

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 1 of 27			

Report for Participants in **RLEUH-PT** program 2021

ML-01-2021

March 2021

Report Status: Final

Sample type:(CSF- Urine- Blood- BAL- Throat swab)

Test type: Clinical Microbiology

Test material Code: ML- 01/2021

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Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاختصاصات EGAC Accredited Proficiency Testing Unit CAB # 719002	المجلس الأعلى للمستشفيات الجامعية RLEUH PTU
Issue / Rev. No.	02/00			
Issue Date	02/06/2020			
Issued by	RLEUH director			
Approved by	Secretary SCUH			
Approval date	02/06/2020			
RLEUH- PTP Report				
Page 2 of 27				

Contents

	Page No
1. Introduction	3
2. Design and objectives of the study	3
3. Participants	3
4. Test Materials	4
4.1. Preparation of test materials	4
4.2 Dispatching	4
4.3 Homogeneity and stability test	4
4.4 Subcontracting	4
5. References	4
6. Results	5
6.1. Analysis of the participant's results	5
6.1.1. Evaluation of the participant performance	5
Overall evaluation of participating laboratories	16
Evaluation of individual laboratory performance	19
Conclusion	21
Annex 1: Detailed evaluation of each sample	24
Annex 2: Homogeneity and Stability tables	29

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 3 of 27			

1. INTRODUCTION

The duties of the RLEUH-PTU are to assess the performance of the designated Governmental laboratories as well as private laboratories. The programs of the proficiency test are organized within ISO/IEC 17043:2010.

Hence, it is a requirement for the accreditation to ISO 15189:2015 that the laboratory takes part in a proficiency testing scheme. Proficiency testing is a legal requirement for these laboratories. Thus, together with the use of validated methods, proficiency testing is an essential element of laboratory quality assurance.

2. DESIGN AND OBJECTIVES OF THE PT RESULTS STUDY

The study consisted in detection and isolation of a microorganism from different five samples spiked with different amounts of microorganisms. The samples are (Blood- BAL-Urine- CSF-Throat swab)

OBJECTIVES

To improve the preparedness of the different governmental laboratories or even private laboratories towards testing clinical samples commodities for the presence of different microorganisms, by applying to the well reputable test methods.

To improve the preparedness of the laboratories towards the detection and isolation of different microorganisms and conducting the antibiotic sensitivity test.

CONFIDENTIALITY

All information held by RLEUH-PTU about participants, including their evaluation, is confidential and will not be disclosed to anyone unless explicitly agreed by the participant for a particular purpose. To preserve this confidentiality participants, receive reports giving all the results for that PT but without identifying individual laboratories. The laboratory code numbers used in reports are assigned in order of receipt of results from participants. Participants will be assigned the same code number in different PTs only by chance. The reports for individual laboratories can be used as a quality control tool to achieve accreditation or measure the testing performance, other interested parties of accreditation bodies can use the PT results as specified in ISO/IEC 17011:2004, 7.15. Also regulatory bodies can evaluate the performance of participants covered by regulations.

3. PARTICIPANTS

Nineteen laboratories representing 16 Governmental University hospitals' laboratories and three laboratories from private sector hospitals are participated in the study. Only medical microbiology

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 4 of 27			

laboratories with a clinical pathologist as coordinator are allowed to participate as per eligibility criteria in the announcement.

Each laboratory received its own individual laboratory numerical code, which is reported in the result tables and in the individual reports.

4. Test Materials

4.1. Preparation of test materials

Samples preparation were subcontracted in the reference laboratory of Egyptian University Hospitals (RLEUH) operated in ASUSH to meet the requirements of ISO:15189, 2012.

The test material was artificially prepared samples inoculated by microorganisms to mimic Clinical samples (Blood, BAL, Urine, CSF, Throat swab) test materials and samples were stored at $-20 \pm 5 / -80$ °C until dispatching.

Metrological traceability: The five Isolates from ATCC Strains or CAP identified strains. (*Reference Table 2)

4.2 Dispatching

All samples were dispatched starting from 4/4/2021 to 6/5/2021. Samples were sent to the laboratories in a cooling Isothermal container that maintained temperature at -20 C within 14 hours and temperature was recorded by data logger (thermometer) on arrival and during transportation.

4.3 Homogeneity and stability test

Twenty samples were selected randomly and were analyzed to test the homogeneity of the samples after preparation of the PT test items and before distribution to participants. Stability of samples is checked after distribution of samples till the deadline of the PT round. Four samples will be stored in worst conditions and longest transportation duration mimic transportation and storage of participating laboratories and tested two times from the dispatching of PTs to the closing date of laboratories results. Samples were analyzed in ASUSH laboratory. Homogeneity and stability were tested according to the requirement of ISO 17043:2010.

Test materials in RLEUH-PTU were not distributed until testing demonstrates that the individual subsamples are of sufficient homogeneity. PTU uses the statistical procedure according to ISO 13528:2015 [2]. Details of the homogeneity and stability testing data are shown in table 2.

4.4 Subcontracting:

RLEUH is subcontracting Ain shams University Specialized Hospital microbiology branched laboratory for Preparation of PT item, performing homogeneity & stability tests of PT item

5. References:

- 1- ISO/IEC 17043: 2010, Conformity assessment – General requirements for proficiency testing provider.
- 2- ISO 13528:2015, Statistical methods for use in proficiency testing by inter-laboratory comparison.

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 5 of 27			

3-Clinical Laboratory Standard Institute Guidelines (CLSI) 2018

4-Proficiency test handling & communication Florida Board of Clinical Laboratory Science CE Supervision/Administration, Quality Control/Quality Assurance, and Safety, Course #: 650809

6. Results

Results (20 response) were sent by 19 medical laboratories by email before the closing date 20/5/2021 (date was extended as per request of newly enrolled university hospitals laboratories and approval by Secretary of Supreme Council for University Hospitals). Each participant was given code, assigned in order of receiving the test material.

6.1. Analysis of the participant's results

6.1.1. Evaluation of the participant performance in the identification of microorganisms, determination of morphological characteristics, antibiotic selection for interpretation the sensitivity test

Performance of each participant was evaluated for five different unknown samples; 20% was given for all true results for each sample an extra mark may be mentioned for some additional tests as bonus.

True sample means that the participant is able to detect the microorganism, identify its morphology, Gram stain, proper selection of antibiotic with accurate interpretation of sensitivity results and final detection Multi Drug Resistance (MRD) and interpretation of results. The performance of each participant in accurate passing of each task was evaluated by assigning specific score. Distribution of score among samples is shown in table1.

No uncertainty measurements

Assigned Value: Not applicable

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاختصاصات EGAC Accredited Proficiency Testing Unit CAB # 719002	المجلس الأعلى للمستشفيات الجامعية RLEUH PTU
Issue / Rev. No.	02/00			
Issue Date	02/06/2020			
Issued by	RLEUH director			
Approved by	Secretary SCUH			
Approval date	02/06/2020			
RLEUH- PTP Report				
Page 6 of 27				

Evaluation of tasks:

Table 1: Over all evaluation of tasks based on Clinical Laboratory Standard Institute Guidelines (CLSI) 2018.

Parameters	ML-01-a CSF	ML-01-b Urine	ML-01-c Blood	ML-01-d BAL	ML-01-e Throat swab
Pathogen Identification	3	3	9	10	9
ID test/media	4	4	8	4	9
Gram Stain /Morphology	2	2	3	5	2
Colony count	-	2	-	1	-
Antibiotic selection	3	3	-	-	-
Antibiotic interpretation	6	4	-	-	-
MDRO test	2	2	-	-	-
Total score	20	20	20	20	20

Table 1-a Scoring system for Sample ML-01-a

Parameters	ML-01-a	Scoring Criteria	
Pathogen Identification	3	-Species ID: Escherchia	1.5
		-Subspecies ID: coli	1.5
ID test/media	4	-Biochemical tests:	
		MIO: Motile	0.3
		LIA: Negative	0.3
		Citrate: Negative	0.3
		Urease: Negative	0.3
		Indole: Positive	0.3
		TSI agar:A/A gas, No H2S	0.5
Gram Stain /Morphology	2	-Colony morphology: Lactose fermenter pink colonieswith pigmentation non hemolytic colonies	2
		-Gram Stain: Gram Negative Bacilli	2

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد  EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 7 of 27			

Abic selection	3	-Selection of appropriate Abics (8 Abic each 0.3)	3
Abic interpretation	6	-Interpretation of each Abic (S,I,R) (each 0.75)	6
MDRO test	2	-ESBL: Negative -Carbapenamase test: Negative	1 1
Total score	20	Pass score 16 (80%)	

Table 1-b: Scoring system for Sample ML-01-b

Parameters	ML-01-b	Scoring Criteria	
Pathogen Identification	3	-Species ID: Proteus -Subspecies ID: Mirabilis	1.5 1.5
ID test/media	4	-Colony morphology: -non hemolytic whitish colonies with swarming on blood agar, -non lactose fermenting colonies on Mac -Biochemical reaction: -oxidase negative -citrate negative -urease positive -TSI Alk/A plus H ₂ S -LIA lysine deamination : negative -SIM motile -Indole negative	1 1 0.3 0.3 0.3 0.3 0.3 0.3 0.2
Gram Stain /Morphology	2	Gram: Gram negative bacilli	2
Colony count	2	>100,000 CFU/ml	2

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 8 of 27			

Abic selection	3	Selection of proper Abic (8 Abics each 0.3)	3
Abic interpretation	4	Interpretation (S,I,R) (0.5 each)	4
MDRO test	2	-ESBL: Negative -Carbapenemase test: Negative	1 1
Total score	20	Pass score 16 (80%)	

Table 1-c Scoring system for Sample ML-01-c

Parameters	ML-01-c	Scoring Criteria	
Pathogen Identification	9	First pathogen -Species ID: Escherchia -Subspecies ID: coli Second pathogen Species: Enterococcus Subspecies: fecalis Third pathogen Species: Salmonella	1.5 1.5 1.5 1.5 3%
ID test/media	8	-Colony morphology: On blood agar: -Enterococcus: grayish small non hemolytic colonies -Ecoli: whitish non hemolytic colonies,Salmonella:Whitish non hemolytic colonies On Mac agar: E.coli: lactose fermenting colonies on mac. Salmonella: non lactose fermenting colonies on mac. -ID tests: Entero: catalase, Bile esculine , 6.5% NaCL solubility test, sutrim disc, Ecoli: (Citrate, urease, TSI, LIA, SIM), Salmonella:Citrate, urease, TSI, LIA, SIM	0.5 0.5 0.5 0.5 0.5% 1% 0.5% ----- --1

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	 EGAC Accredited Proficiency Testing Unit CAB # 719002 RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 9 of 27			

		<u>Enterococcus</u> :Cat negative, BE positive, soluble in 6.5% NaCl, sutrim resistant, <u>Ecoli</u> :citrate negative, urease negative, TSI A/A gas no H ₂ s, LIA negative, SIM motile and indole positive, <u>Salmonella</u> :TSI Alk/Acid plus H ₂ S , Citrate +ve ,urease -ve, Motile , positive decarboxylation plus H ₂ s	2% 1
Gram Stain /Morphology	3	Enterococcus:Gram positive cocci in chains E.coli:GNB Salmonella:GNB	1 1 1
Total score	20	Pass score 16 (80%)	

Table 1-d Scoring system for Sample ML-01-d

Parameters	ML-01-d BAL	Scoring criteria	
Pathogen Identification	10	-Species ID: Candida -Species ID: non-albicans Subspecies: Parapsilosis	5 3 2
ID test/media	4	-Selection of ID test: Germ tube test -Interpretation of ID test: Negative	2 2
Gram Stain /Morphology	5	-Selection of Media: Sabaroud's dextrose agar, blood agar -Colony morphology: Creamy white colonies, white non hemolytic colonies on blood -Gram Stain: Gram positive Budding yeast	1 2 2
Colony count	1	>10 ⁴ CFU/ml	1
Total score	20	Pass score 16 (80%)	

Table 1-e Scoring system for Sample ML-01-e

Parameters	ML-01-e	Scoring criteria
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Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 10 of 27			

Pathogen Identification	9	Presence of group A (3)beta hemolytic (1)streptococcus pyogenes(3+2)	9
ID test/media	9	-Colony morphology: Beta hemolytic small colonies on blood agar -Selection of ID tests: catalase, BE and Bacitracine disc Interpretation: Catalase:Negative, BE: negative Bacitracin sensitive	1.5 3 1.5 1.5 1.5
Gram Stain /Morphology	2	Gram positive cocci, single and in chain	2
Total score	20	Pass score 16 (80%)	

Table 2: Results of Pathogen identification of PT Samples

Sample code	Type	Bacteria	*Reference
ML01a	CSF	E.coli	ATCC 25922
ML01b	Urine	Proteus mirabilis	ATCC 35659
ML01c	Blood	E.coli Enterococcus faecalis Salmonella spp	ATCC 25922 ATCC 51299 CAP identified D19-2014
ML01d	BAL	Candida parapsilosis	CAP identified F3-03/2019
ML01e	Throat swab	Group A Beta hemolytic streptococcus pyogenes	ATCC 19615

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد  EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 11 of 27			

Table 3: Homogeneity data for samples ML-01 (according to ISO: 13528: 2015 [2]).

Antibiotics ML-01-a	overall Avg.	SD of Avg.	Sw	SS	σ_{pt}	check value	Homogeneity is
Ampicillin/sulbactam	20.550	0.369	0.500	0.105	0.385	0.115	OK
ceftazidime	25.300	0.350	0.447	0.149	0.577	0.173	OK
Meropenem	29.450	0.369	0.500	0.105	0.509	0.153	OK
Pip/Tazo	20.700	0.483	0.632	0.183	0.770	0.231	OK
Imipenam	30.050	0.369	0.500	0.105	0.385	0.115	OK
Trimthoprim/sulfa	25.700	0.483	0.632	0.183	0.839	0.252	OK
Tobramycin	17.833	0.500	0.671	0.158	0.577	0.173	OK
Ceftriaxone	29.650	0.530	0.742	0.075	0.385	0.115	OK
Cefoxitine	26.300	0.350	0.447	0.149	0.509	0.153	OK
Cefepime	30.300	0.350	0.447	0.149	0.577	0.173	OK
Cefotaxime	28.667	0.433	0.548	0.194	0.694	0.208	OK
Gentamycin	19.450	0.369	0.500	0.105	0.385	0.115	OK
Amikacin	19.550	0.369	0.500	0.105	0.509	0.153	OK

Antibiotics ML-01-b	overall Avg.	SD of Avg.	Sw	SS	σ_{pt}	check value	Homogeneity is
Pip/Tazo	30.850	0.530	0.742	0.075	0.333	0.100	OK
Cefepime	31.55	0.437798	0.591608	0.129099	0.7698	0.23094	OK
Amikacin	19.7	0.349603	0.447214	0.149071	0.509175	0.152753	OK
Ampicillin/sulbactam	30.3	0.349603	0.447214	0.149071	0.509175	0.152753	OK
Imipenem	24.700	0.483	0.632	0.183	0.694	0.208	OK
Gentamycin	19.550	0.438	0.592	0.129	0.770	0.231	OK
Cefoxitin	28.700	0.587	0.775	0.211	0.770	0.231	OK
Nitrofurantoin	13.45	0.368932	0.5	0.105409	0.3849	0.11547	OK
Amox/Clavulanat	30.3	0.349603	0.447214	0.149071	0.509175	0.152753	OK
Meropenem	28.7	0.421637	0.547723	0.166667	0.57735	0.173205	OK
Ceftazidime	30.45	0.368932	0.5	0.105409	0.509175	0.152753	OK
Trimethoprim/Sulpha	26.550	0.369	0.500	0.105	0.385	0.115	OK
Ciprofloxacin	30.650	0.530	0.742	0.075	0.839	0.252	OK
Levofloxacin	30.450	0.369	0.500	0.105	0.509	0.153	OK
Tobramycin	19.55	0.437798	0.591608	0.129099	0.693889	0.208167	OK
Ceftriaxone	34.3	0.349603	0.447214	0.149071	0.509175	0.152753	OK
Cefotaxime	34.3	0.349603	0.447214	0.149071	0.509175	0.152753	OK

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	الاجلس الوطني للاعتماد  EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 12 of 27			

Table 4: Stability data for samples ML-01 (according to ISO: 13528: 2015 [2]).

Antibiotics	Overall average	Homogeneity mean	Diff from homogeneity mean	opt	Stability is
Ampicillin/sulbactam	20	20.550	-0.550	0.385	OK
ceftazidime	25	25.300	-0.300	0.577	OK
Meropenem	29.25	29.450	-0.200	0.509	OK
Pip/Tazo	20.25	20.700	-0.450	0.770	OK
Imipenam	30	30.050	-0.050	0.385	OK
Trimthoprim/sulfa	25.25	25.700	-0.450	0.839	OK
cefoxitine	26	26.300	-0.300	0.509	OK
Ceftriaxone	29.75	29.650	0.100	0.385	OK
Cefepime	30.25	30.300	-0.050	0.577	OK
Gentamycin	19.5	19.450	0.050	0.385	OK
Tobramycin	17.75	17.833	-0.083	0.577	OK
Cefotaxime	28.25	28.667	-0.417	0.694	OK
Amikacin	19.25	19.550	-0.300	0.509	OK

Antibiotics ML-01-b	Overall average	Homogeneity mean	Diff from homogeneity mean	opt	Stability is
Pip/Tazo	30.5	30.850	-0.350	0.333	OK
imipenem	24.5	24.700	-0.200	0.694	OK
Nitrofurantoin	13.5	13.45	0.05	0.3849	OK
Amikacin	19.5	19.700	-0.200	0.509	OK
Gentamycin	19.5	19.550	-0.050	0.770	OK
Cefoxitin	28.5	28.700	-0.200	0.770	OK
Meropenem	28.5	28.7	-0.2	0.57735	OK
Tobramycin	19.5	19.55	-0.05	0.693889	OK
Cefepime	31.5	31.550	-0.050	0.000	OK
Amoxacilin/clav	30.25	30.3	-0.05	0.509175	OK
Trimethoprim/Sulpha	26.5	26.550	-0.050	0.385	OK
Ciprofloxacin	30.5	30.650	-0.150	0.839	OK
Levofloxacin	30.5	30.450	0.050	0.509	OK
Ampicillin/sulbactam	30	30.3	-0.3	0.509175	OK
Ceftazidime	30.5	30.45	0.05	0.509175	OK
Ceftriaxone	34.25	34.3	-0.05	0.509175	OK
Cefotaxime	34	34.3	-0.3	0.509175	OK

Detailed and complete homogeneity and stability file annex 2 page 29

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية Reference Council of University Hospitals RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 13 of 27			

Laboratories Scores in PT samples

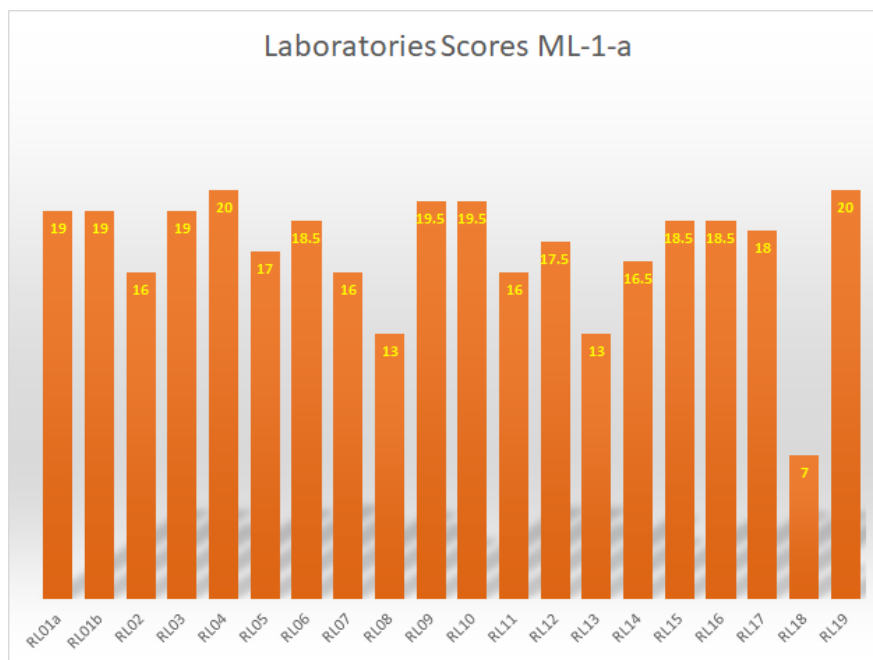


Figure 1: Evaluation of sample ML_01_a

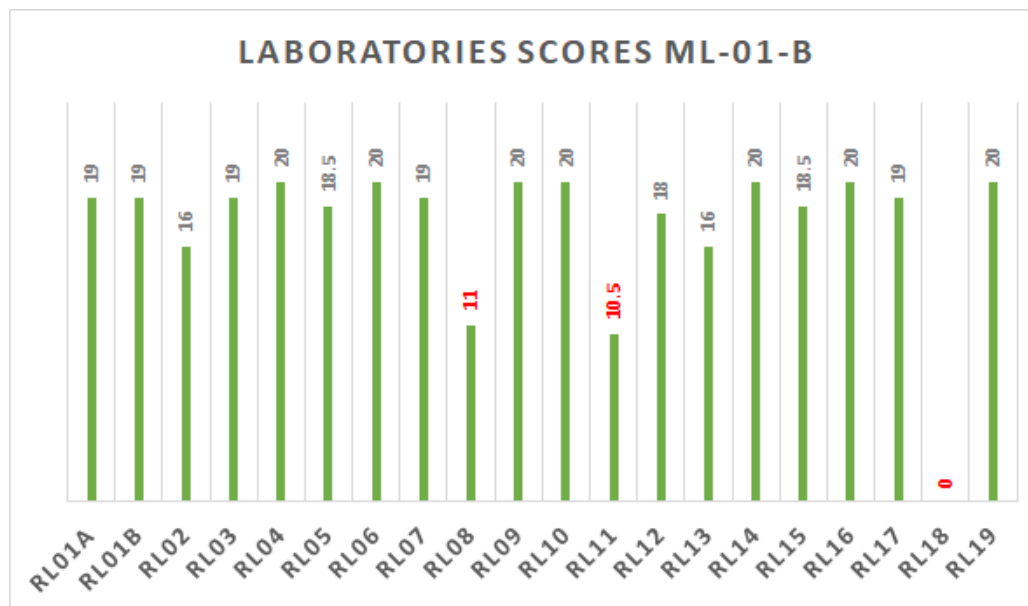


Figure 2: Evaluation of sample ML_01_b

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 14 of 27			

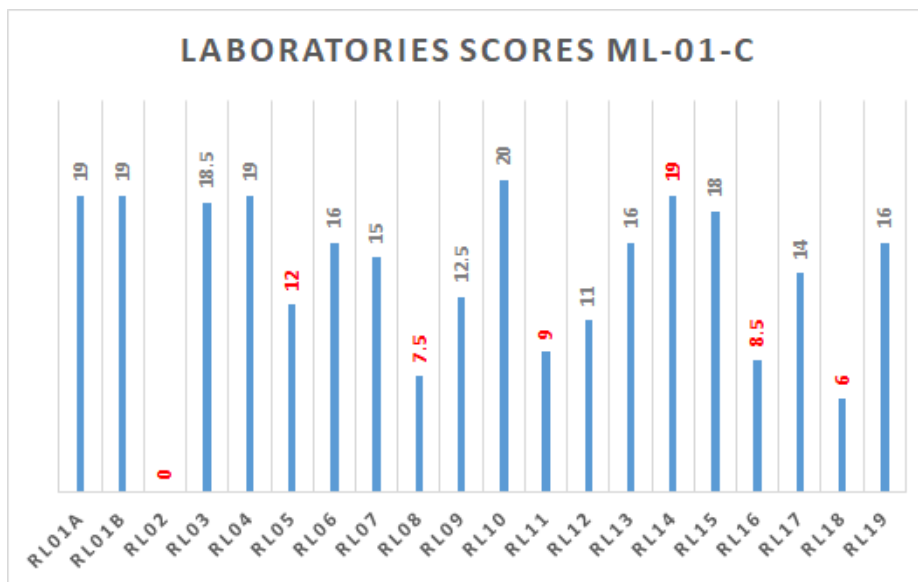


Figure 3: Evaluation of sample ML_01_c

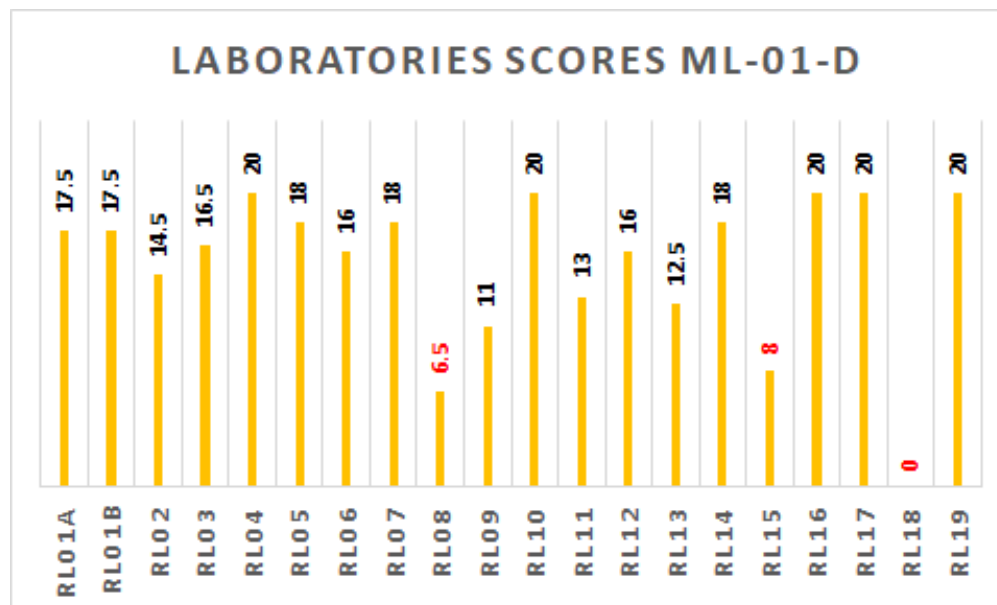


Figure 4: Evaluation of sample ML_01_d

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 15 of 27			

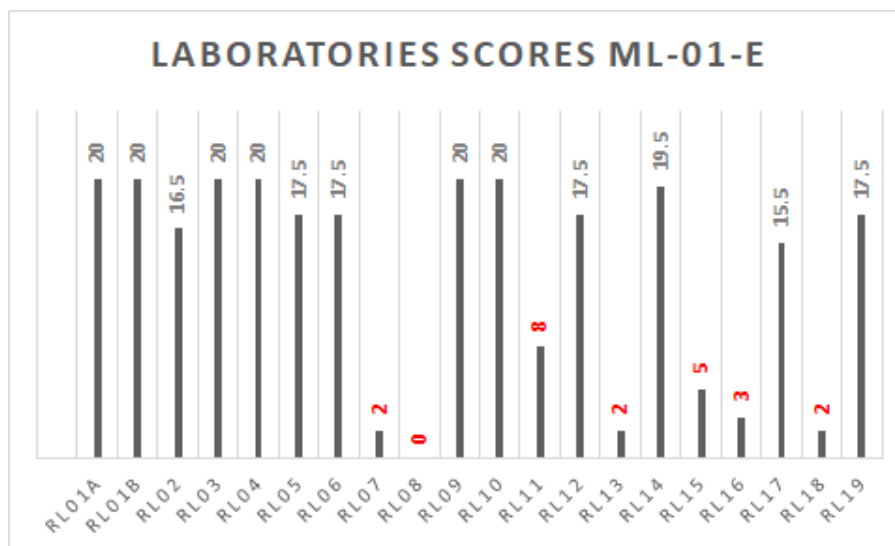


Figure 5: Evaluation of sample ML_01_e

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 16 of 27			

Table 5: Overall evaluation of participating laboratories:

Code	ML-01-a	ML-01-b	ML-01-c	ML-01-d	ML-01-e	Total
RL01a	19	19	19	17.5	20	94.5
RL01b	19	19	19	17.5	20	94.5
RL02	16	16	0	14.5	16.5	63
RL03	19	19	18.5	16.5	20	93
RL04	20	20	19	20	20	99
RL05	17	18.5	10	18	17.5	81
RL06	18.5	20	13.5	16	17.5	85.5
RL07	16	19	15	18	2	70
RL08	13	11	7.5	6.5	0	38
RL09	19.5	20	12.5	11	20	83
RL10	19.5	20	20	20	20	99.5
RL11	16	10.5	9	13	8	56.5
RL12	17.5	18	11	16	17.5	80
RL13	13	16	16	12.5	2	59.5
RL14	16.5	20	19	18	19.5	93
RL15	18.5	18.5	18	8	5	68
RL16	18.5	20	8.5	20	3	70
RL17	18	19	14	20	15.5	86.5
RL18	7	0	6	0	2	15
RL19	20	20	16	20	17.5	93.5

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 17 of 27			

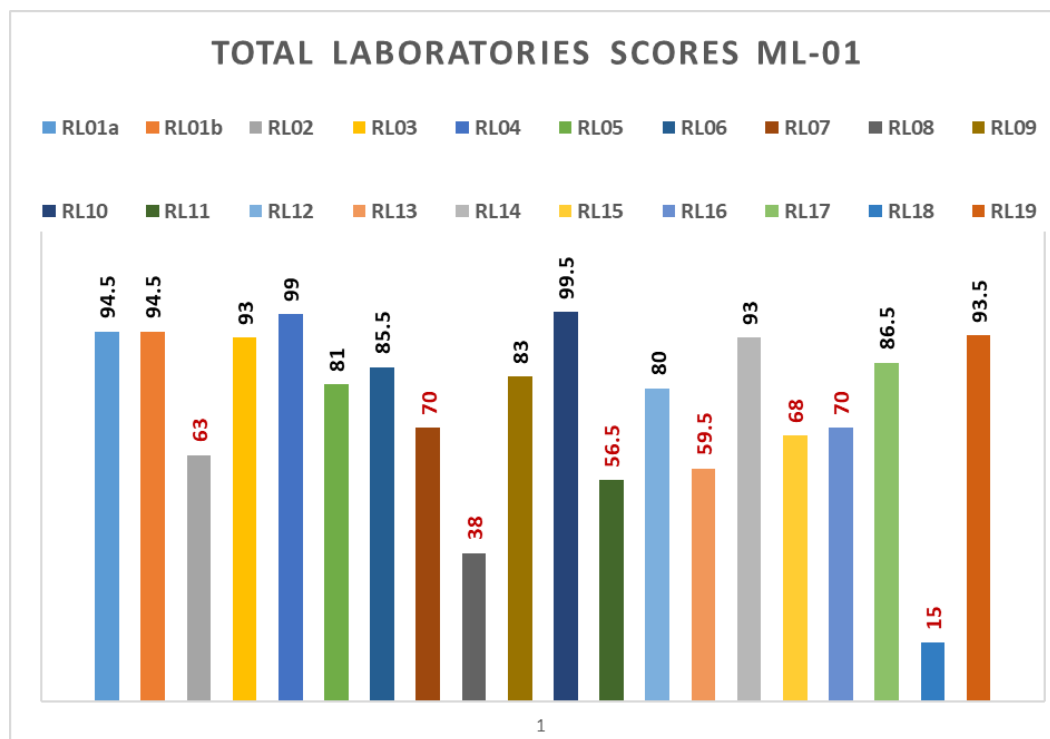


Figure 6: Overall scores of participating laboratories (Pass score 80%)

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد  EGAC Accredited Proficiency Testing Unit CAB # 719002  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 18 of 27			

Evaluation of individual laboratory performance

*Laboratories (11 laboratories with 12 results) **RL01a, RL01b, RL03, RL04, RL05, RL06, RL09, RL10, RL12, RL14, RL17, RL19** showed excellent performance and trustable results (Scores 81-99.5%). Recommended to maintain their outstanding performance and consistent implementation of CLSI-2018 guidelines with its updates. A reward workshop “Validation study in microbiology laboratory” will be prepared for them. An Award will be given by the end of the program for laboratories with outstanding performance.

*Laboratories (8 laboratories) did not reach the pass score. However, six out of the eight (**RL02, RL07, RL11, RL13, RL15, RL16**) showed scores 60-70% and can improve their performance and suggested actions will be send. They are encouraged to work on minor non-conformities and stick to CLSI guidelines, implementation of QC and RLEUH will support by the following workshop: “Quality assurance program in microbiology laboratory”. Two laboratories **RL08 (38%) and RL18 (15%)** need to revise their laboratory work instructions, staff competencies, reagents quality and stick to SOPs to follow CLSI and QC program. An on job training will be delivered to them as well as SOPs. “Standard microbiologic techniques Workshop” will be prepared and staff will be hosted by RLEUH to ensure they are on the track.

Gaps and Suggested improvements

RL02: Showed score 63%, missing the following:

- 1-No reporting of ESBL and Carbapenemase tests for gram negative organism in Sample a-b.
- 2-Incorrect Identification of other pathogens in sample (c).
- 3-incorrect species identification of Candida with inappropriate description of colony morphology and gram stain results and missing reporting colony count in sample (d).

Suggested improvement:

- 1-Testing for ESBL and Carbapenemase.
- 2-Implementation of SOPs that follows CLSI guidelines to ensure proper culture technique for good separation of colonies and better identification of all pathogens with appropriate tests for identifications and biochemical reactions. In addition to proper colony counting and better description of organism morphology and QC on gram stain.

RL07: Showed score 70%, missing the following:

- 1-no reporting of colony morphology as requested.
- 2- Inappropriate selection of antimicrobials for treatment of neonatal meningitis.

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	المجلس الوطني للاعتماد  EGAC Accredited Proficiency Testing Unit CAB # 719002 المجلس الأعلى للمستشفيات الجامعية  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 19 of 27			

3-Failed Identification of E.coli in sample c

4- failed detection of group A beta hemolytic streptococci in sample e

Suggested improvement

1-Reporting colony morphologies.

2-appropriate selection of antimicrobials for treatment of a case of meningitis

3- Proper culture technique for good separation of colonies and better identification of all pathogens with appropriate tests for identifications and biochemical reactions.

4- Check Appropriate culture, incubation conditions and temperature and interpretation of organism in sample e

RL08: Showed score 38%, missing the following:

1-Inappropriate selection of antimicrobials for treatment of meningitis and according to CLSI 2018

2-Failed ESBL and carbapenemase test reporting.

3-Inappropriate selection of antimicrobials according to CLSI 2018 in sample b

4-Failed identification of other 2 pathogens in sample c

5-Failed identification of candida species as candida parapsilosis of non albicans, with no tests for identification reported (Germ tube test) and no colony count reported and incorrect terms of identification in gram stain.

6- failed detection of group A beta hemolytic streptococci in sample e

Suggested improvement:

1-Appropriate selection of antimicrobials for treatment of a case of meningitis and according to CLSI 2018

2-Testing for ESBL and Carbapenemase as requested

3-Proper culture technique for good separation of colonies and better identification of all pathogens with appropriate tests for identifications and biochemical reactions.

4-Candida species identification or even as candida non-albicans by germ tube test performance

5-Check Appropriate culture, incubation conditions and temperature and interpretation of organism in sample e

RL11: Showed score 56.5% and missing the following:

1-Inappropriate choice of antimicrobials for treatment of a case of neonatal meningitis and use of nitrofurantoin and Norfloxacin which are used in case of UTI

2-Incorrect pathogen identification in sample b with wrong Biochemical reaction results and wrong antimicrobial susceptibility results.

3- Failed identification of other 2 pathogens in sample c with improper colony morphology reporting

4-Wrong identification of candida as albicans with wrong germ tube test results

5- no reporting of presence of group A beta hemolytic streptococci

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 20 of 27			

Suggested improvement:

- 1-Appropriate choice of antimicrobials used in case of neonatal meningitis and according to CLSI 2018
- 2-better interpretation of colony morphology and BR. Results
- 3- Proper culture technique for good separation of colonies and better identification of all pathogens with appropriate tests for identifications and biochemical reactions.

RL13: Showed score 59.5% and missing the following:

- 1-Inappropriate selection of antimicrobials for treatment of neonatal meningitis.
- 2-No reporting of tests used for identification of isolates and the results of the test
- 3-Missing detection of group A beta hemolytic streptococci in sample e

Suggested improvement:

- appropriate selection of antimicrobials for treatment of a case of meningitis and according to CLSI 2018
- 2- Check appropriate culture, incubation conditions and temperature and interpretation of organism in sample e

RL15: Showed score 68%, missing the following:

- 1-Missing identification of candida species or as candida non-albicans with no reporting of colony morphology or tests used for identification or their results as requested
- 2- Failed detection of the presence of group A beta hemolytic streptococci

Suggested improvement

- 1-Candida species identification or even as candida non-albicans by Germ tube test performance
- Check appropriate culture, incubation conditions, temperature and interpretation of organisms like Streptococci sample e

RL16: Showed score 70% missing the following:

- 1- Missing identification of other 2 pathogens in sample c
- 2-Missing detection of the presence of group A beta hemolytic streptococci

Suggested improvement:

- 1- Proper culture technique for good separation of colonies and better identification of all pathogens with appropriate tests for identifications and biochemical reactions.
- 2- Check appropriate culture, incubation conditions and temperature and interpretation of organism in sample e

RL18: Showed score 15% missing the following:

- 1-incorrect identification of pathogen in sample a with no reporting of tests used for identification

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 21 of 27			

2-Inappropriate choice of antimicrobials for treatment of a case of neonatal meningitis and selection was not following to CLSI 2018

3-No reporting of pathogen identified in sample b with failed tests used for identification of Proteus and inappropriate choice of antimicrobials

3-Wrong identification of all the three pathogens in sample c

4-Failure of growth of candida parapsilosis

5-Failure detection of group A beta hemolytic streptococci in sample e

Suggested improvement:

1- Proper culture technique for good separation of colonies and better identification of all pathogens with appropriate tests for identifications and biochemical reactions

2-Appropriate choice of antimicrobials used in case of neonatal meningitis and according to CLSI 2018

3-better interpretation of colony morphology and BR. Results

4- Check appropriate culture, incubation conditions and temperature and interpretation of organism in sample e

PT- Unit team appreciate your participation and encourage you to persist and consider this as baseline to show your upgrade and effort.

Conclusion:

Twelve laboratories out of nineteen pass successfully the cut off and showed excellent laboratory results only one laboratory showed overall score 99.5% same like RLEUH-PT Unit results, one laboratory showed score <40% & one laboratory showed score <20%

Annex 1: Detailed score of samples, ML-01-2021(a,b,c,d,e).

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	  RLEUH PTU
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 22 of 27			

Please send any comments or suggestions regarding this report or
RLEUH-PTU program
through the following

Post Code :11588, Cairo, EGYPT

Email: uhd@scu.eg- ipcu@scu.eg

URL: www.scu.eg

Tel.: 02 24025537

It is an honor to receive your feedback or complains (attached form)

Signature of issue person: *Dr. Ghada Ismail*

Date of issue: 10/6/2021

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	 EGAC Accredited Proficiency Testing Unit CAB # 719002	 RLEUH PTU
Issue / Rev. No.	02/00			
Issue Date	02/06/2020			
Issued by	RLEUH director			
Approved by	Secretary SCUH			
Approval date	02/06/2020			
RLEUH- PTP Report				
Page 23 of 27				

Annex 1: Detailed score of samples, ML-01-2021(a,b,c,d,e).

Laboratory Code	Pathogen	ID test	morphology	gram stain	Abic selection	Abic interpretation	ESBL	Carbapenemase	Scores ML-01-a
RL01a	5	0	2	2	3	6	1	0	19
RL01b	5	0	2	2	3	6	1	0	19
RL02	3	2	2	2	2	5	0	0	16
RL03	5	0	2	2	3	6	1	0	19
RL04	5	0	2	2	3	6	1	1	20
RL05	3	2	2	2	1	5	1	1	17
RL06	3	1	1.5	2	3	6	1	1	18.5
RL07	5	0	0	2	2	5	1	1	16
RL08	5	0	1.5	2	1.5	3	0	0	13
RL09	5	0	2	2	2.5	6	1	1	19.5
RL10	5	0	1.5	2	3	6	1	1	19.5
RL11	3	2	2	2	2	4	1	0	16
RL12	5	0	2	2	2.5	5	1	0	17.5
RL13	3	1	2	2	1	4	0	0	13
RL14	5	0	2	2	1.5	4	1	1	16.5
RL15	3	1.5	2	2	3	6	1	0	18.5
RL16	5	0	1.5	2	2.5	5.5	1	1	18.5
RL17	5	0	2	2	2	5	1	1	18
RL18	0	1	1	2	1	2	0	0	7
RL19	3	2	2	2	3	6	1	1	20

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	 EGAC Accredited Proficiency Testing Unit CAB # 719002	 RLEUH PTU
Issue / Rev. No.	02/00			
Issue Date	02/06/2020			
Issued by	RLEUH director			
Approved by	Secretary SCUH			
Approval date	02/06/2020			
RLEUH- PTP Report				
Page 24 of 27				

Laboratory Code	Pathogen	ID test	Morphology	Gram stain	colony count	Abic Select	Abic Interpret	ESBL interpr	carbapenem	Total Score ML-01-b
RL01a	5	0	2	2	2	3	4	1	0	19
RL01b	5	0	2	2	2	3	4	1	0	19
RL02	2	2	2	2	2	2.5	3.5	0	0	16
RL03	5	0	2	2	2	3	4	1	0	19
RL04	5	0	2	2	2	3	4	1	1	20
RL05	2	1.5	2	2	2	3	4	1	1	18.5
RL06	3	2	2	2	2	3	4	1	1	20
RL07	5	0	2	2	1	3	4	1	1	19
RL08	5	0	1	2	0	1	2	0	0	11
RL09	5	0	2	2	2	3	4	1	1	20
RL10	5	0	2	2	2	3	4	1	1	20
RL11	0	1	0.5	1	2	3	2	1	0	10.5
RL12	5	0	2	2	2	3	4	0	0	18
RL13	3	1	2	2	2	2.5	3.5	0	0	16
RL14	5	0	2	2	2	3	4	1	1	20
RL15	3	1.5	2	2	2	3	4	1	0	18.5
RL16	5	0	2	2	2	3	4	1	1	20
RL17	5	0	2	2	2	2.5	3.5	1	1	19
RL18	0	0	0	0	0	0	0	0	0	2
RL19	5	0	2	2	2	3	4	1	1	20

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	 EGAC Accredited Proficiency Testing Unit CAB # 719002	 RLEUH PTU
Issue / Rev. No.	02/00			
Issue Date	02/06/2020			
Issued by	RLEUH director			
Approved by	Secretary SCUH			
Approval date	02/06/2020			
RLEUH- PTP Report				
Page 25 of 27				

Laboratory Code	Pathogen	ID test	Morphology	Gram stain	Scores ML-01-c
RL01a	9	6	1	3	19
RL01b	9	6	1	3	19
RL02	0	2	1	2	5
RL03	7.5	6	2	3	18.5
RL04	9	6	1	3	19
RL05	4.5	3.5	2	2	12
RL06	7.5	3.5	2	3	16
RL07	8	5	1	2	16
RL08	4.5	0	1	2	7.5
RL09	9	0	1.5	2	12.5
RL10	9	6	2	3	20
RL11	3	2	2	2	9
RL12	6	1	1	3	11
RL13	7.5	5.5	0	3	16
RL14	9	6	1	3	19
RL15	7.5	2	5.5	3	18
RL16	4.5	2	1	1	8.5
RL17	8	4	2	0	14
RL18	0	2	2	1	6
RL19	6	6	2	2	16

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 26 of 27			

Laboratory Code	Pathogen	Germ tube test	Germ tube interpret	Media used	Morphology	Gram Stain	Colony count	Scores ML-01-d
RL01a	14	0	0	0.5	1	2	0	17.5
RL01b	14	0	0	0.5	1	2	0	17.5
RL02	8	0.5	1	2	2	1	0	14.5
RL03	8	0.5	2	2	2	2	0	16.5
RL04	14	0	0	1	2	2	1	20
RL05	8	1	2	2	2	2	1	18
RL06	8	1	1	2	2	2	0	16
RL07	8	2	2	2	2	2	0	18
RL08	5	0	0	0.5	1	0	0	6.5
RL09	5	2	0	0.5	1.5	2	0	11
RL10	14	0	0	1	2	2	1	20
RL11	5	1	2	2	0	2	1	13
RL12	6	1	2	2	2	2	1	16
RL13	8	0.5	1	0	0	2	1	12.5
RL14	8	1	2	2	2	2	1	18
RL15	5	0.5	0	0	0	1.5	1	8
RL16	14	0	0	1	2	2	1	20
RL17	10	1	2	2	2	2	1	20
RL18	0	0	0	0	0	0	0	0
RL19	14	0	0	1	2	2	1	20

Form Code	RL-RP 017/F01	المجلس الأعلى للمستشفيات الجامعية Proficiency Testing Unit Reference laboratory for Egyptian University Hospitals	 EGAC Accredited Proficiency Testing Unit CAB # 719002
Issue / Rev. No.	02/00		
Issue Date	02/06/2020		
Issued by	RLEUH director		
Approved by	Secretary SCUH		
Approval date	02/06/2020		
RLEUH- PTP Report			
Page 27 of 27			

Laboratory Code	Pathogen	ID test	Morphology	Gram Stain	Scores ML-01-e
RL01a	16.5	0	1.5	2	20
RL01b	16.5	0	1.5	2	20
RL02	9	4	1.5	2	16.5
RL03	16.5	0	1.5	2	20
RL04	16.5	0	1.5	2	20
RL05	9	5	1.5	2	17.5
RL06	9	5	1.5	2	17.5
RL07	0	0	0	2	2
RL08	0	0	0	0	0
RL09	16.5	0	1.5	2	20
RL10	16.5	0	1.5	2	20
RL11	0	5	1	2	8
RL12	9	5	1.5	2	17.5
RL13	0	0	0	2	2
RL14	16.5	0	1	2	19.5
RL15	0	2	1	2	5
RL16	0	0	1	2	3
RL17	9	3	1.5	2	15.5
RL18	0	0	0	2	2
RL19	9	5	1.5	2	17.5

ML-1-c

Tests	organism name							
Pathogen Identification	E coli							
	Enterococcus fecalis							
	Salmonella spp							
ID media								
Colony morphology on Blood agar:	E coli	Whitish non hemolytic colonies						
	Enterococcus fecalis	grayish small non hemolytic colonies						
	Salmonella spp	Whitish non hemolytic colonies						
Colony morphology on	E coli	lactose fermenting colonies						
morphology on	Salmonella spp	Non lactose fermenting colonies						
ID tests	E coli	citrate positive, urease negative, TSI A/A gas no H ₂ S, LIA negative, SIM motile and indole positive,						
	Enterococcus fecalis	Cat negative, BE positive, soluble in 6.5% NaCl, sutrim resistant,						
	Salmonella spp	TSI Alk/Acid plus H ₂ S , Citrate and urease -ve, Motile , positive decarboxylation plus H ₂ S						
Gram Stain /Morphology	E coli	Gram negative bacilli						
	Enterococcus fecalis	Gram positive cocci in chains						
	Salmonella spp	Gram negative bacilli						
Data entry:	Dr. Ghada Egendy							
Validated by:	Dr. Abeer Elsayed							
Revised By:	Dr. Nashwa Naguib							
Approved by:	Prof.Ghada Ismail							

[illegible]

ML-01-d

Tests	organism name
Pathogen Identification	Candida Parapsilosis
ID media	
Colony morphology on Sabaroud's dextrose and blood agar	Creamy white colonies
ID tests	
Germ tube test	Negative
Gram Stain /Morphology	Gram positive Budding yeast
Colony count	>104 CFU/ml
Data entry:	Dr. Ghada Egendy
Validated by:	Dr. Abeer Elsayed
Revised By:	Dr. Nashwa Naguib
Approved by:	Prof.Ghada Ismail

HOMOGENIETY AND STABILITY OF SAMPLES ML-01 C,D,E -2021

Replicate1	R2	R3	R4	R5	R6	R7	R8	R9	R10	R11	R12	R13	R14	R15	R16	R17	R18	R19	R20	Reproducibility	P1	P2	P3	P4	P6	P7	P8	P9	Stability S1	S2	S3	S4	homogeneity	Stability		
OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK	OK
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ML-01-e

Tests	organism name
Pathogen Identification	group A beta hemolytic streptococcus pyogenes
ID media	
Colony morphology on Blood agar	Beta hemolytic small colonies
ID tests	
Catalase test	Negative
BE test	negative
Bacitracin disc	sensitive
Gram Stain /Morphology	Gram positive cocci, single or in chain
Data entry:	Dr. Ghada Egendy
Validated by:	Dr. Abeer Elsayed
Revised By:	Dr. Nashwa Naguib
Approved by:	Prof.Ghada Ismail

HOMOGENIETY AND STABILITY OF SAMPLES ML-01 C,D,E -2021

Replacet1	R2	R3	R4	R5	R6	R7	R8	R9	R10	R11	R12	R13	R14	R15	R16	R17	R18	R19	R20	roducibility	P2	P3	P4	P6	P7	P8	P9	Stability S1	S2	S3	S4	homogenit	Stability	
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