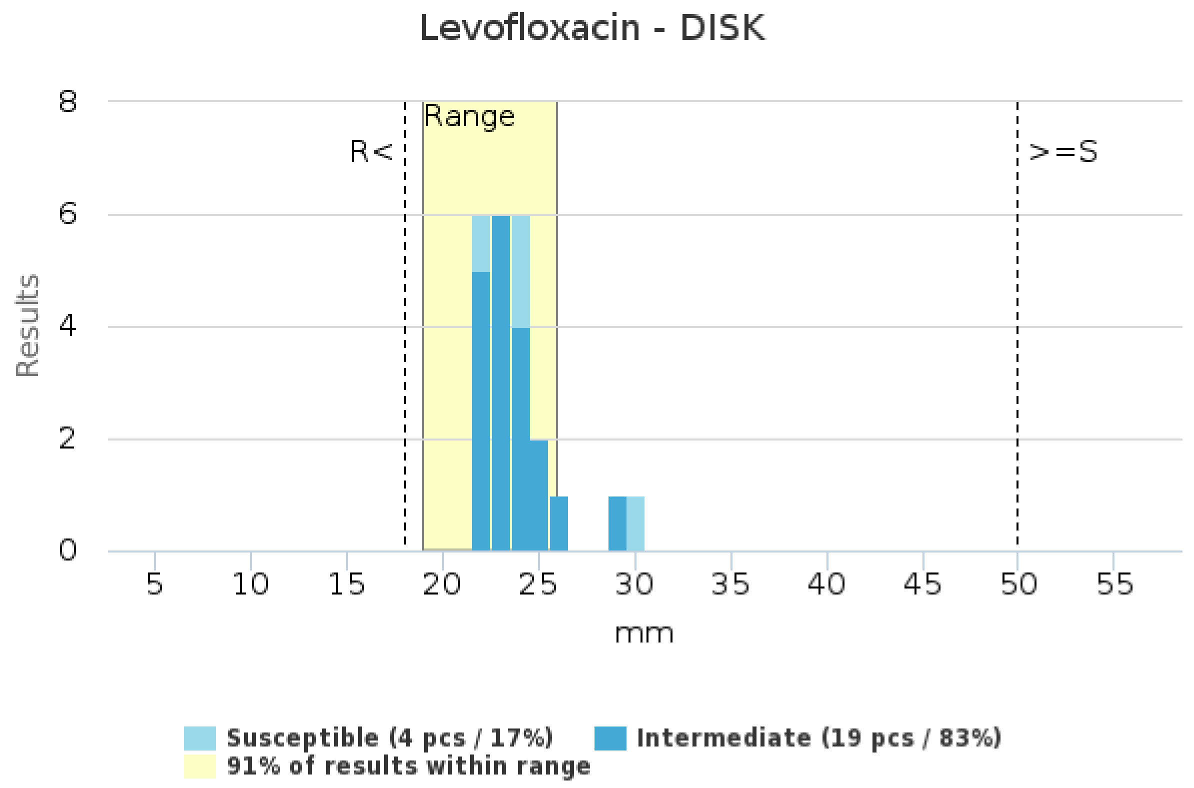
Antimicrobial susceptibility testing results

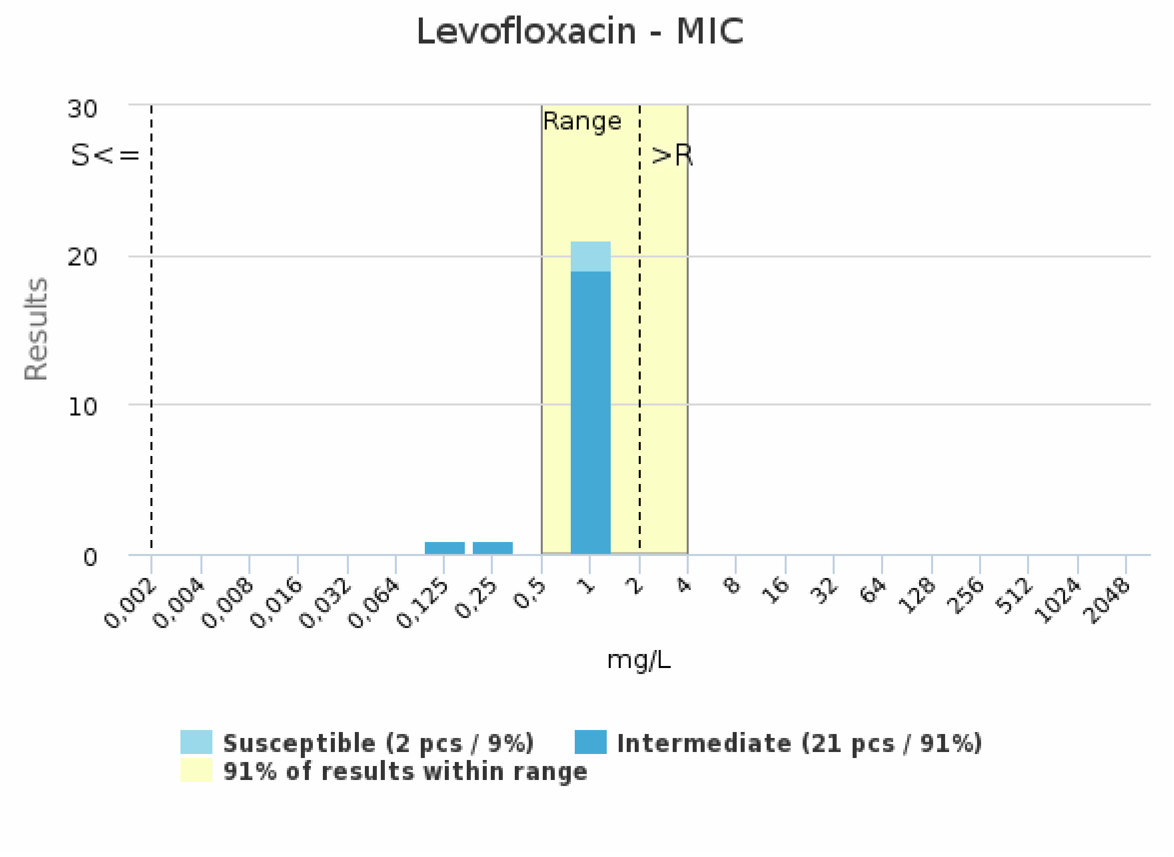






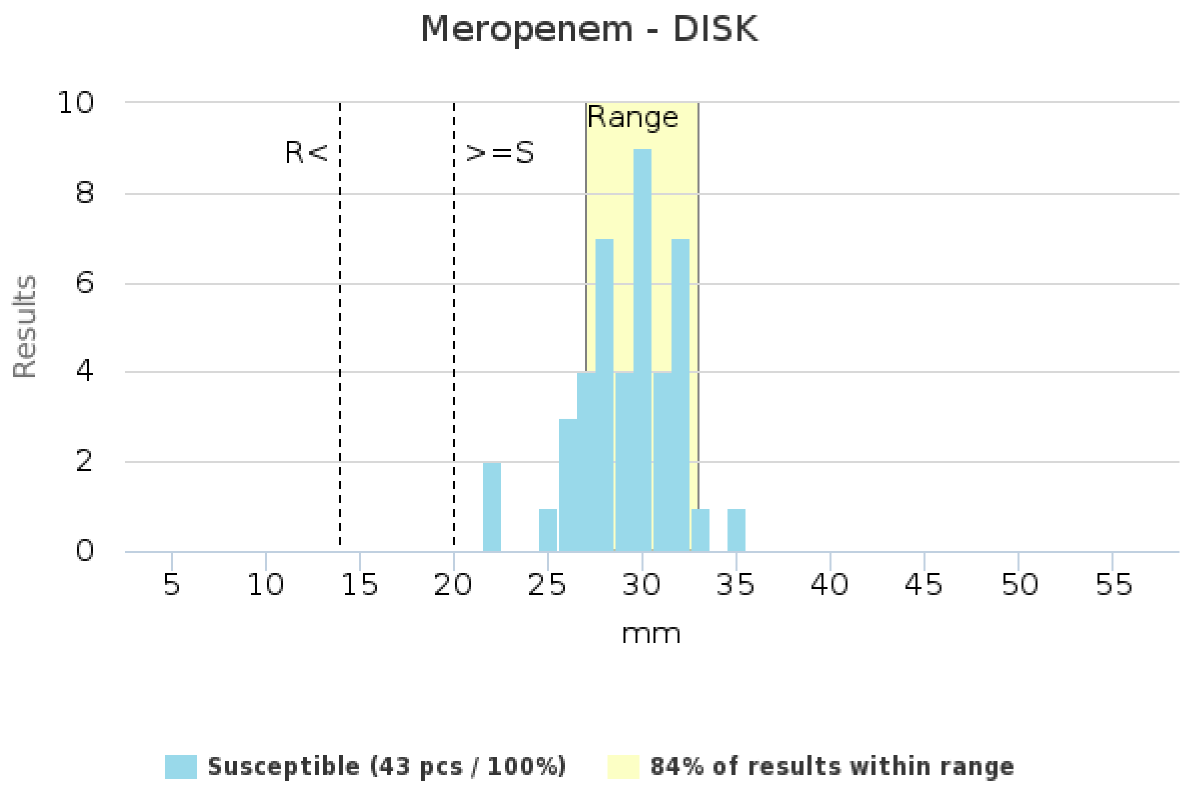


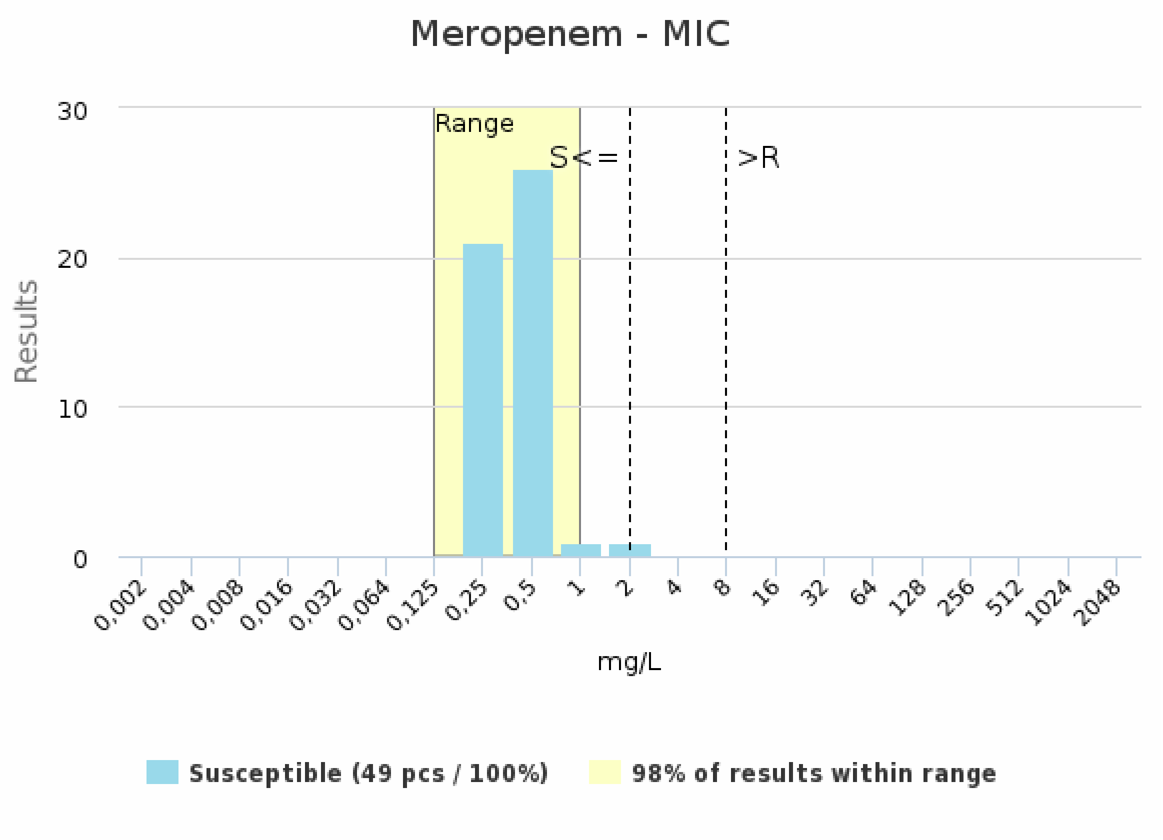


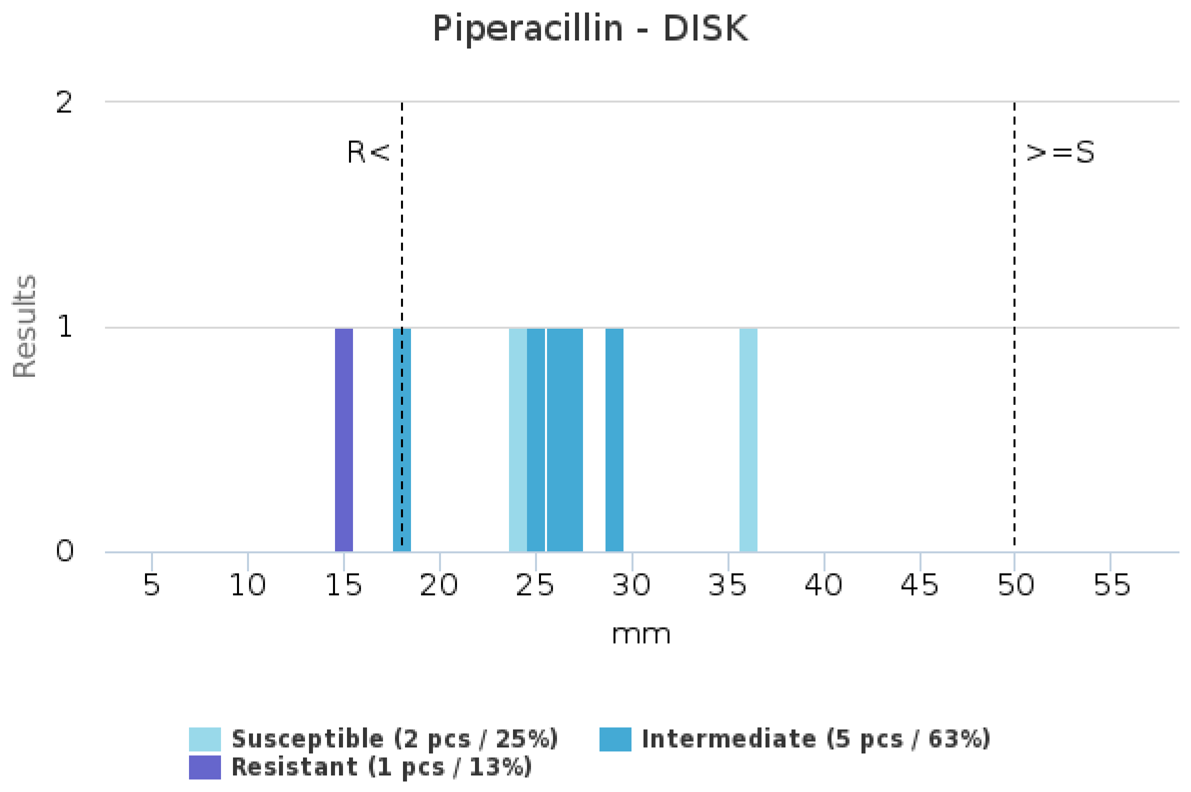


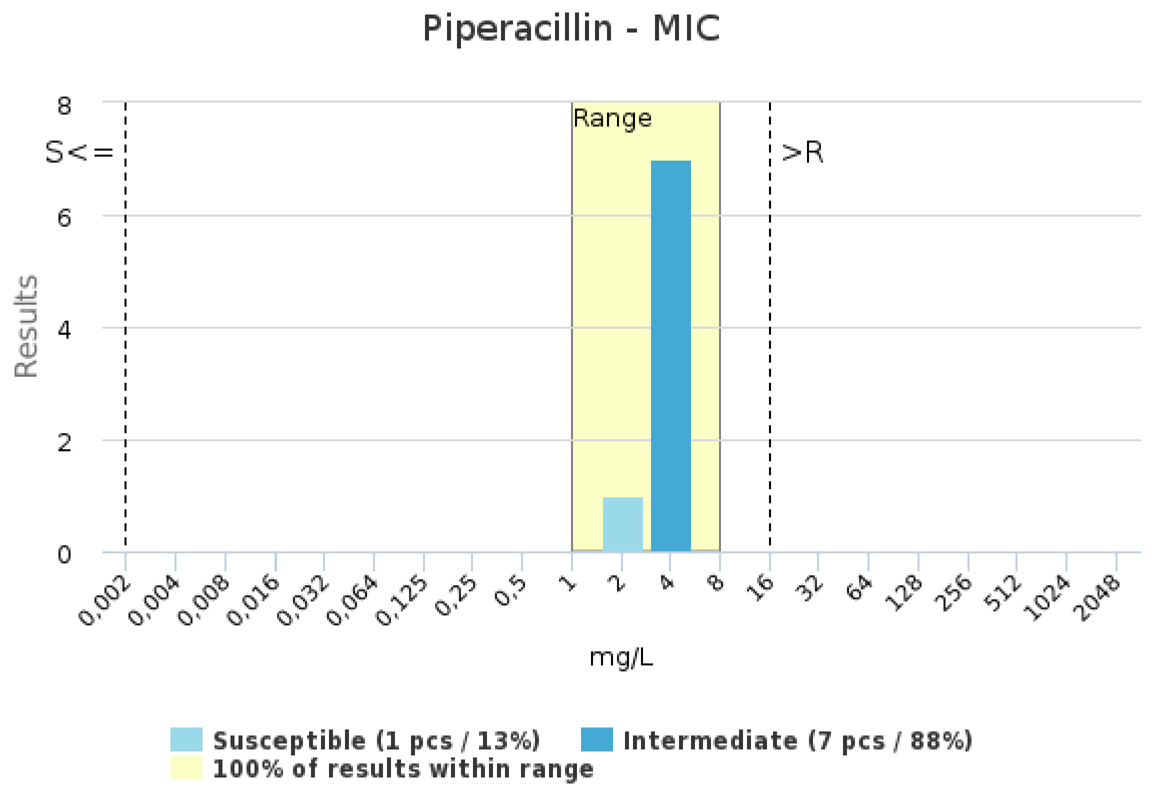
General Bacteriology, March, 1-2023

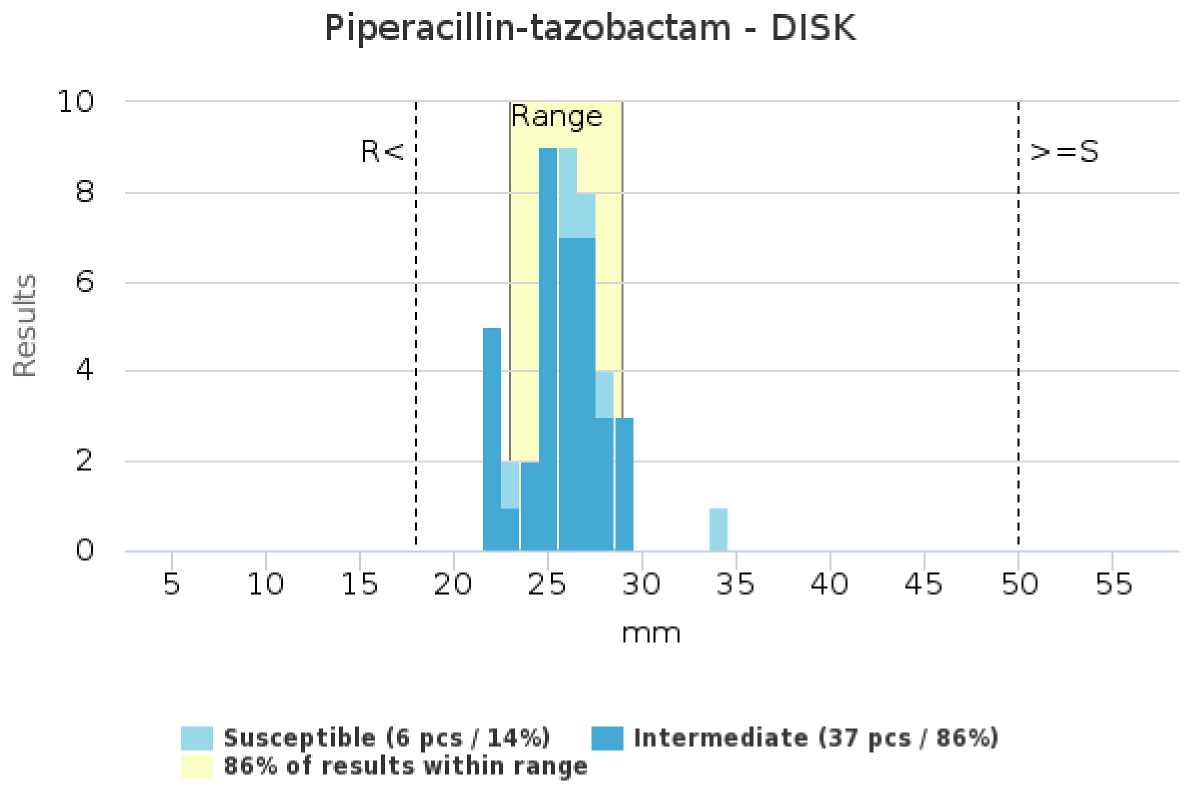
Antimicrobial susceptibility testing results

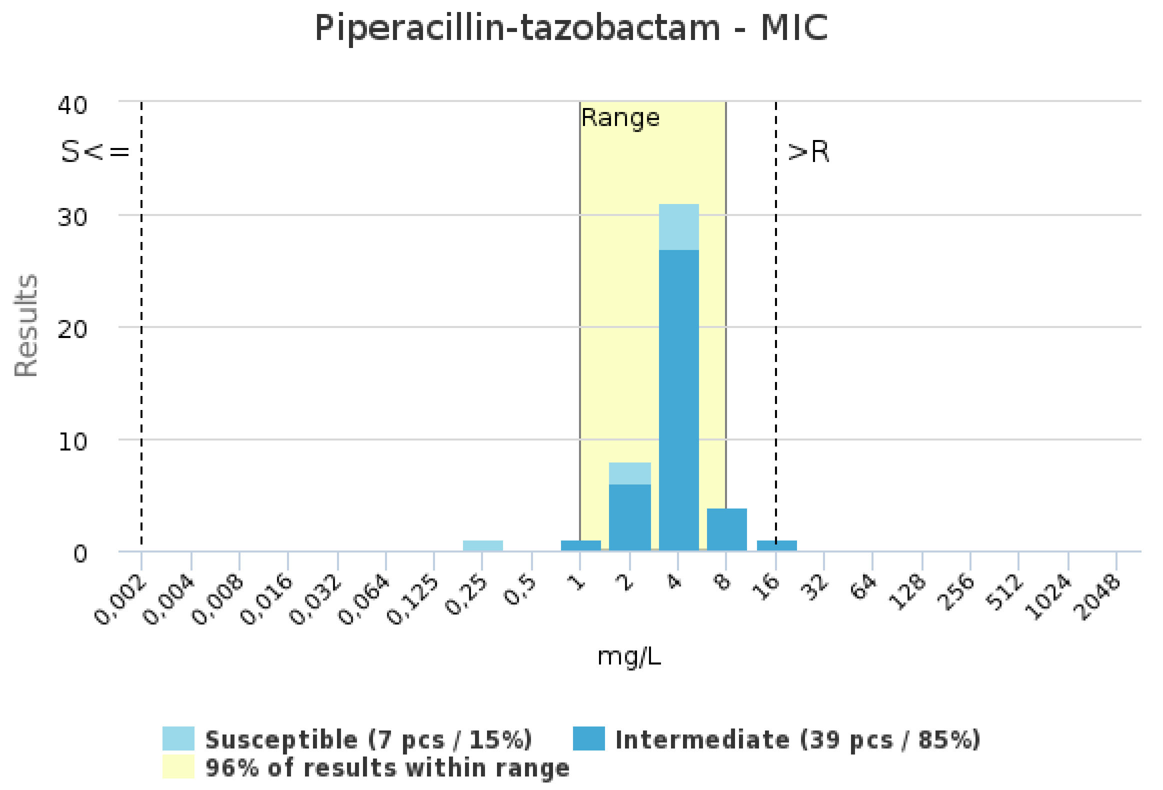

Meropenem - DISK

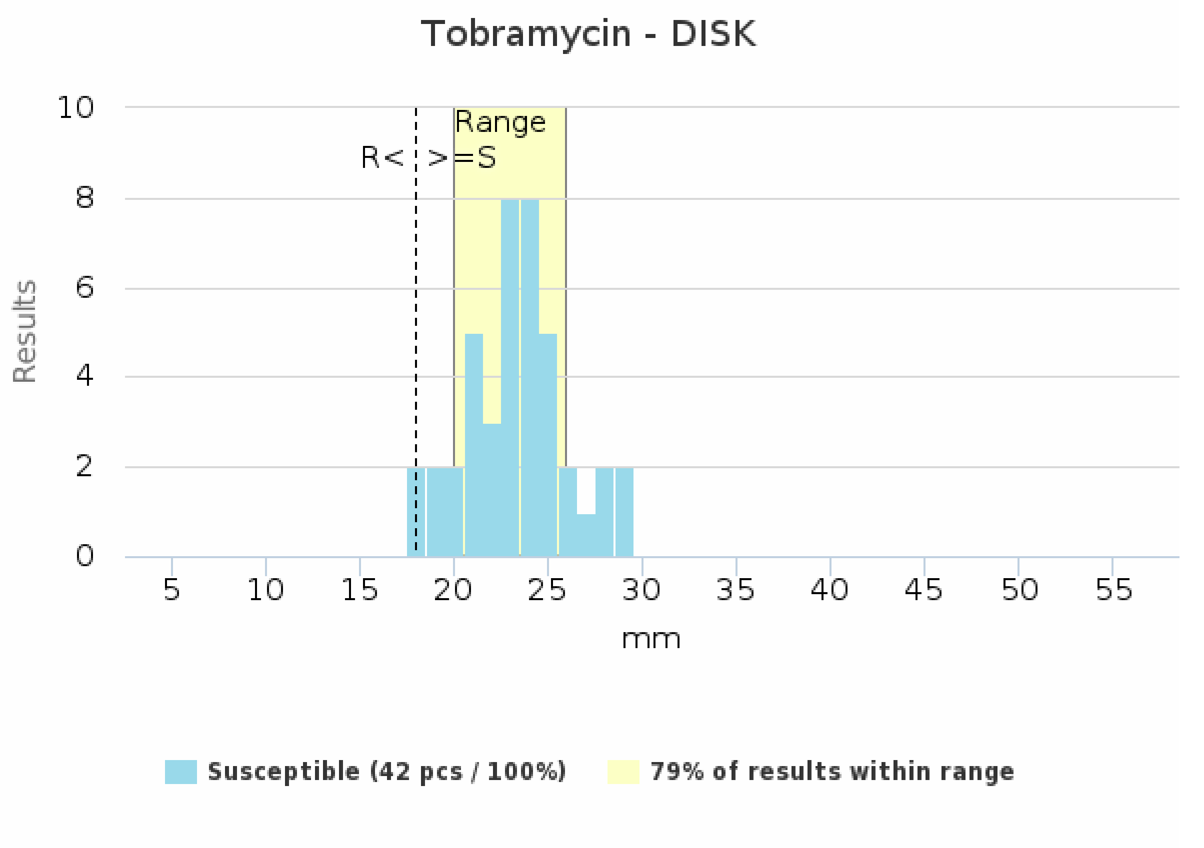

Meropenem - MIC

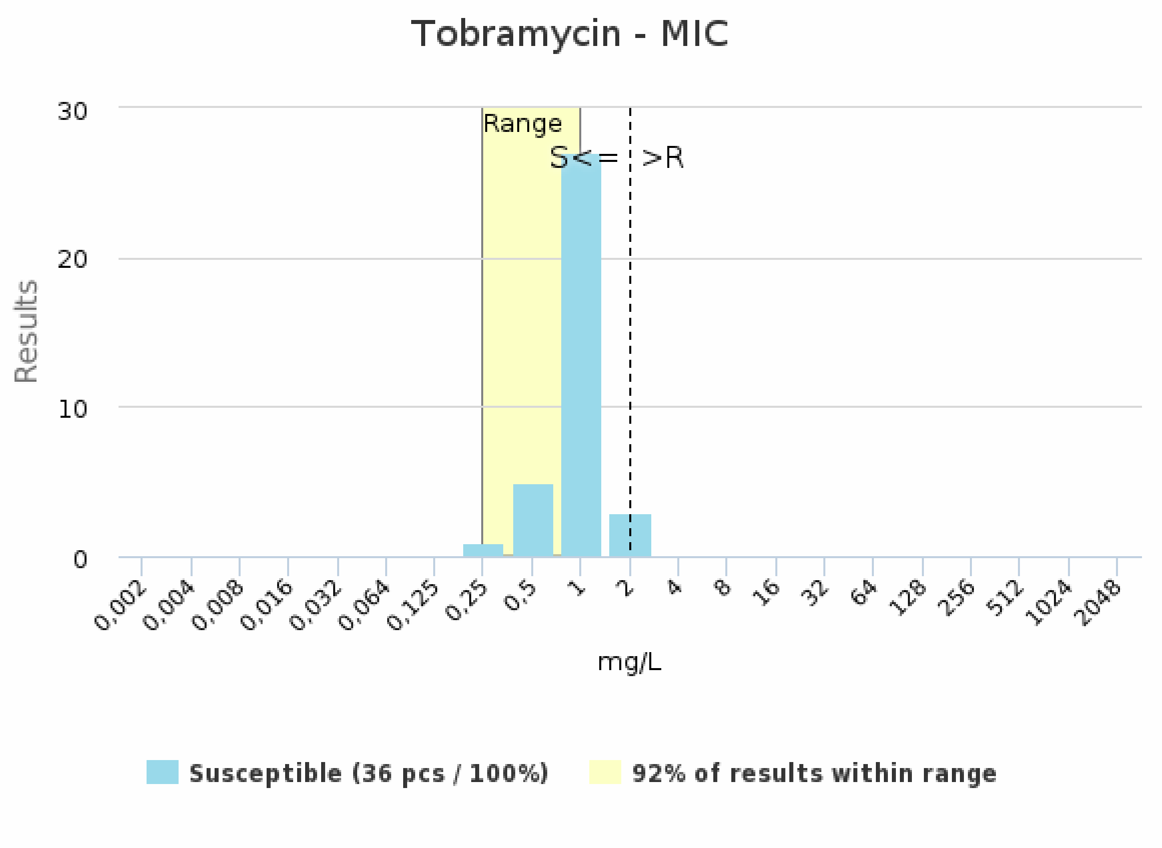

Piperacillin - DISK


Piperacillin - MIC


Piperacillin-tazobactam - DISK


Piperacillin-tazobactam - MIC


Tobramycin - DISK
Results
10
8
6
4
2
0
Range
R<
>=S
5
10
15
20
25
30
35
40
45
50
55
mm
Susceptible (42 pcs / 100%)
79% of results within range


Tobramycin - MIC
Results
30
20
10
0
Range
S<=
>R
0,002
0,004
0,008
0,016
0,032
0,064
0,125
0,25
0,5
1
2
4
8
16
32
64
128
256
512
1024
2048
mg/L
Susceptible (36 pcs / 100%)
92% of results within range

Sample 001 | Additional questions

Report info

Participants

Altogether 94 laboratories from 22 countries participated in this EQA round.

Report info

The antimicrobial susceptibility testing results are shown in laboratory specific summary tables and histograms. Histograms are drawn for each antimicrobial agent if the laboratory's result is included in a group of at least three results. By “group” is meant results which are obtained and interpreted according to the same standard (EUCAST, CLSI or CA-SFM).
Laboratory's own results are indicated with a black radio button in the table and an orange dot in the histograms. Average (x) is used as a reference value for disk results and mode (Mo) is used for MIC results. According to the experts' assessment some antimicrobials may be excluded from the final summary tables, e.g., antimicrobial agents to which the microbe is intrinsically resistant or to which only one result has been reported.
If you have not reported antimicrobial susceptibility testing results, or, your results have been excluded, you will get a note: “You have not reported antimicrobial susceptibility results, only global report is available.”
For information on report interpretation and performance evaluation, please see the "EQAS Interpretation guidelines" in LabScala User instructions. In case you have any questions regarding the reports, please contact the EQA Coordinator.

General Bacteriology, March, 1-2023

Report to the clinician

GLOBAL REPORT

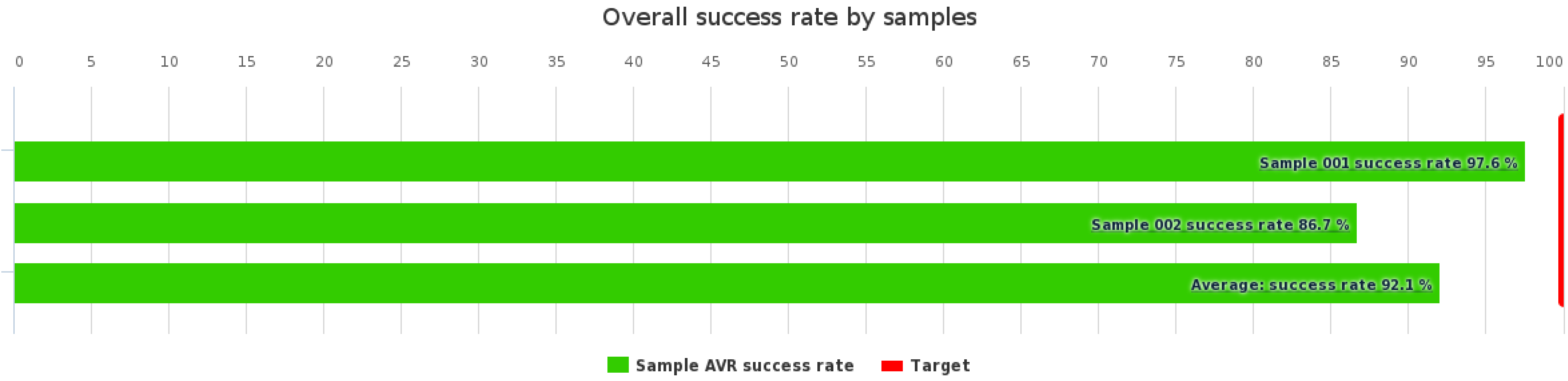
	No of participants	No of responded participants	Response percentage
General Bacteriology 1 (aerobes and anaerobes), March, 1-2023	59	58	98.3 %
General Bacteriology 2 (aerobes), March, 1-2023	35	33	94.3 %

Summary

General Bacteriology 1 (aerobes and anaerobes) (5080)

Summary	AVR success rate
Sample 001	99.3 %
Sample 002	97.9 %
Sample 003	90.7 %
Sample 004	86.7 %
Average:	93.6 %

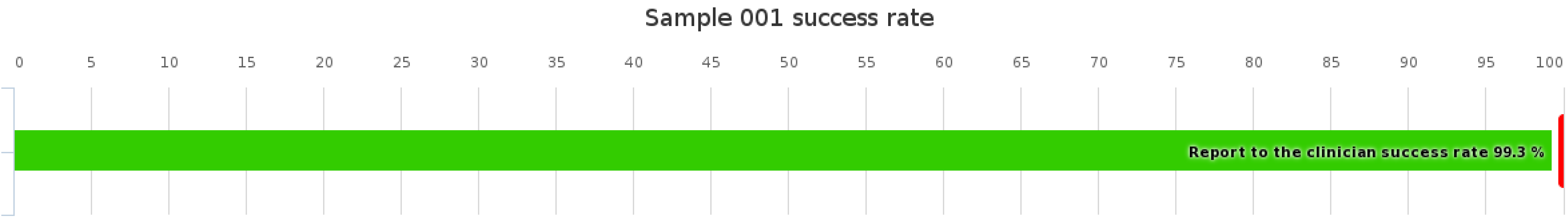
General Bacteriology 2 (aerobes) (5081)



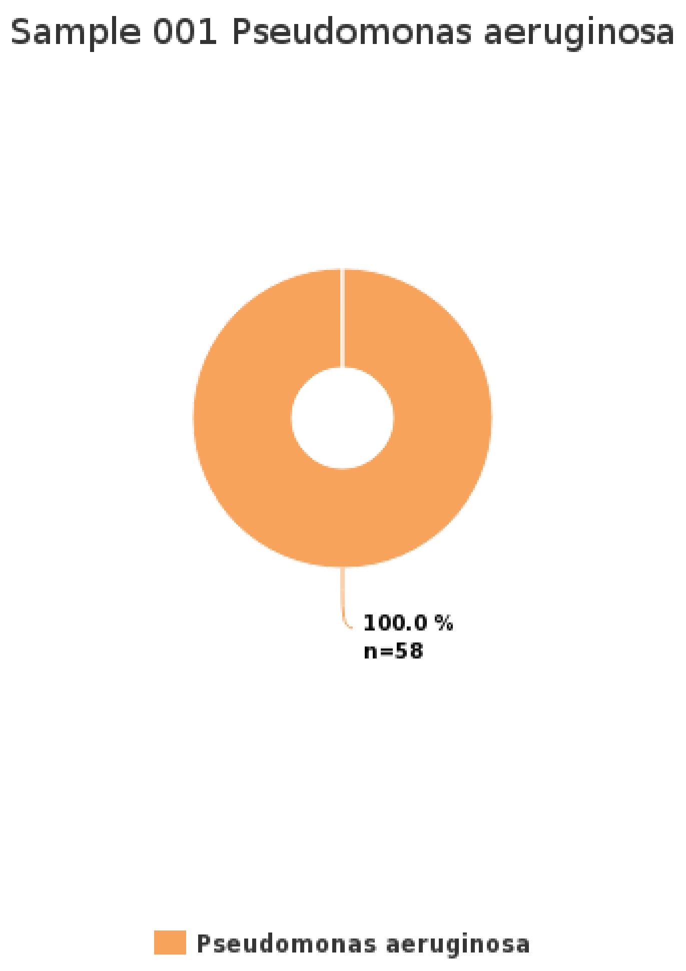
Summary	AVR success rate
Sample 001	97.6 %
Sample 002	86.7 %
Average:	92.1 %

Sample 001 | Pseudomonas aeruginosa

General Bacteriology 1 (aerobes and anaerobes) (5080)



Sample 001 results	Responded	AVR success rate	Count
	Report to the clinician	99.3 %	58
Total:		99.3 %	58



REPORT TO THE CLINICIAN

Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Pseudomonas aeruginosa		**58**						**99.3 %**
	Pseudomonas aeruginosa	58	56	1	1	2	56	
Total:		58						99.3 %

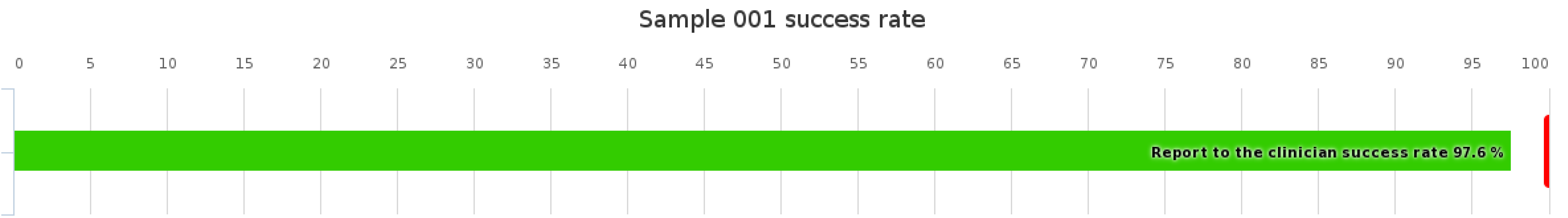
SCORING SUMMARY

Finding group	Finding	Finding score	Significant pathogen	Max score
Pseudomonas aeruginosa				**5**
	Pseudomonas aeruginosa	4	1	5
Total:				5

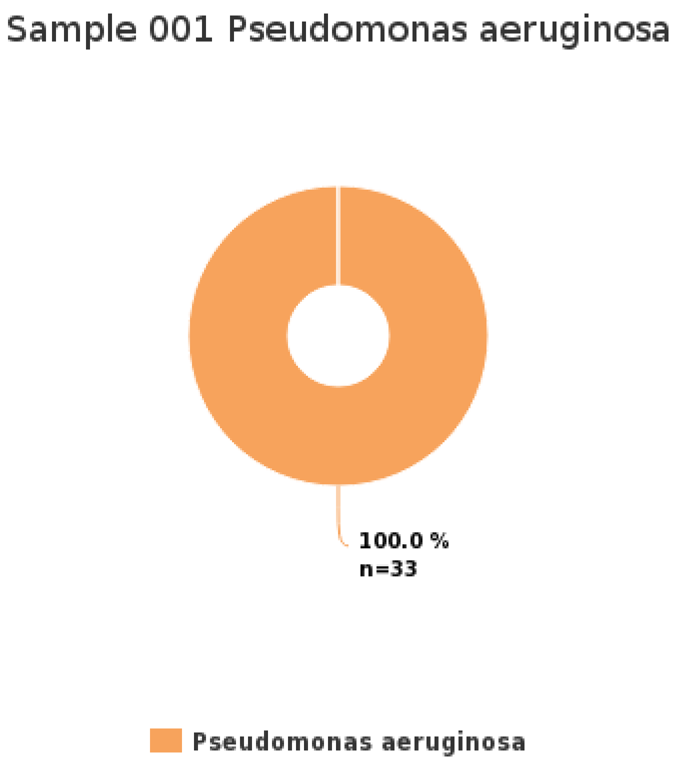
General Bacteriology 2 (aerobes) (5081)

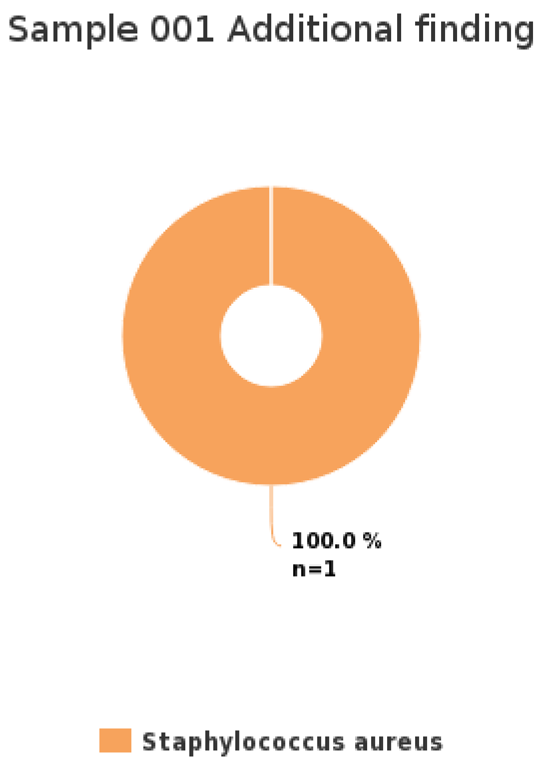
General Bacteriology, March, 1-2023

Report to the clinician



Sample 001 results	Responded	AVR success rate	Count
	Report to the clinician	97.6 %	34
Total:		97.6 %	34





REPORT TO THE CLINICIAN

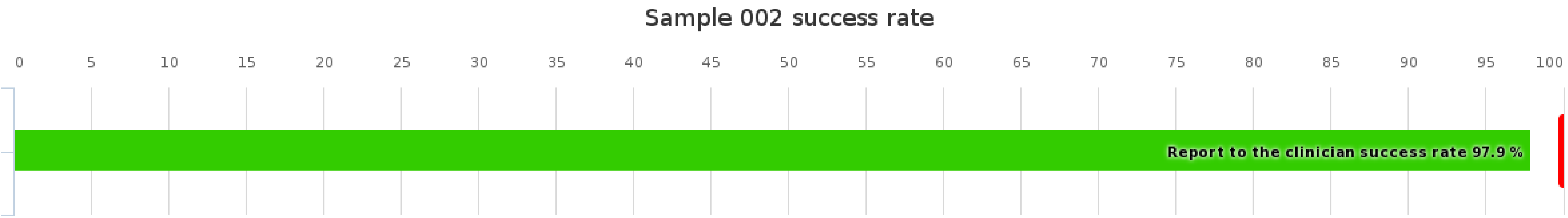
Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Referred	Not referred	AVR success rate
Pseudomonas aeruginosa		**33**					**97.6 %**
	Pseudomonas aeruginosa	33	29	4	1	32	
Additional finding		**1**					**-**
	Staphylococcus aureus	1	1			1	
Total:		34					97.6 %

SCORING SUMMARY

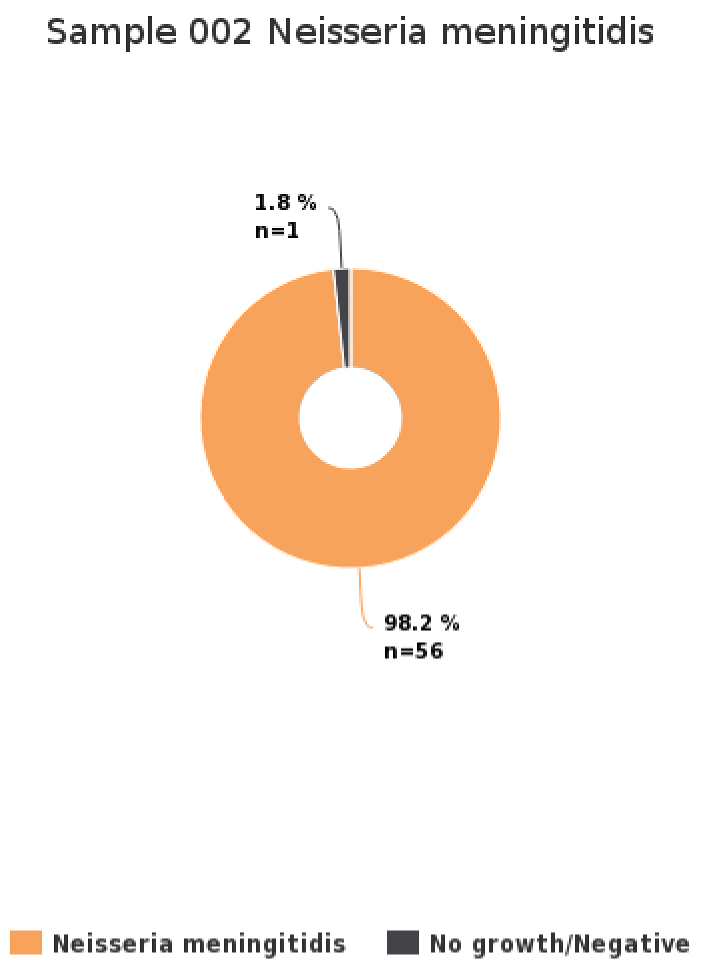
Finding group	Finding	Finding score	Significant pathogen	Max score
Pseudomonas aeruginosa				**5**
	Pseudomonas aeruginosa	4	1	5
Additional finding				**-**
	Staphylococcus aureus	-		-
Total:				5

Sample 002 | Neisseria meningitidis

General Bacteriology 1 (aerobes and anaerobes) (5080)



Sample 002 results	Responded	AVR success rate	Count
	Report to the clinician	97.9 %	57
Total:		97.9 %	57



REPORT TO THE CLINICIAN

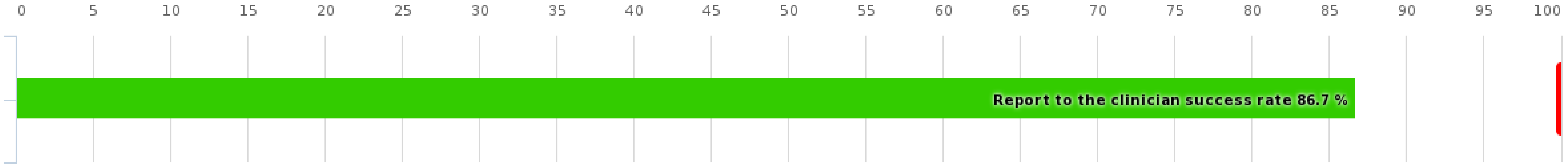
Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Neisseria meningitidis		**57**						**97.9 %**
	Neisseria meningitidis	56	55	1		38	18	
	No growth/Negative	1			1		1	
Total:		57						97.9 %

SCORING SUMMARY

Finding group	Finding	Finding score	Significant pathogen	Max score
Neisseria meningitidis				**5**
	Neisseria meningitidis	4	1	5
	No growth/Negative	0		5
Total:				5

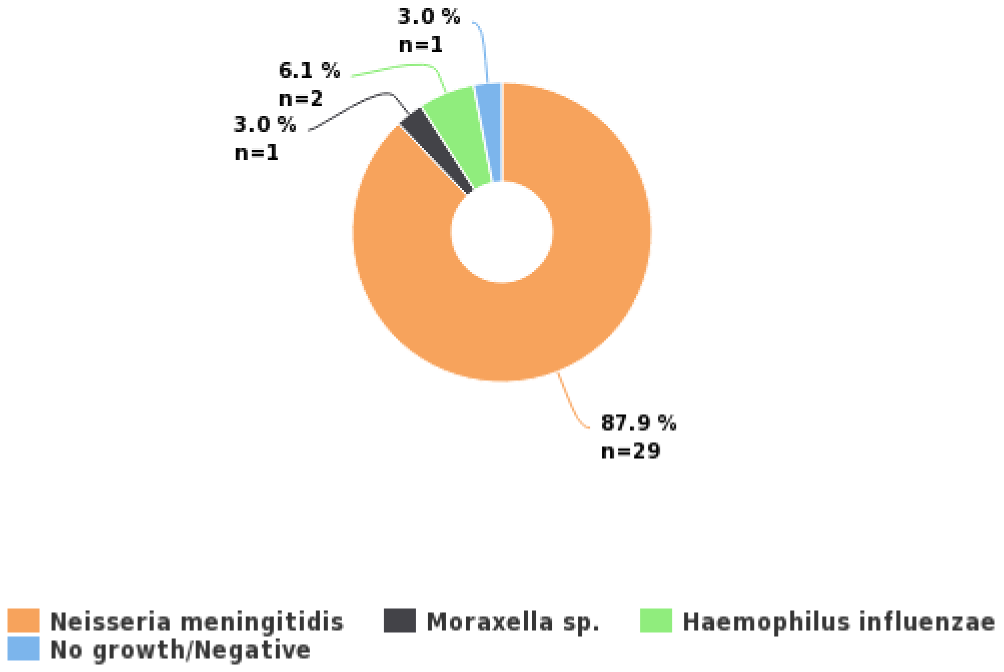
General Bacteriology 2 (aerobes) (5081)

Sample 002 success rate



Sample 002 results	Responded	AVR success rate	Count
	Report to the clinician	86.7 %	33
Total:		86.7 %	33

Sample 002 Neisseria meningitidis



REPORT TO THE CLINICIAN

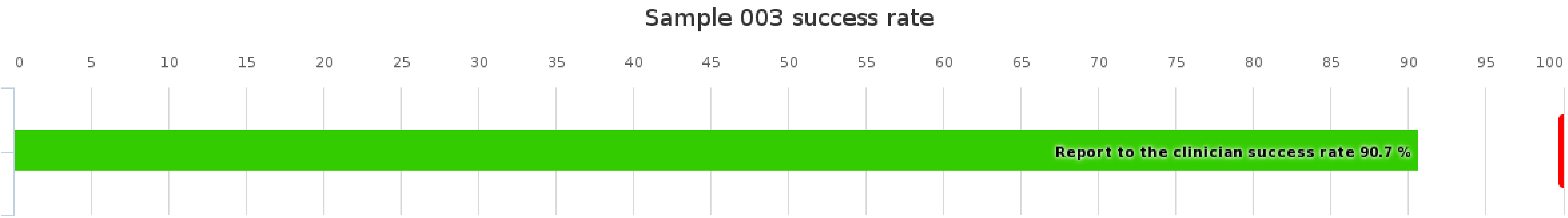
Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Neisseria meningitidis		**33**						**86.7 %**
	Neisseria meningitidis	29	27	2		13	16	
	Moraxella sp.	1	1				1	
	Haemophilus influenzae	2	1	1			2	
	No growth/Negative	1			1		1	
Total:		33						86.7 %

SCORING SUMMARY

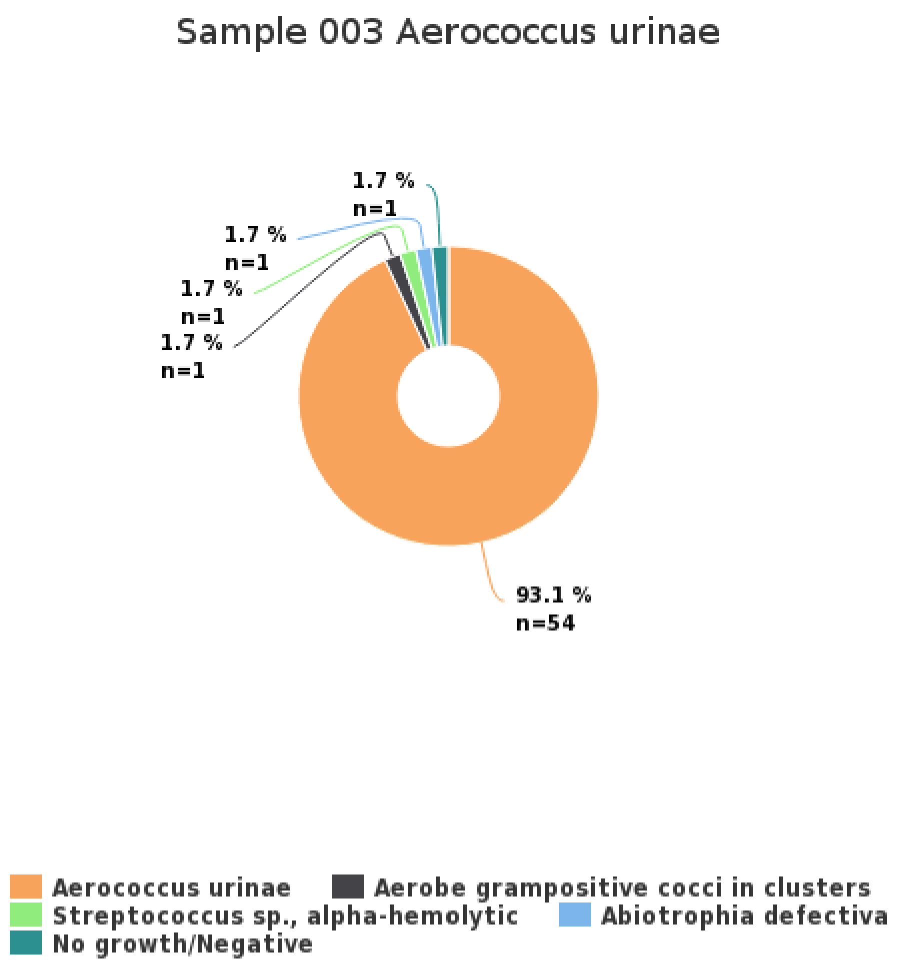
Finding group	Finding	Finding score	Significant pathogen	Max score
Neisseria meningitidis				**5**
	Neisseria meningitidis	4	1	5
	Moraxella sp.	0		5
	Haemophilus influenzae	0		5
	No growth/Negative	0		5
Total:				5

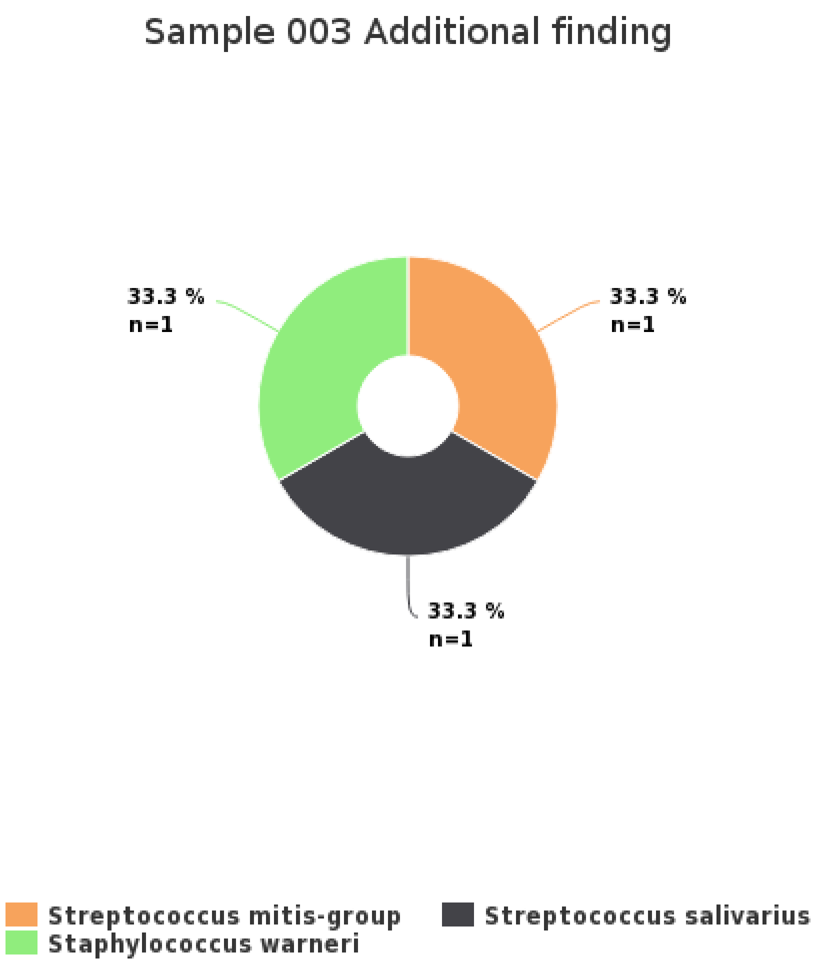
Sample 003 | Aerococcus urinae

General Bacteriology 1 (aerobes and anaerobes) (5080)



Sample 003 results	Responded	AVR success rate	Count
	Report to the clinician	90.7 %	61
Total:		90.7 %	61





REPORT TO THE CLINICIAN

Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Aerococcus urinae		**58**						**90.7 %**
	Aerococcus urinae	54	45	9		3	51	
	Aerobe grampositive cocci in clusters	1	1			1		
	Streptococcus sp., alpha-hemolytic	1	1				1	
	Abiotrophia defectiva	1						
	No growth/Negative	1			1		1	
Additional finding		**3**						**-**
	Streptococcus mitis-group	1			1		1	
	Streptococcus salivarius	1		1			1	
	Staphylococcus warneri	1	1				1	
Total:		61						90.7 %

SCORING SUMMARY

Finding group	Finding	Finding score	Significant pathogen	Referred	Max score
Aerococcus urinae					**5**
	Aerococcus urinae	4	1		5
	Aerobe grampositive cocci in clusters	1		1	5

	Streptococcus sp., alpha-hemolytic	0			5
	Abiotrophia defectiva	0			5
	No growth/Negative	0			5
Additional finding					**-**
	Streptococcus mitis-group	-			-
	Streptococcus salivarius	-			-
	Staphylococcus warneri	-			-
Total:					5

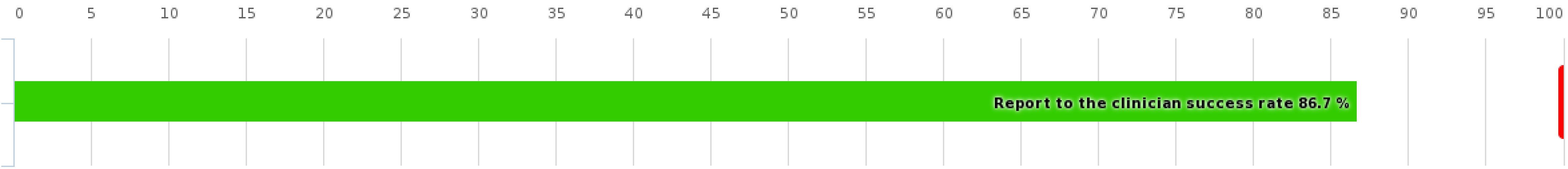
General Bacteriology, March, 1-2023

Report to the clinician

Sample 004 | Streptococcus constellatus, Fusobacterium necrophorum

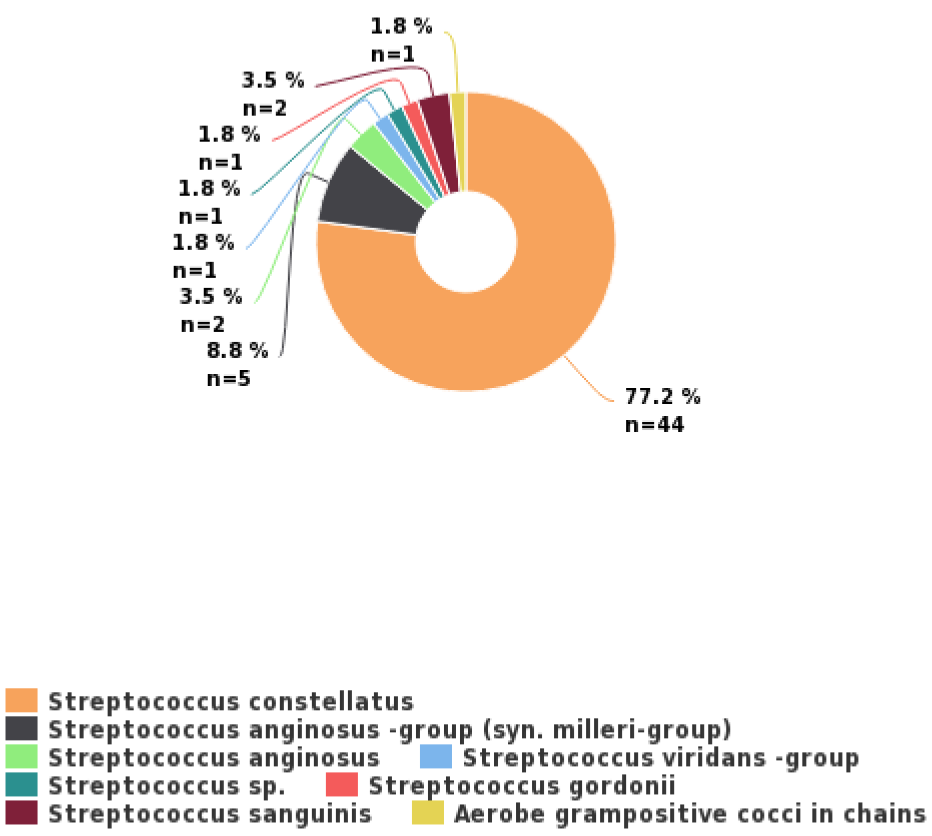
General Bacteriology 1 (aerobes and anaerobes) (5080)

Sample 004 success rate

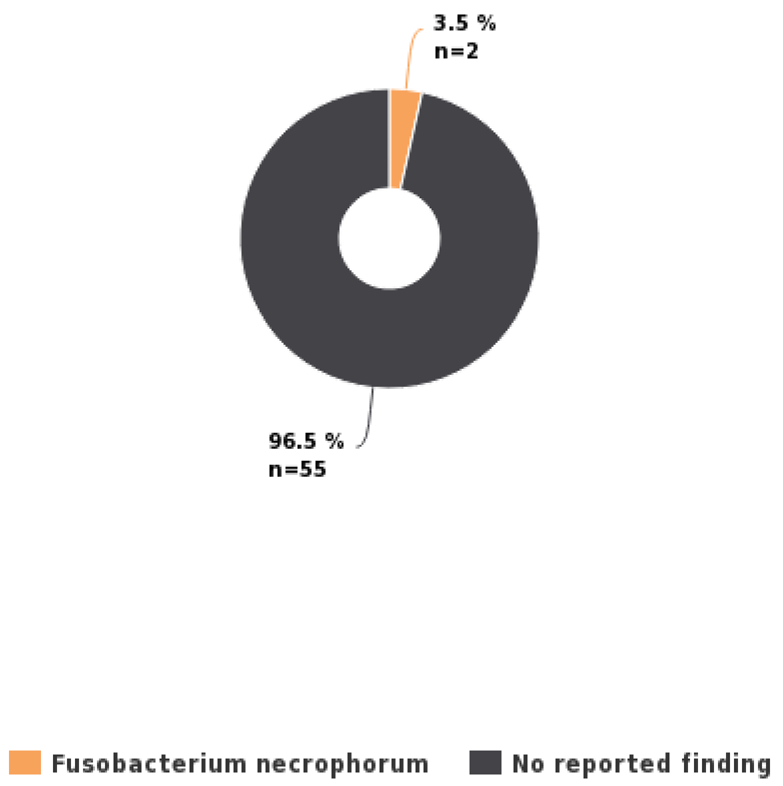


Sample 004 results	Responded	AVR success rate	Count
	Report to the clinician	86.7 %	115
Total:		86.7 %	115

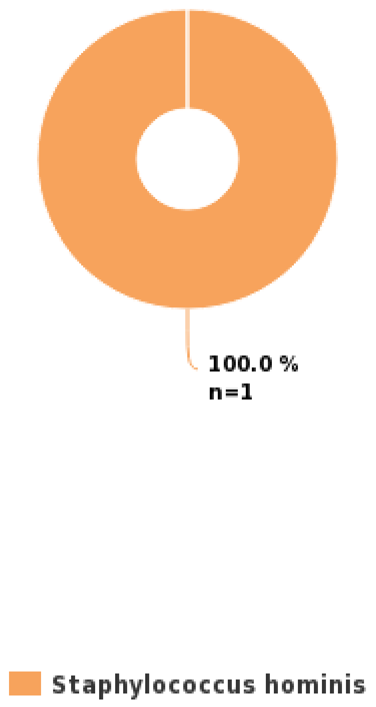
Sample 004 Streptococcus constellatus



Sample 004 Fusobacterium necrophorum



Sample 004 Additional finding



REPORT TO THE CLINICIAN

General Bacteriology, March, 1-2023

Report to the clinician

Finding group	Finding	Finding count	Significant pathogen	Possible pathogen	Non-significant finding	Referred	Not referred	AVR success rate
Streptococcus constellatus		**57**						**86.7 %**
	Streptococcus constellatus	44	28	11	5		44	
	Streptococcus anginosus -group (syn. milleri-group)	5	5				5	
	Streptococcus anginosus	2	1	1		1	1	
	Streptococcus viridans -group	1	1				1	
	Streptococcus sp.	1		1			1	
	Streptococcus gordonii	1		1			1	
	Streptococcus sanguinis	2	1	1			2	
	Aerobe grampositive cocci in chains	1		1			1	
Fusobacterium necrophorum		**57**						**-**
	Fusobacterium necrophorum	2	2				2	
	No reported finding	55						
Additional finding		**1**						**-**
	Staphylococcus hominis	1			1		1	
Total:		115						86.7 %

SCORING SUMMARY

Finding group	Finding	Finding score	Significant pathogen	Possible pathogen	Max score
Streptococcus constellatus					**5**
	Streptococcus constellatus	4	1	1	5
	Streptococcus anginosus -group (syn. milleri-group)	4	1		5
	Streptococcus anginosus	2			5
	Streptococcus viridans -group	1			5
	Streptococcus sp.	1			5
	Streptococcus gordonii	0			5
	Streptococcus sanguinis	0			5
	Aerobe grampositive cocci in chains	1			5
Fusobacterium necrophorum					**-**
	Fusobacterium necrophorum	-			-
	No reported finding	-			-
Additional finding					**-**
	Staphylococcus hominis	-			-
Total:					5

Report Info

PARTICIPANTS

Altogether 94 laboratories from 22 countries participated in this EQA round.

REPORT INFO

On the front page you can see summaries of overall success rate and sample specific success rates which have been calculated from the scores. The reported results and the scores are presented in the same report but in separate tables. The global summary report contains the results of schemes General Bacteriology 1 (5080) and General Bacteriology 2 (5081), but in separate tables. The participant specific summary includes the results of your own reference group (product) merely.
In general, the expected results are marked with green color. Accepted results may also be indicated with yellow color. Laboratory’s own results are indicated with a black radio button If you have not reported results, you will get a note: “You have not responded in time, only global report is available.”
For information on report interpretation and performance evaluation, please see the "EQAS Interpretation guidelines" in LabScala User instructions. In case you have any questions regarding the reports, please contact the EQA Coordinator.

SCORING

The results in the “Report to the clinician” part can be scored when at least 60% of the participants have reported the correct/expected result and when there are at least three reported results. The report includes a sample specific scoring summary. Laboratory’s scores have been converted to percentage (own success rate, % from maximum scores) with a target at 100%. Own success rate is compared with the success rate of all results.

The scoring range/finding is 0-5 points. The scoring comprises the following elements:
species identification, a maximum of 4 points is given (see below)
the interpretation of the significance of the finding, a maximum of 1 point is given
in case of insufficient species identification, an additional score (maximum 1 point) might be given to participants that would have referred the isolate for further identification
The following general rules are applied regarding the scoring of the species identification:
4 points is reached by reporting the expected result
1-3 points is given to results that are partly correct/insufficient regarding the expected finding
0 points is given for an incorrect/false result

General Bacteriology, March, 1-2023

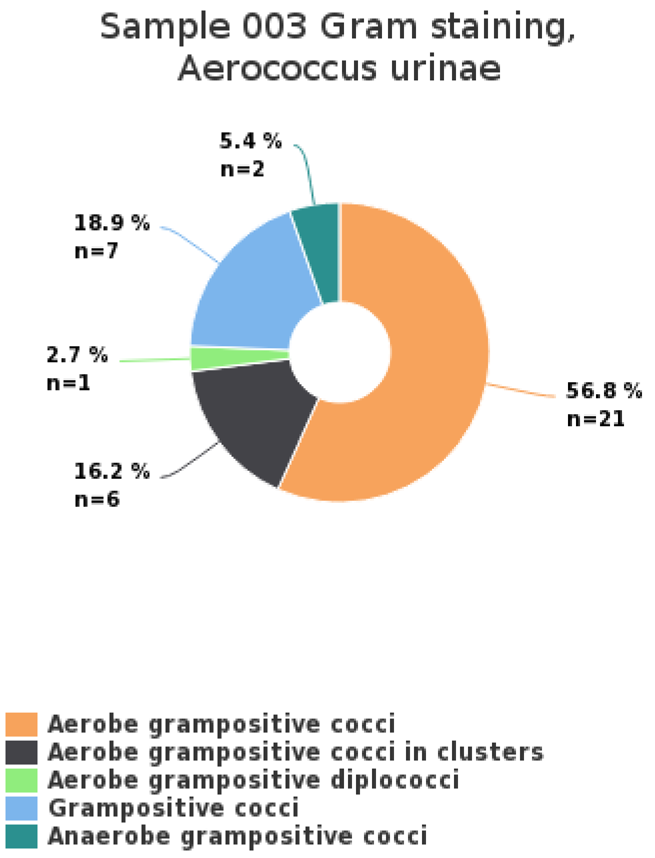
Identification test results

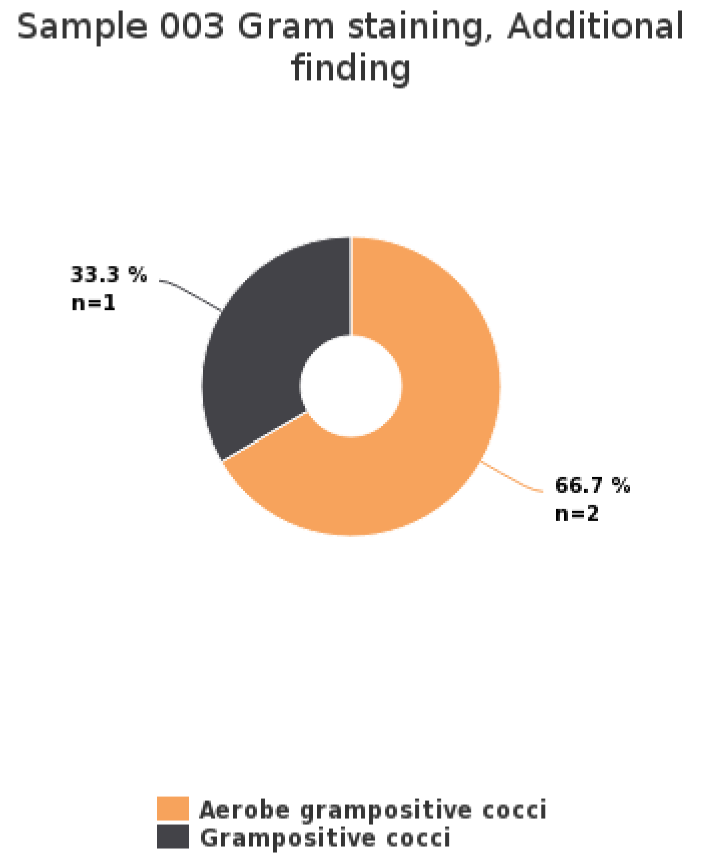
GLOBAL REPORT

	No of participants	No of responded participants	Response percentage
General Bacteriology 1 (aerobes and anaerobes), March, 1-2023	59	57	96.6 %

Sample 003 | Aerococcus urinae

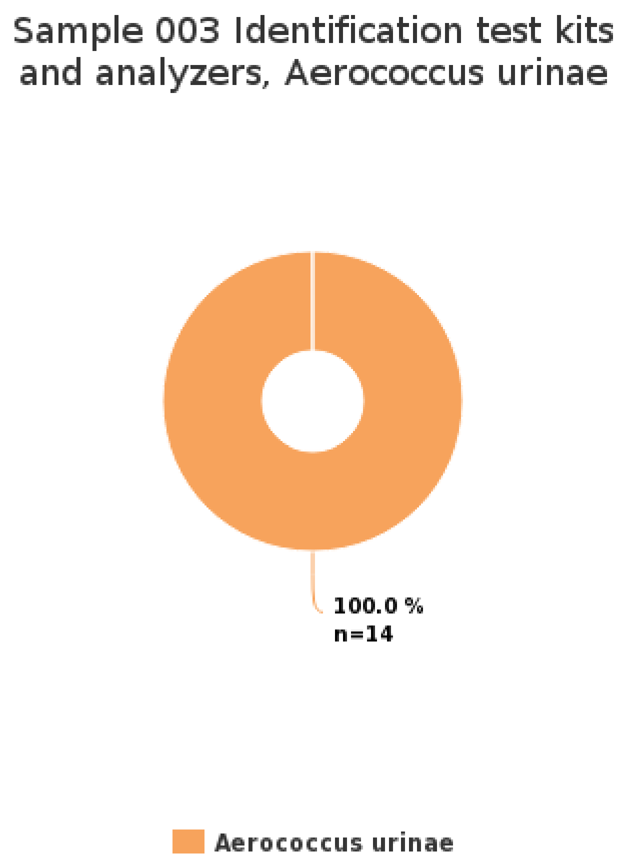
Sample 003 results	Responded	Count
	Gram staining	40
	Identification test kits and analyzers	15
	Identification tests: MALDI-TOF	47
	Identification tests: NAT and DNA-sequencing	1
Total:		103

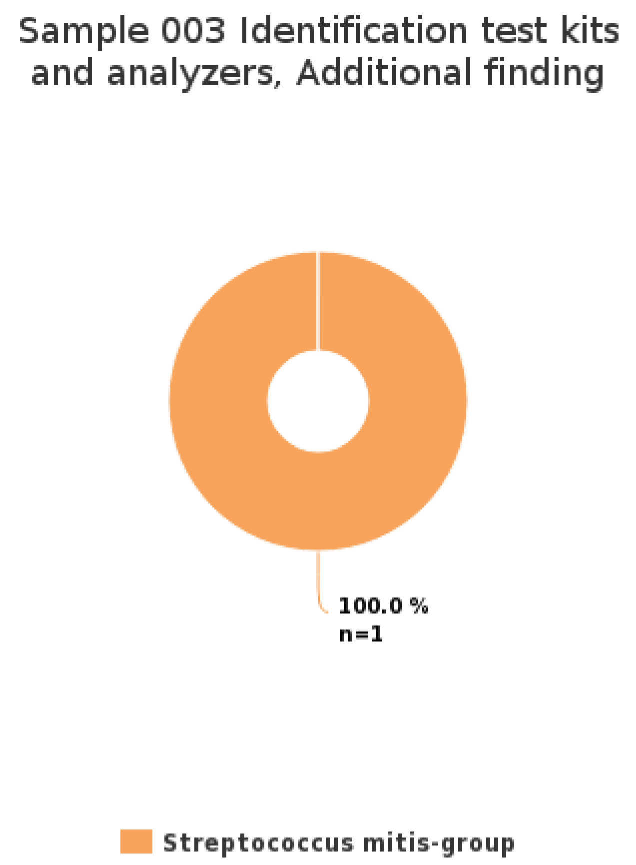

Sample 003 Gram staining, Aerococcus urinae

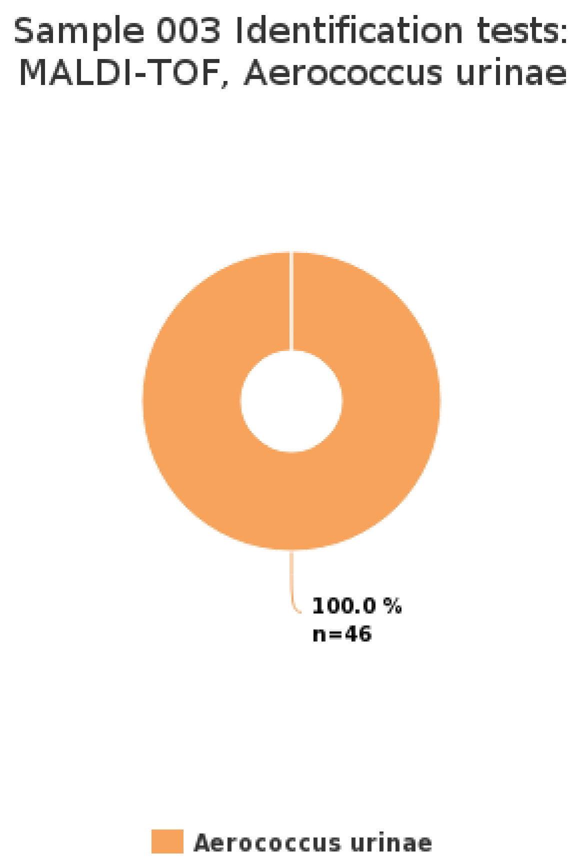

Sample 003 Gram staining, Additional finding

GRAM STAINING

Finding group	Result	Result count
Aerococcus urinae		**37**
	Aerobe grampositive cocci	21
	Aerobe grampositive cocci in clusters	6
	Aerobe grampositive diplococci	1
	Grampositive cocci	7
	Anaerobe grampositive cocci	2
Additional finding		**3**
	Aerobe grampositive cocci	2
	Grampositive cocci	1
Total:		40


Sample 003 Identification test kits and analyzers, Aerococcus urinae

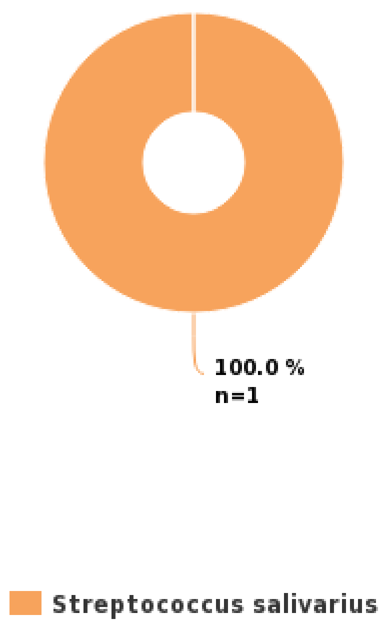

Sample 003 Identification test kits and analyzers, Additional finding


Sample 003 Identification tests: MALDI-TOF, Aerococcus urinae

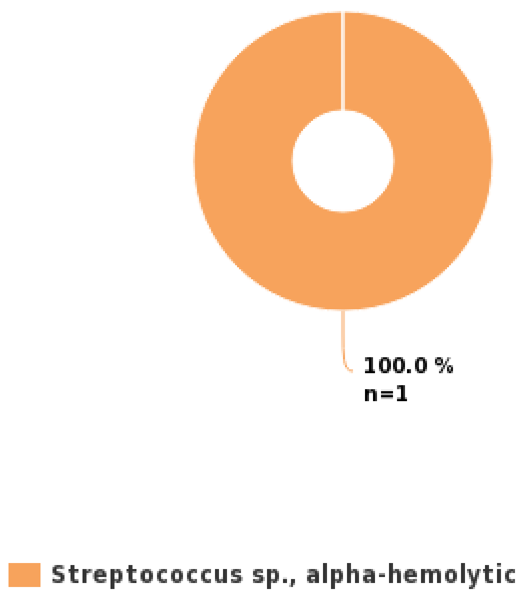
Sample 003 Identification tests:

Sample 003 Identification tests: NAT

MALDI-TOF, Additional finding



and DNA-sequencing, Aerococcus urinae



IDENTIFICATION TEST KITS AND ANALYZERS

Finding group	Method	Result	Profile number	Profile number count
Aerococcus urinae	BD Phoenix PMIC/ID panel (Becton Dickinson)	Aerococcus urinae	N/A	1
	VITEK 2 (bioMerieux)	Aerococcus urinae	000070700040111	1
			000070500050011	1
			000070500040030	1
			000030520040011	1
			000030500050411	1
			000030500040011	1
			000030100040011	1
			N/A	1
	VITEK 2 Compact 15 (bioMerieux)	Aerococcus urinae	000030700040011	1
	VITEK 2 Compact 30 (bioMerieux)	Aerococcus urinae	000030720150111	1
			000030100040010	1
			GP 000030700140011	1
			N/A	1
Additional finding	VITEK 2 Compact 30 (bioMerieux)	Streptococcus mitis-group	021110364305511	1
Total:				15

IDENTIFICATION TESTS: MALDI-TOF

Finding group	Method	Result	Score / Probability %	Score / Probability % count
Aerococcus urinae	MALDI Biotyper (Bruker)	Aerococcus urinae	≥2	25
	VITEK MS (bioMérieux)	Aerococcus urinae	99,9 %	19
			99 %	2
Additional finding	MALDI Biotyper (Bruker)	Streptococcus salivarius	≥2	1
Total:				47

IDENTIFICATION TESTS: NAT AND DNA-SEQUENCING

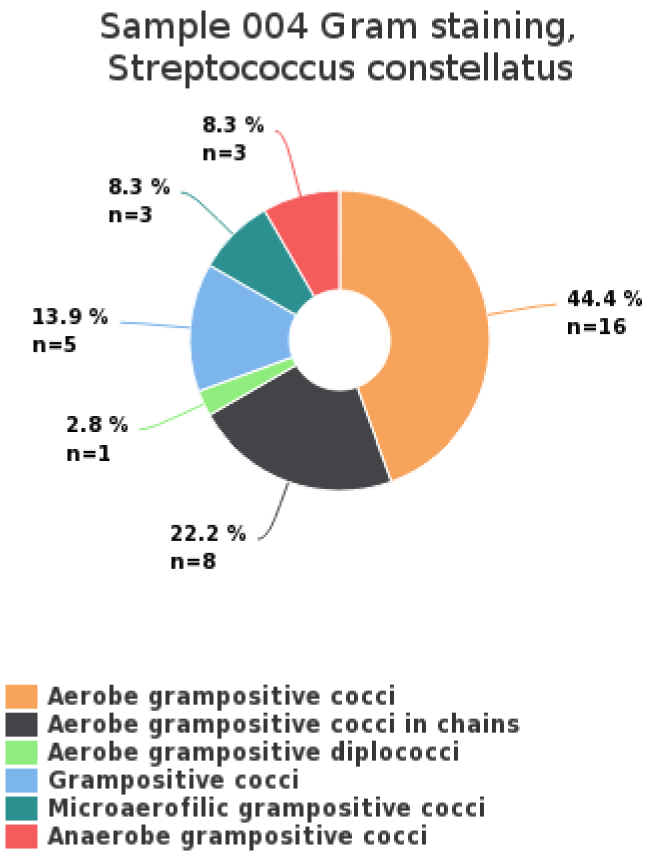
Finding group	Method	Result	Result count
Aerococcus urinae	NAT, In house	Streptococcus sp., alpha-hemolytic	1
Total:			1

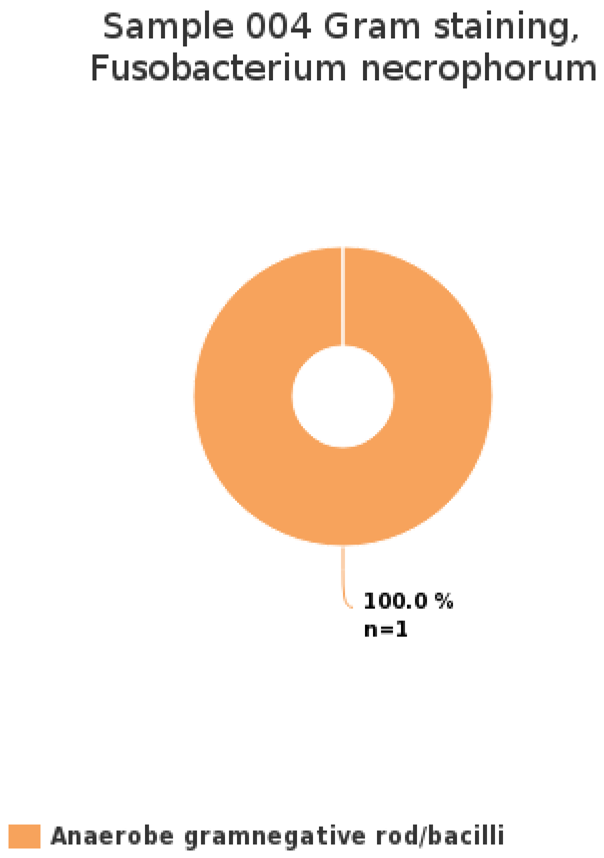
General Bacteriology, March, 1-2023

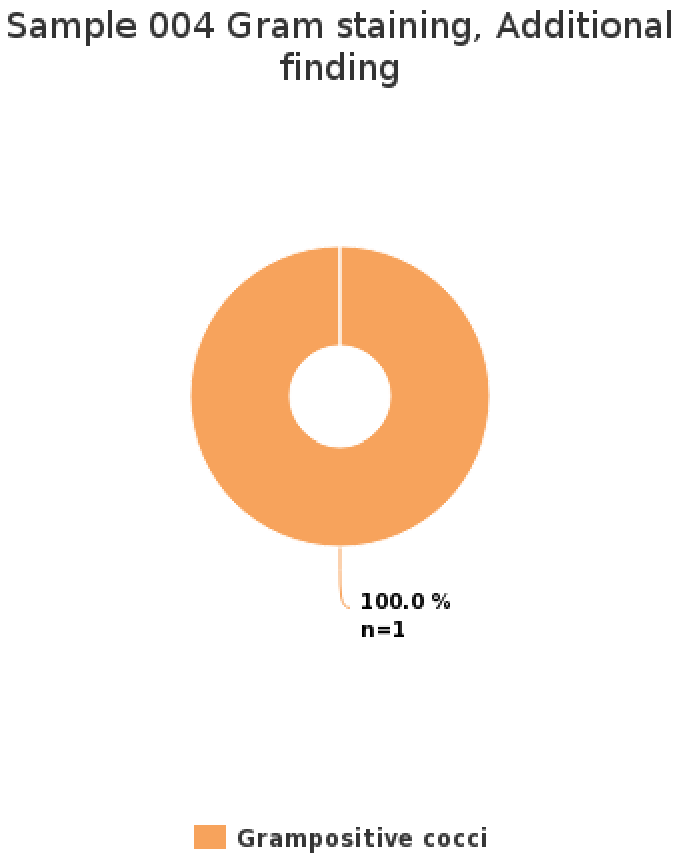
Identification test results

Sample 004 | Streptococcus constellatus, Fusobacterium necrophorum

Sample 004 results	Responded	Count
	Gram staining	38
	Identification test kits and analyzers	11
	Identification tests: MALDI-TOF	50
	Identification tests: NAT and DNA-sequencing	1
Total:		100


Sample 004 Gram staining, Streptococcus constellatus


Sample 004 Gram staining, Fusobacterium necrophorum

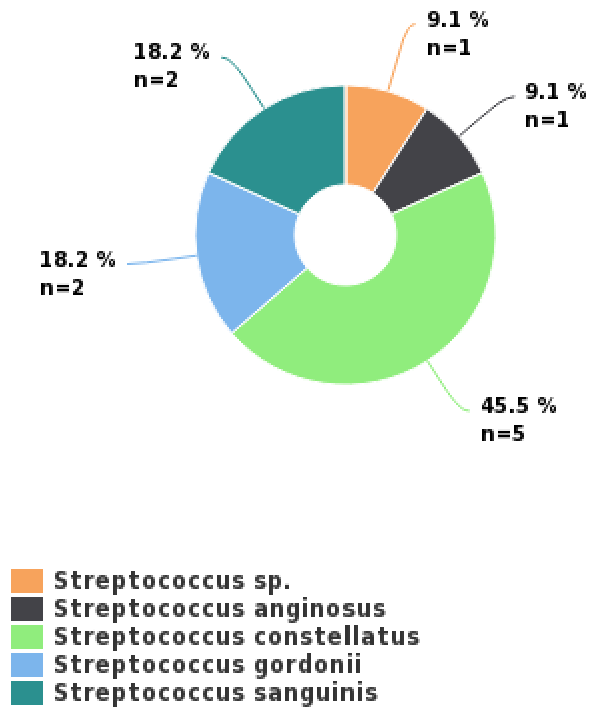

Sample 004 Gram staining, Additional finding

GRAM STAINING

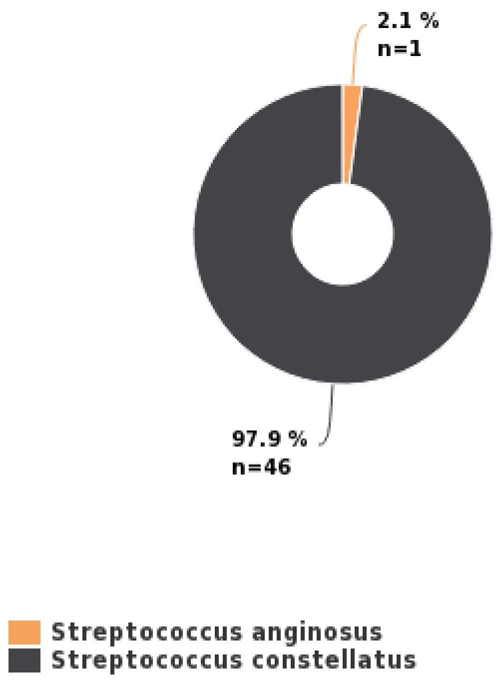
Finding group	Result	Result count
Streptococcus constellatus		**36**
	Aerobe grampositive cocci	16
	Aerobe grampositive cocci in chains	8
	Aerobe grampositive diplococci	1
	Grampositive cocci	5
	Microaerofilic grampositive cocci	3
	Anaerobe grampositive cocci	3
Fusobacterium necrophorum		**1**
	Anaerobe gramnegative rod/bacilli	1
Additional finding		**1**
	Grampositive cocci	1
Total:		38

General Bacteriology, March, 1-2023

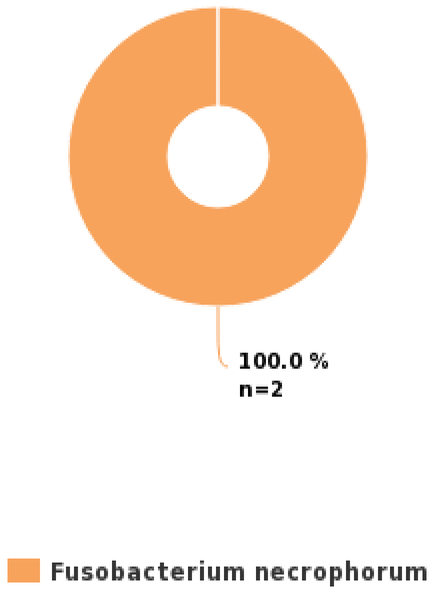
Identification test results



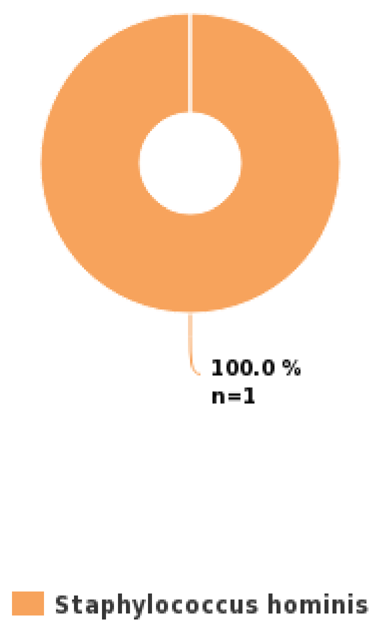
Sample 004 Identification test kits and analyzers, Streptococcus constellatus



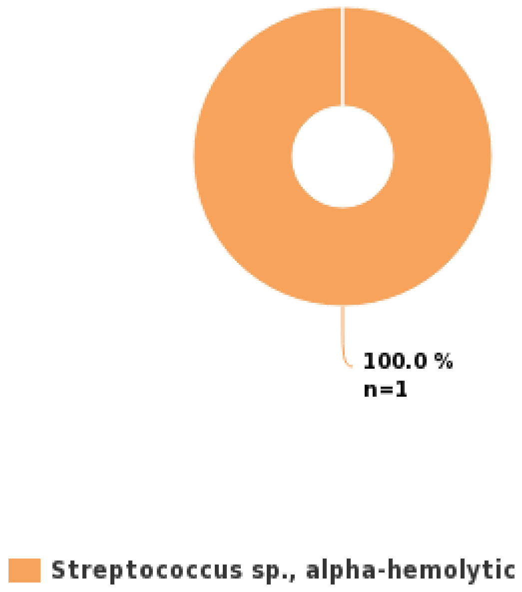
Sample 004 Identification tests: MALDI-TOF, Streptococcus constellatus



Sample 004 Identification tests: MALDI-TOF, Fusobacterium necrophorum



Sample 004 Identification tests: MALDI-TOF, Additional finding



Sample 004 Identification tests: NAT and DNA-sequencing, Streptococcus constellatus

IDENTIFICATION TEST KITS AND ANALYZERS

Finding group	Method	Result	Profile number	Profile number count
Streptococcus constellatus	BD Phoenix SMIC/ID panel (Becton Dickinson)	Streptococcus anginosus	N/A	1
	RapID STR (Thermo Scientific)	Streptococcus constellatus	30211strep	1
	VITEK 2 (bioMerieux)	Streptococcus sp.	N/A	1
		Streptococcus constellatus	051410360713671	1
		Streptococcus gordonii	011410120313471	1
		Streptococcus sanguinis	011010340301431	1
	VITEK 2 Compact 15 (bioMerieux)	Streptococcus sanguinis	001010120203431	1
	VITEK 2 Compact 30 (bioMerieux)	Streptococcus constellatus	051410360713471	1
			011410360713431	1
			N/A	1
		Streptococcus gordonii	N/A	1
Total:				11

IDENTIFICATION TESTS: MALDI-TOF

Finding group	Method	Result	Score / Probability %	Score / Probability % count
Streptococcus constellatus	MALDI Biotyper (Bruker)	Streptococcus constellatus	≥2	22
			≥1.7..<2	3
	VITEK MS (bioMérieux)	Streptococcus anginosus	99,9 %	1
		Streptococcus constellatus	99,9 %	19
			99 %	1

			98 %	1
Fusobacterium necrophorum	MALDI Biotyper (Bruker)	Fusobacterium necrophorum	≥2	1
	VITEK MS (bioMérieux)	Fusobacterium necrophorum	99,9 %	1
Additional finding	MALDI Biotyper (Bruker)	Staphylococcus hominis	≥1.7..<2	1
Total:				50

IDENTIFICATION TESTS: NAT AND DNA-SEQUENCING

Finding group	Method	Result	Result count
Streptococcus constellatus	NAT, In house	Streptococcus sp., alpha-hemolytic	1
Total:			1

LABQUALITY

External Quality Assessment Scheme

General Bacteriology 1
Round 1, 2023

This report replaces the preliminary report. The final report also includes the expert comments on the susceptibility testing results. We apologize for the inconvenience caused by the delay in publication.

Specimens
The round included four lyophilized specimens. The sample lots were tested in an accredited Finnish reference laboratory and the results were consistent with the certificates provided by the sample manufacturer. As an exception, *Fusobacterium necrophorum* included in sample S004 was not isolated in the pretesting. Based on the quality controls conducted by the sample material manufacturer, pre-testing and the results obtained in the round, the sample lots are to be considered as homogeneous, stable and suitable for external quality assessment. The materials were sent without temperature control packaging.

The use of samples only for external quality assessment. The consent of Labquality must be requested for the use of the microbial strains contained in the samples for other purposes.

The samples included the following microbes:

Sample S001 (LQ760123011)
Pseudomonas aeruginosa ATCC® 27853™

Sample S002 (LQ760123012)
Neisseria meningitidis C090156

Sample S003 (LQ760123013)
Aerococcus urinae C070025

Sample S004 (LQ760123014)
Streptococcus constellatus C100637
Fusobacterium necrophorum ATCC® 25286™ (scarce growth)

Report info
Please see the description of the data analysis on the last page of the laboratory-specific reports and global reports. It is important to read the Final report first, as it contains important information of the samples and results in each round. The results reported by participants of General Bacteriology 1 and General Bacteriology 2 have been commented on as one group.

Comments – Experts
Sample S001
Background information: Keratitis in patient using contact lenses.
Finding: *Pseudomonas aeruginosa* as a significant pathogen.

Patient and specimen
P. aeruginosa may cause serious eye infections and should be regarded as a significant pathogen in specimen obtained from an eye.

Culture and identification
Only one pathogen was growing well on both blood and chocolate plates. Gram stain revealed straight and rather long and narrow gram-negative rods. Isolate produced green pigment and had an odor typical for *P. aeruginosa.*

2023-05-24

FINAL REPORT

Product no. 5080

Subcontracting: Sample pretesting

Samples sent	2023-03-21
Round closed	2023-04-14
Expected results	2023-04-18
Preliminary report	2023-05-15
Final report	2023-05-24

Request for correction
Typing errors in laboratory's result forms are on laboratory's responsibility. Labquality accepts responsibility only for result processing. Requests must be notified by writing within three weeks from the date of this letter.

Authorized by
EQA Coordinator
Yvonne Björkman
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Experts
Chief Physician Tapio Seiskari, Fimlab, Tampere, Finland.
Chief Physician Antti Hakanen and, specialist Juha O. Grönroos, Turku University Hospital, Finland.

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FINAS
Finnish Accreditation Service
PT02 (EN ISO/IEC 17043)

Only the analysis phase is accredited.

Quality Management
DQS
ISO 9001:2015

Several automated instruments, such as MALDI TOF based methods can be used in identifying *P. aeruginosa*.

Comments on susceptibility testing results
Pseudomonas aeruginosa ATCC® 27853™ is a susceptibility control strain recommended by EUCAST. It has no acquired resistance.

The majority of the reported susceptibility testing results were within the reference range, and most of the interpretations were correct. Well done!

Table 1. The MIC results reported for the *P. aeruginosa* ATCC® 27853™ strain by two Finnish reference laboratories. Both laboratories followed the EUCAST guideline.

Antimicrobial agent	Ref. laboratory 1 MIC (mg/L)	SIR	Ref. laboratory 2 MIC (mg/L)	SIR
Amikacin	3	S	≤4	S
Aztreonam	3	I	4	I
Ceftazidime	2	I	2	I
Ceftolozane-tazobactam	0.5	S	1	S
Ciprofloxacin	0.25	I	0.25	I
Colistin	2	S	2	S
Meropenem	0.75	S	0.25	S
Piperacillin-tazobactam	3	I	4	I
Tobramycin	0.75	S	≤1	S

Sample S002
Background information: CSF. Suspected meningitis.
Finding: *Neisseria meningitidis* as a significant finding.

Patient and specimen
Meningococcal meningitis is a serious infection associated with high fatality and severe complications.

Culture and identification
Only one species was isolated from the specimen, growing as rather large greenish colonies that had strong positive oxidase reaction. Gram stain showed gram-negative diplococci. When observed from CSF from a meningitis patient, this should cause a suspicion of *N. meningitidis*.

The species was identified as *N. meningitidis* using e.g., MALDI TOF based methods.

Sample S003
Background information: Cardiac valve. Patient with endocarditis.
Finding: *Aerococcus urinae* as a significant finding.

Patient and specimen
A. urinae has been reported to cause infective endocarditis.

Culture and identification
Alpha-hemolytic catalase-negative colonies resembling streptococci were observed on culture plates. Gram stain revealed bacteria growing in clusters rather than chains, which is typical for *A. urinae*. E. g. MALDI TOF based methods can be used in identifying *A. urinae*.

Sample S004
Background information: Tooth abscess, sample taken by puncture.
Finding: *Streptococcus constellatus* as a significant or possibly significant pathogen and *Fusobacterium necrophorum* (very scarce growth) as a significant pathogen.

Patient and specimen
Tooth abscesses are often multimicrobial and caused by pathogens that are present in oral flora.

Culture and identification

Two bacterial species were isolated.

On aerobically and anaerobically cultured plates, gram-positive small alpha-hemolytic and catalase-negative colonies typical for streptococci, were observed. Isolate could be identified as *S. constellatus* using e.g., MALDI TOF based methods.

The second species was a strictly anaerobic pathogen. Gram stain showed pleomorphic gram-negative rods. Indole and lipase reactions were positive suggesting that *F. necrophorum* might be involved. E.g., MALDI TOF based methods can be used in identifying *F. necrophorum*.

The quantity of *F. necrophorum* in the sample was very low and therefore it will not be scored.

Exceptions in scoring

The *F. necrophorum* finding included in sample S004 is not scored due to poor growth (<60% of the participants reported the expected finding).

End of report