

**Administration Office**

c/o EMQN CIC, Unit 4, Enterprise House  
Manchester Science Park Pencroft Way,  
Manchester, M15 6SE, United Kingdom.  
Tel: +44 161 757 4952  
Fax: +44 161 850 1145  
Email: [admin@erndim.org](mailto:admin@erndim.org)

**Scientific Advisor**

Dr Sabine Scholl-Bürgi  
Tirol Kliniken  
Anichstr. 35, A-6020 Innsbruck  
Austria  
Tel: +43 512 504 23600  
Fax: +43 512 504 25886  
Email: [sabine.scholl-buergi@tirol-kliniken.at](mailto:sabine.scholl-buergi@tirol-kliniken.at)

**Scheme Organisers**

**Administration Office**

c/o EMQN CIC, Unit 4, Enterprise House  
Manchester Science Park Pencroft Way,  
Manchester, M15 6SE, United Kingdom.  
Tel: +44 161 757 4952  
Fax: +44 161 850 1145  
Email: [admin@erndim.org](mailto:admin@erndim.org)

## 2023 First Round Interim Report (DOC5136)

Version Number<sup>1</sup>: 01

Date of issue: 8<sup>th</sup> September 2023

**ERNDIM Code:**

**Please Note:**

- This interim report is intended for participants of the ERNDIM AAI scheme. The contents should not be used for any publication without permission of the Scientific Advisor.
- **This is an interim report and it includes provisional scores only.** All scores are subject to change following moderation at the Scientific Advisory Board meeting in autumn of this year. For final scores and performance data the ERNDIM AAI Annual Report should be referred to.
- The fact that your laboratory participates in this scheme is not confidential, however, the raw data and performance scores are confidential and will only be shared within ERNDIM for the purpose of evaluating your laboratories performance, unless ERNDIM is required to disclose performance data by a relevant government agency. For details please see the ERNDIM Privacy Policy on [www.erndim.org](http://www.erndim.org).

### 1. Results Submission

The deadline for submission of the 2023 first round results was 30<sup>th</sup> May 2023. Participants were able to view the cases and submit their results using the ERNDIM Formdesk website.

135 laboratories registered for the 2023 AAI scheme, of these 131 labs (97%) submitted results for the first round.

### 2. Scoring System

As for the previous circulations, each of the three aspects, analytical findings, diagnosis, and further tests, were scored equally with a maximum of two points for each category. Plasma amino acid concentrations together with the laboratories reference ranges were provided.

The tables (Table 1-3) show scoring to which the evaluators agreed previously. Scoring was done by two blinded evaluators each (the evaluators were blinded to both, the ERN number and to the scores of the second evaluator). If the scores were not concordant the scheme advisor scored in addition. Further close evaluation based on agreed/revised scoring criteria was used to determine on the final score.

Part. No.	Case 1 abnormalities, scoring by	1	2	3	2023.01 abnormalities	Case 1 diagnosis, scoring by	1	2	3	2023.01 diagnosis	Case 1 further testing recommendations, scoring by	1	2	3	2023.01 recommendations	Critical Error (participant overbook UCD)	2023.01 Sum
	elevated gln and ala 1 point, low cit 1 point, maximum 2 points					urea cycle, CPS, OTC, NAGS deficiency each 1 point, maximum 2 points					each 1 point (maximum 2 points): orotic acid, organic acids in urine, molecular genetic analyses of UCD genes, enzymatic analyses of UCD enzymes						
x	Hyperammonemia Metabolic acidosis Gln, Glu increased (hyperammonemia) Ala, Pro increased (hyperlactatemia) Cit, Arg decreased! Lys increased	●	●	●	2.0	Hyperammonemia probably due to OTC deficiency, DD CPS1 deficiency, NAGS deficiency	●	●	●	2.0	Analyse orotic acid in urine Organic acids in urine Acylcarnitine in blood Confirm diagnosis with genetic/enzymatic testing	●	●	●	2.0	no	6.0

Figure 1: Example of scoring for case 2023-1.

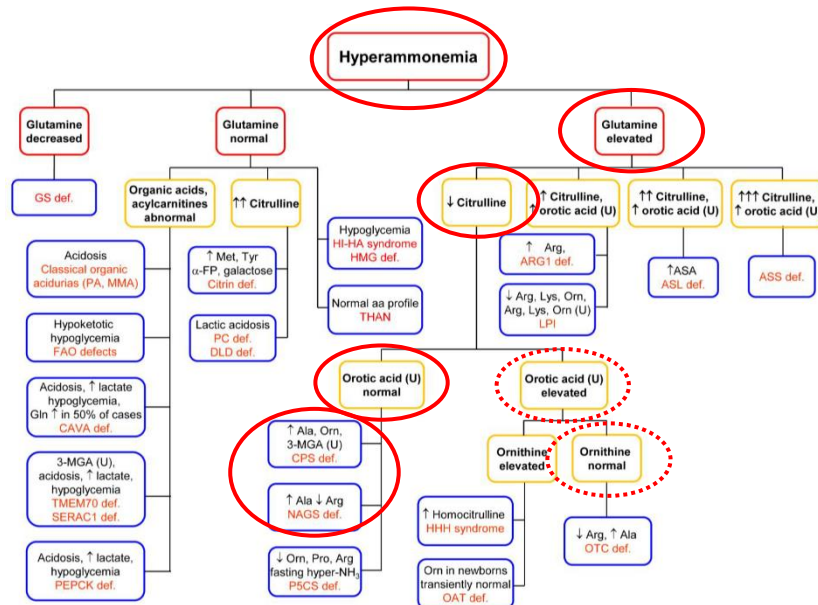
<sup>1</sup> If this Report is not Version 1 for this scheme year, go to APPENDIX 2 (page 9) for details of the changes made since the last version of this document.

### 3. Results of samples and evaluation of reporting

#### 3.1. Case 2023-1: Carbamylphosphat synthetase deficiency (CPS deficiency)

##### 3.1.1. Sample Details

The results provided were from a boy on the 2nd day of life, who has to be resuscitated for a short time during ventricular fibrillation. As sepsis was suspected, empirical antibiotic therapy was started. Because infection parameters were negative a metabolic work up was performed, which showed a hyperammonemia with ammonia concentrations up to max. 2700 µmol/l. Plasma amino acid profile revealed beside elevated glutamine and alanine, low citrulline concentration. No orotic acid excretion detectable (not reported here). Carbamylphosphat synthetase deficiency (CPS deficiency) was confirmed by the detection of two pathogenic nonsense mutations.



Investigations in plasma if not stated otherwise; U: urine; 3-MGA: 3-methylglutaconic aciduria (Rokicki et al. 2017) |

**Figure 2:** Application of the diagnostic algorithm on case 1, as concentration of orotic acid was not reported OTC, NAGS or CPS deficiency would be possible (see: [UCD GUIDELINE – 1st REVISION 2018 \(awmf.org\)](https://www.awmf.org/))

##### 3.1.2. Scoring details

**Table 1:** Scoring details for case 2023-1.

	Interpretation		Score (points)
<b>Findings, abnormalities [A, maximum 2 points]</b>	elevated	gln, ala	1
	low	cit	1
<b>Diagnosis [D, maximum 2 points]</b>	proximal urea cycle deficiency		2
	urea cycle deficiency		1
	CPS deficiency		1
	OTC deficiency		1
	NAGS deficiency		1
	CAVA deficiency		1
<b>Further tests (if molecular genetics recommended, specify the gene) [R, maximum 2 points]</b>	orotic acid, organic acids in urine		1
	molecular genetic analyses of UCD genes		1
	enzymatic analyses of UCD enzymes		1

Scores for participating laboratories are in APPENDIX 1 on page 6.

##### 3.1.3. Comments on overall performance

Overall proficiency was 95%. The proficiency for diagnosis was lowest at 90%, the most common "misdiagnosis" was carbonic anhydrase VA (CA-VA) deficiency.

### 3.1.4. Best interpretation (scored with 2 points each)

- **Findings:** There is a very strong hyperammonaemia with an elevated glutamine, glutamate, alanine, proline and lysine. Citrulline is non-detectable and arginine is low. Argininosuccinate is not reported (Lab. 37).
- **Diagnosis:** Ornithine transcarbamylase (OTC), carbamoyl phosphate synthetase (CPS), or N-acetyl glutamate synthase (NAGS) deficiency. Elevated lysine may be secondary to shortage of alpha-ketoglutarate (Lab. 116).
- **Further tests:** Determination of orotic acid. If orotic acid is high: enzymatic activity in liver and mutational analysis of OTC gene. If orotic acid is low: mutational analysis of CPS1 and NAGS gene. Organic acids in urine (Lab. 40).

## 3.2. Case 2023-2: Adenosine kinase deficiency

### 3.2.1. Sample details

The results of the amino acid analysis in plasma were obtained from a 2.5 month old boy who presented with cholestatic jaundice with normal coloured stools, hepatomegaly, global muscular hypotonia and eye movement disorders. He also had dysmorphic features such as micrognathia, high arched palate and unique transverse palmar folds. Adenosine kinase deficiency has been shown to be the cause of the clinical symptoms and biochemical changes.

### 3.2.2. Scoring details

**Table 2:** Scoring details for case 2023-2.

	Interpretation		Score (points)
<b>Findings, abnormalities [A, maximum 2 points]</b>	elevated	met	1
	elevated	tyr, thr	1
	normal	cit	
	elevated (unspecific)	lys	
<b>Diagnosis [D, maximum 2 points]</b>	Hepatic dysfunction leading to increased met and tyr		1
	Adenosine kinase deficiency		2
	Tyrosinaemia type I		1
	MAT I/III		
<b>Further tests (if molecular genetics recommended, specify the gene) [R, maximum 2 points]</b>	homocysteine		1
	SAH/SAM		1
	organic acids		1
	molecular genetic analysis ( <i>ADK, MATI/III</i> )		1

Scores for participating laboratories are in APPENDIX 1 on page 6.

### 3.2.3. Comments on overall performance

The overall proficiency is relatively low at 88%, whereas the description of the laboratory results was correct in almost 99% of the participants. Almost all laboratories recognised the abnormalities with significantly elevated methionine and tyrosine concentrations. Proficiency in interpreting the results was low at 84%. The proficiency of the recommendation was also low (81%). This may be due to the fact that the constellation of findings allowed two directions of interpretation (with different recommendations), first a liver disease, then methionine degradation disorders including an adenosine kinase deficiency.

### 3.2.4. Best interpretation (scored with 2 points each)

- **Findings:** Markedly increased tyrosine, methionine and moderately increased threonine and slightly increased lysine, ornithine, arginine (Lab. 121).
- **Diagnosis:** Results together with clinical suggest adenosine kinase deficiency. Need to exclude tyrosinaemia type-1 as a cause of liver dysfunction. Consider congenital disorders of glycosylation (Lab. 20).
- **Further tests:** Analyse SAM, SAH in blood, analyse homocysteine in blood, analyse succinylacetone in blood, confirm diagnosis with genetic testing (Lab. 2).

### 3.3. Case 2023-3: Classical MSUD

#### 3.3.1. Sample details

The results of the amino acid analysis in plasma were obtained from ten days old girl with cerebral seizures, somnolence, shrill screaming and weight loss (ammonia 160  $\mu\text{mol/L}$ ). Based on the results of the analysis of plasma amino acids and organic acids, the diagnosis of MSUD was made and confirmed by molecular genetics.

#### 3.3.2. Scoring details

**Table 3:** Scoring details for case 2023-3.

	Interpretation		Score (points)
	<b>Findings, abnormalities [A, maximum 2 points]</b>	elevated	leu, ile, val
elevated		allo ile	1
low		ala	1
<b>Diagnosis [D, maximum 2 points]</b>	MSUD		2
<b>Further tests</b> (if molecular genetics recommended, specify the gene) <b>[R, maximum 2 points]</b>	organic acids in urine		1
	molecular genetic analyses of <i>BCKDC</i>		1
	enzymatic analyses of BCKDC		1

Scores for participating laboratories are in APPENDIX 1 on page 6.

#### 3.3.3. Comments on overall performance

The overall performance was very good with 97%. All participants made the right diagnosis! This was due to the clear and well-known abnormalities in the plasma aminogram. Some of the recommendations for further examinations only included the recommendation to carry out a genetic examination. There was no mention of which gene should be examined, nor was there any mention of other examinations such as the analysis of organic acids. For this reason, some participants lost points, but overall the performance was also high with 92%.

#### 3.3.4. Best interpretation (scored with 2 points each)

- **Findings:** Markedly elevated branched-chain amino acids (leucine, valine, isoleucine) including alloisoleucine. Low alanine, borderline low glutamine (Lab. 124).
- **Diagnosis:** Increased branched chain amino acids with pathognomonic increase of allo-isoleucine are diagnostic for Maple Syrup Urine Disease (MSUD). Clinical information is consistent with this diagnosis. (Lab. 4)
- **Further tests:** Urine organic acid profile analysis. Analysis of the genes encoding subunits of the BCKD complex. (If necessary, enzymatic assay of complex activity in cultured fibroblasts.) (Lab. 5)

### 3.4. Comments on the whole of the first circulation results 2023

Overall, the number of participants is pleasingly high. Four out of 135 participants did not enter any results.

In order to make the evaluation system transparent, the evaluation was determined before the test and is included in the report. There was a high level of agreement between the scorers. In the first round of this interpretation scheme, there were two clear cases (1 and 3) and one "difficult" case (2). This is reflected in the respective performance. However, the overall performance across all results is good at 93%.

**Table 4:** Laboratory methods for the analysis of amino acids used by the participants

Method	No of responses
Ion-exchange chrom Ninhydrin 0 Int. Std	8
Ion-exchange chrom Ninhydrin 1/2 Int. Std	42
LC-MS	6
LC-MS/MS	56
Reverse phase HPLC/UPLC with non MS detection	15
Other	4
<b>Total</b>	<b>131</b>

**Table 5:** Overall scores for the first circulation in the amino acid interpretation scheme

	2023.01				2023.02				2023.03				2023.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Totals
<b>Total Points</b>	258	237	250	<b>745</b>	260	220	212	<b>692</b>	259	262	241	<b>762</b>	<b>2199</b>
<b>% proficiency</b>	98%	90%	95%	<b>95%</b>	99%	84%	81%	<b>88%</b>	99%	100%	92%	<b>97%</b>	<b>93%</b>

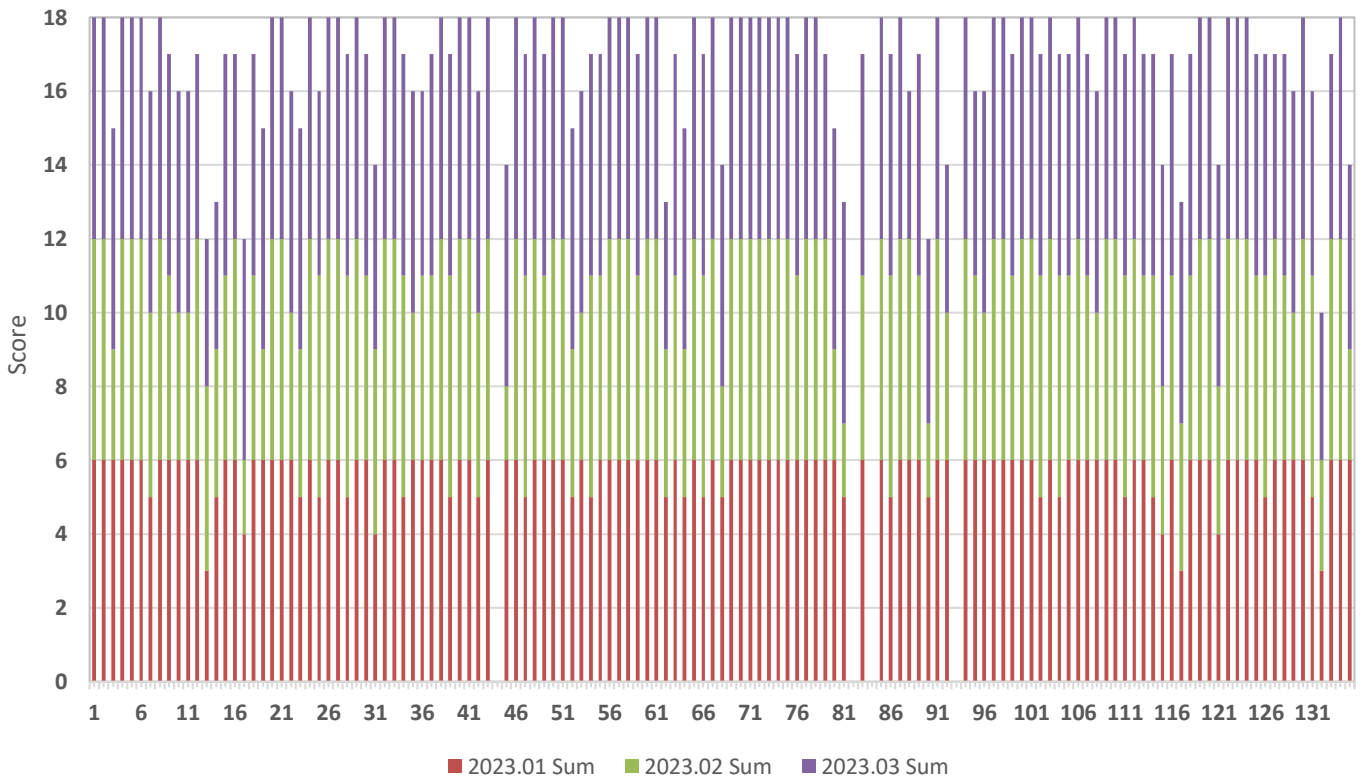
**Key**

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

Results first circulation Amino Acid Interpretation scheme 2023



**Figure 3:** Detailed scores for the first circulation in the amino acid interpretation scheme

*We encourage participants to send us comments and suggestions regarding this scheme and do not hesitate to contact us if you question any of our scoring.*

Date: 08 September 2023

The Scientific Evaluators

Sabine Scholl-Bürgi, Scientific Advisor

Scheme Assessors: Brian Fowler, Rachel Carling, Mary Anne Preece, Daniela Karall, Apolline Imbard and Olivier Braissant

**APPENDIX 1. Detailed scores for submitting laboratories****Key**

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

DNS = did not submit any results

Your laboratory's anonymised lab number in the table below is: XX

Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
1	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
2	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
3	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	15.0
4	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
5	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
6	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
7	2.0	1.0	2.0	5.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	16.0
8	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
9	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
10	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
11	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
12	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	17.0
13	1.0	1.0	1.0	3.0	2.0	2.0	1.0	5.0	2.0	2.0	0.0	4.0	12.0
14	2.0	2.0	1.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	0.0	4.0	13.0
15	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
16	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	17.0
17	2.0	1.0	1.0	4.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	12.0
18	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
19	2.0	2.0	2.0	6.0	1.0	0.0	2.0	3.0	2.0	2.0	2.0	6.0	15.0
20	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
21	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
22	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
23	2.0	2.0	1.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	15.0
24	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
25	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	16.0
26	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
27	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
28	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
29	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
30	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
31	2.0	1.0	1.0	4.0	2.0	1.0	2.0	5.0	2.0	2.0	1.0	5.0	14.0
32	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
33	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
34	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
35	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
36	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	1.0	5.0	16.0

Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
37	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
38	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
39	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
40	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
41	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
42	2.0	1.0	2.0	5.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	16.0
43	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
44													DNS
45	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	14.0
46	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
47	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
48	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
49	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
50	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
51	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
52	2.0	1.0	2.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	15.0
53	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
54	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
55	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
56	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
57	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
58	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
59	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
60	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
61	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
62	2.0	2.0	1.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	0.0	4.0	13.0
63	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
64	2.0	1.0	2.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	15.0
65	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
66	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
67	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
68	2.0	1.0	2.0	5.0	2.0	0.0	1.0	3.0	2.0	2.0	2.0	6.0	14.0
69	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
70	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
71	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
72	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
73	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
74	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
75	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
76	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
77	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
78	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
79	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	17.0
80	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	15.0
81	2.0	1.0	2.0	5.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	13.0

Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
82													DNS
83	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
84													DNS
85	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
86	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
87	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
88	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	0.0	4.0	16.0
89	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
90	2.0	1.0	2.0	5.0	2.0	0.0	0.0	2.0	2.0	2.0	1.0	5.0	12.0
91	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
92	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	1.0	2.0	1.0	4.0	14.0
93													DNS
94	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
95	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	1.0	2.0	2.0	5.0	16.0
96	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
97	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
98	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
99	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
100	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
101	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
102	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
103	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
104	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
105	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
106	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
107	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
108	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
109	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
110	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
111	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
112	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
113	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
114	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
115	2.0	1.0	1.0	4.0	2.0	2.0	0.0	4.0	2.0	2.0	2.0	6.0	14.0
116	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
117	1.0	1.0	1.0	3.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	13.0
118	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
119	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
120	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
121	2.0	1.0	1.0	4.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	14.0
122	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
123	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
124	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
125	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
126	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0



Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
127	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	17.0
128	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
129	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	16.0
130	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
131	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	16.0
132	1.0	1.0	1.0	3.0	2.0	1.0	0.0	3.0	2.0	2.0	0.0	4.0	10.0
133	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	17.0
134	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
135	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	2.0	2.0	1.0	5.0	14.0

## APPENDIX 2. Change log (changes since the last version)

Version Number	Published	Amendments
1	08 September 2023	<ul style="list-style-type: none"> <li>2023 first round interim report published</li> </ul>

END OF REPORT