Amino Acids Interpretation (AAI) PILOT

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First Round Interim Report 2022 *(DOC5136)*

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Please Note:

- This interim report is intended for participants of the ERNDIM AAI Pilot 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 pilot 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.

1. Results Submission

The deadline for submission of the 2022 first round results was 7th March 2022. Participants were able to view the cases and submit their results using the ERNDIM Formdesk website.

105 laboratories registered for the 2022 AAI pilot scheme but only 99 labs (94%) 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.

Figure 1 shows an example of scoring

19	Elevated biomarkers of liver disease. Generalized hyperaminoacidemia with significant increase of tyrosine.	○	#	●	#	○	#	1,0	Tyrosinemia, type 1 (OMIN 276700) Tyrosinemia, type 2 (OMIN 276600) Tyrosinemia, type 3 (OMIN 276710)	○	#	○	#	○	#	1,0	Organic acid analysis: determination of succinylacetone in urine Genetic test Referral to metabolic team	○	#	●	#	○	#	1,0

Figure 1: Example of scoring for case 2022-1.

3. Results of samples and evaluation of reporting

3.1. Case 2022-1: Classical galactosemia with liver failure.

3.1.1. Sample Details

The results provided were from a boy with positive new-born screening due to slightly elevated galactose concentration (21.8 mg/dL, cut off 20 mg/dL). New-born screening was taken at the third day of life. A control was requested from the new-born screening laboratory. Amino acid concentrations were determined at the age of 11 days

[1] **If this Report is not Version 1 for this scheme year, go to APPENDIX 2 (page 8) for details of the changes made since the last version of this document.**

when the patient came to the emergency department due to vomiting, hyperbilirubinemia, and weight loss. Plasma amino acids showed as well as other elevated amino acids, elevated tyrosine (822 µmol/L) and phenylalanine (165 µmol/L) and low isoleucine concentrations (7 µmol/L). Additionally, activities of liver enzymes were elevated, and coagulation parameters were altered.

The diagnosis of classical galactosemia was confirmed by elevated galactose concentration, decreased GALT activity and mutation analysis showing compound heterozygosity for pathogenic mutations in the GALT-gene. Current treatment comprises lactose free, low galactose intake.

3.1.2. Scoring details

Table 1: Scoring details for case 2022-1.

	Interpretation		Score (points)
Findings, abnormalities [A, maximum 2 points]	Elevated	Tyr, phe	2
	Decreased	Ile	1
	Tyrosinemia		1
Diagnosis [D, maximum 2 points]	Galactosemia		2
	Liver failure not metabolic		1
	Molecular genetic investigation (tyr, gal)		1
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**	Succinylacetone in urine		1
	GALT activity		1
	Galactose-1-phosphate		1

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

3.1.3. Comments on overall performance

Overall proficiency was 80%. The diagnosis was difficult to make as two diagnoses were possible, tyrosinemia type I and classical galactosemia.

3.1.4. Best interpretation (scored with 2 points each)

- **Findings:** Tyrosine highly increased. Normal methionine. Slight increase of majority of amino acids (esp. phenylalanine). Signs of hepatic dysfunction.
- **Diagnosis**: Classical galactosemia. DD: transient neonatal tyrosinemia, tyrosinemia type I.
- **Further tests:** Reducing substances in urine, galactose-1-phosphate, GALT activity, organic acids profile and succinylacetone.

3.2. Case 2022-2: Prolidase deficiency

3.2.1. Sample details

The results were from a sample from a 14 years old boy presenting with splenomegaly (chronic EBV-infection and other infections), intermittent mild pancytopenia, mental retardation, dysmorphism since early childhood. The patient has prolidase deficiency due to a mutation in the *PEPD*-gene.

The chromatogram of the analysis was provided for the participants showing the typical unidentified/unusual peaks (iminodipeptides, see figure 2).

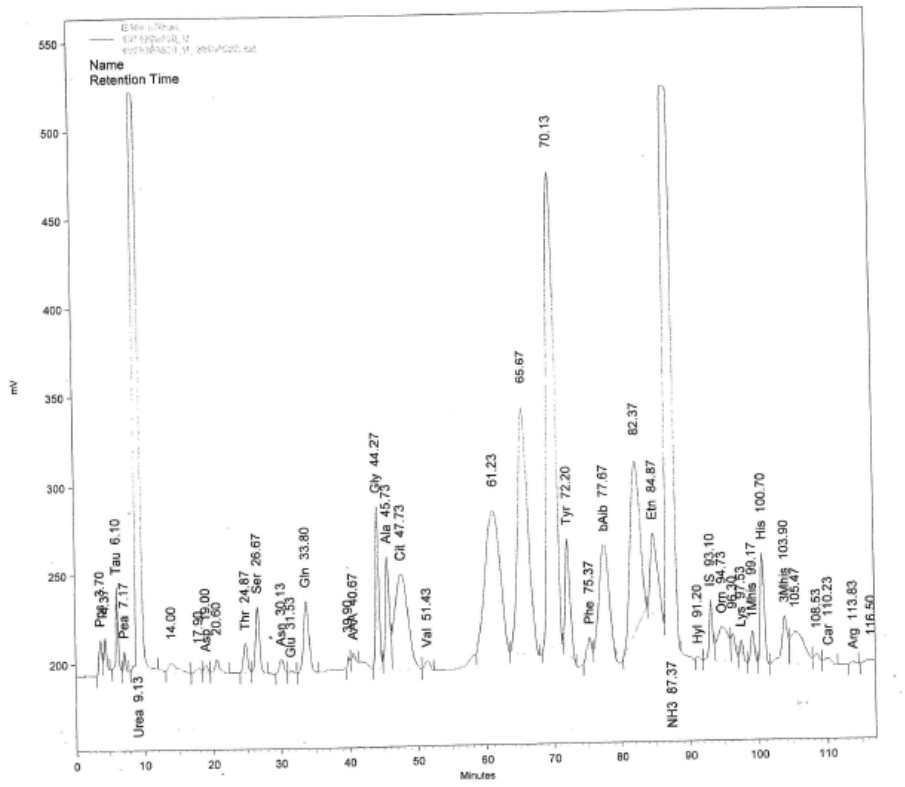

Figure 2: Chromatogram for case 2022-1, showing the unidentified peaks.

3.2.2. Scoring details

Table 2: Scoring details for case 2022-2.

	Interpretation		Score (points)
Findings, abnormalities [A, maximum 2 points]	Elevated	Tyr	1
	Detection of	Unidentified / unusual peaks	2
		iminodipeptides	2
Diagnosis [D, maximum 2 points]	Prolidase deficiency		2
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**	Acidic hydrolysis		1
	Molecular genetic analysis of *PEPD* gene		1
	Prolidase activity		1

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

3.2.3. Comments on overall performance

Performance was 60% for overall proficiency. This case was difficult for some of the participants as they don`t use “classical” amino acid analysis (HPLC with ninhydrin detection).

3.2.4. Best interpretation (scored with 2 points each)

- **Findings:** Iminodipeptiduria. Large and broad peaks in the positions of citrulline, cystine, methionine which are alanylproline and glycylproline.
- **Diagnosis:** Prolidase deficiency.
- **Further tests: Measure proline after acid hydrolysis of the urine. Molecular genetic studies in the PEPD gene.**

3.3. Case 2021-3: Hypotonia-cystinuria syndrome

3.3.1. Sample details

The sample was from a 6-month-old male who had muscular hypotonia ("floppy infant"), dystrophia and dysmorphism. Parents were consanguineous (cousins I°). The extended examination showed reduced tubular reabsorption of dibasic amino acids (COLA = cysteine, ornithine, lysine, and arginine). Later, it could be shown that

the patient had hypotonia-cystinuria syndrome with homozygous microdeletion of part of the *SLC3A1* and *PREPL* genes on chromosome 2p21. Patients with hypotonia-cystinuria syndrome show cystinuria, hypotonia, growth retardation, facial dysmorphism, mental retardation and later obesity (see Jaeken et al 2006).

3.3.2. Scoring details

Table 3: Scoring details for case 2022-3.

	Interpretation		Score (points)
Findings, abnormalities [A, maximum 2 points]	Elevated	Cys, orn, lys, arg	2
Diagnosis [D, maximum 2 points]	Cystinuria		1
	Hypotonia-cystinuria syndrome		2
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**	Molecular genetic analysis of PREPL gene		1
	WES, GCH array		2

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

3.3.3. Comments on overall performance

Overall proficiency was 82% although proficiency for further tests was low (72%).

3.3.4. Best interpretation (scored with 2 points each)

- **Findings:** Very high increase of urinary excretion of cystine, ornithine, lysine, and arginine. Really low tubular reabsorption for these amino acids.
- **Diagnosis:** Hypotonia-cystinuria syndrome.
- **Further tests:** Array-CGH analysis for search of a homozygous microdeletion in 2p21.

3.4. Comments on the whole of the first circulation results 2022

- The amino acid interpretation scheme is a pilot scheme with 105 participants.
- We tried to include cases where changes in amino acid concentrations can be primary or secondary to the underlying inborn disorder of metabolism.
- In case 2 (prolidase deficiency) a chromatogram was provided for HPLC with ninhydrin detection. Some of the participants don`t use this method. It has to be discussed how to proceed in the future with this situation.
- As well as testing the participants competence for more routine disorders, this scheme also aims to give them the opportunity of expanding their knowledge. Therefore, we included prolidase deficiency and hypotonia-cystinuria syndrome in this circulation. Additionally, we included the concept of “best interpretation”.

Table 4: Overall scores for the first circulation in the amino acid interpretation scheme

	2022.01				2022.02				2022.03				2022.01 - .03
	A	**D**	**R**	**Sum**	**A**	**D**	**R**	**Sum**	**A**	**D**	**R**	**Sum**	**Totals**
Total Points	175	154	145	**474**	150	118	108	**376**	198	163	143	**504**	**1354**
% proficiency	88%	78%	73%	**80%**	76%	60%	55%	**63%**	100%	82%	72%	**85%**	**76%**

Key

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

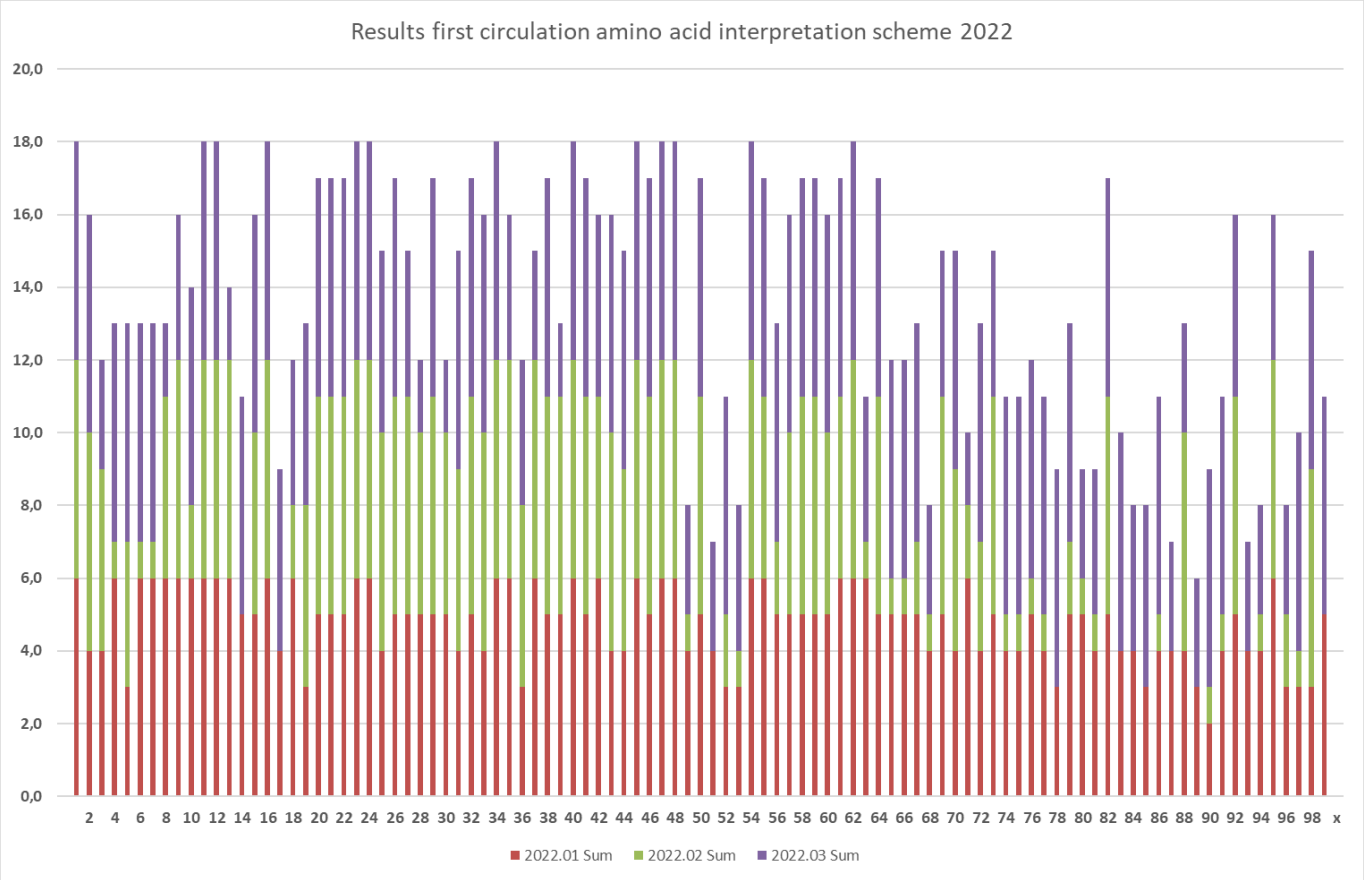

Figure 3: Detailed scores for the first circulation in the amino acid interpretation scheme

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: 08.07.2022

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

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

Anon. lab number	2022.01				2022.02				2022.03				2022.01 - .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	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**16.0**
3	2.0	1.0	1.0	**4.0**	1.0	2.0	2.0	**5.0**	2.0	1.0	0.0	**3.0**	**12.0**
4	2.0	2.0	2.0	**6.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**13.0**
5	1.0	1.0	1.0	**3.0**	2.0	2.0	0.0	**4.0**	2.0	2.0	2.0	**6.0**	**13.0**
6	2.0	2.0	2.0	**6.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**13.0**
7	2.0	2.0	2.0	**6.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**13.0**
8	2.0	2.0	2.0	**6.0**	2.0	2.0	1.0	**5.0**	2.0	0.0	0.0	**2.0**	**13.0**
9	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**
10	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**
11	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**
12	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**
13	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	**14.0**
14	2.0	1.0	2.0	**5.0**	0.0	0.0	0.0	**0.0**	2.0	2.0	2.0	**6.0**	**11.0**
15	2.0	1.0	2.0	**5.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**16.0**
16	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**
17	1.0	2.0	1.0	**4.0**	0.0	0.0	0.0	**0.0**	2.0	2.0	1.0	**5.0**	**9.0**
18	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	2.0	1.0	1.0	**4.0**	**12.0**
19	1.0	1.0	1.0	**3.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	1.0	**5.0**	**13.0**
20	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**
21	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**
22	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**
23	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**
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	1.0	**4.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	1.0	**5.0**	**15.0**
26	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**
27	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**15.0**
28	2.0	2.0	1.0	**5.0**	2.0	2.0	1.0	**5.0**	2.0	0.0	0.0	**2.0**	**12.0**
29	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**
30	1.0	2.0	2.0	**5.0**	2.0	2.0	1.0	**5.0**	2.0	0.0	0.0	**2.0**	**12.0**
31	1.0	2.0	1.0	**4.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**15.0**
32	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**
33	2.0	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**16.0**
34	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**
35	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
36	1.0	1.0	1.0	**3.0**	2.0	2.0	1.0	**5.0**	2.0	1.0	1.0	**4.0**	**12.0**
37	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	0.0	**3.0**	**15.0**

Anon. lab number	2022.01				2022.02				2022.03				2022.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
38	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**
39	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	**13.0**
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	1.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**17.0**
42	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**
43	1.0	1.0	2.0	**4.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**16.0**
44	1.0	2.0	1.0	**4.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**15.0**
45	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**
46	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**
47	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**
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	1.0	1.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	1.0	0.0	**3.0**	**8.0**
50	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**
51	2.0	1.0	1.0	**4.0**	0.0	0.0	0.0	**0.0**	2.0	1.0	0.0	**3.0**	**7.0**
52	1.0	1.0	1.0	**3.0**	2.0	0.0	0.0	**2.0**	2.0	2.0	2.0	**6.0**	**11.0**
53	1.0	1.0	1.0	**3.0**	1.0	0.0	0.0	**1.0**	2.0	1.0	1.0	**4.0**	**8.0**
54	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**
55	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**
56	2.0	2.0	1.0	**5.0**	1.0	0.0	1.0	**2.0**	2.0	2.0	2.0	**6.0**	**13.0**
57	2.0	2.0	1.0	**5.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**16.0**
58	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**
59	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**
60	2.0	1.0	2.0	**5.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**16.0**
61	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
62	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**
63	2.0	2.0	2.0	**6.0**	1.0	0.0	0.0	**1.0**	2.0	1.0	1.0	**4.0**	**11.0**
64	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**
65	2.0	2.0	1.0	**5.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**12.0**
66	2.0	2.0	1.0	**5.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**12.0**
67	1.0	2.0	2.0	**5.0**	2.0	0.0	0.0	**2.0**	2.0	2.0	2.0	**6.0**	**13.0**
68	2.0	1.0	1.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	1.0	0.0	**3.0**	**8.0**
69	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**15.0**
70	2.0	1.0	1.0	**4.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**15.0**
71	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	2.0	0.0	0.0	**2.0**	**10.0**
72	2.0	1.0	1.0	**4.0**	1.0	0.0	2.0	**3.0**	2.0	2.0	2.0	**6.0**	**13.0**
73	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**15.0**
74	2.0	1.0	1.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**11.0**
75	1.0	1.0	2.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**11.0**
76	2.0	2.0	1.0	**5.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**12.0**
77	2.0	1.0	1.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**11.0**
78	1.0	1.0	1.0	**3.0**	0.0	0.0	0.0	**0.0**	2.0	2.0	2.0	**6.0**	**9.0**
79	2.0	2.0	1.0	**5.0**	2.0	0.0	0.0	**2.0**	2.0	2.0	2.0	**6.0**	**13.0**
80	2.0	2.0	1.0	**5.0**	1.0	0.0	0.0	**1.0**	2.0	1.0	0.0	**3.0**	**9.0**
81	2.0	1.0	1.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	0.0	**4.0**	**9.0**
82	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**

Anon. lab number	2022.01				2022.02				2022.03				2022.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
83	2.0	1.0	1.0	**4.0**	0.0	0.0	0.0	**0.0**	2.0	2.0	2.0	**6.0**	**10.0**
84	1.0	1.0	2.0	**4.0**	0.0	0.0	0.0	**0.0**	2.0	1.0	1.0	**4.0**	**8.0**
85	2.0	0.0	1.0	**3.0**	0.0	0.0	0.0	**0.0**	2.0	2.0	1.0	**5.0**	**8.0**
86	2.0	1.0	1.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**11.0**
87	2.0	1.0	1.0	**4.0**	0.0	0.0	0.0	**0.0**	2.0	1.0	0.0	**3.0**	**7.0**
88	1.0	2.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	0.0	**3.0**	**13.0**
89	1.0	1.0	1.0	**3.0**	0.0	0.0	0.0	**0.0**	2.0	1.0	0.0	**3.0**	**6.0**
90	2.0	0.0	0.0	**2.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**9.0**
91	2.0	2.0	0.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**11.0**
92	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	**16.0**
93	2.0	1.0	1.0	**4.0**	0.0	0.0	0.0	**0.0**	2.0	1.0	0.0	**3.0**	**7.0**
94	1.0	2.0	1.0	**4.0**	1.0	0.0	0.0	**1.0**	2.0	1.0	0.0	**3.0**	**8.0**
95	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
96	2.0	1.0	0.0	**3.0**	1.0	0.0	1.0	**2.0**	2.0	1.0	0.0	**3.0**	**8.0**
97	1.0	1.0	1.0	**3.0**	1.0	0.0	0.0	**1.0**	2.0	2.0	2.0	**6.0**	**10.0**
98	1.0	1.0	1.0	**3.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**15.0**
99	1.0	2.0	2.0	**5.0**	0.0	0.0	0.0	**0.0**	2.0	2.0	2.0	**6.0**	**11.0**

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

Version Number	Published	Amendments
1	08 July 2022	• 2022 first round interim report published

END OF REPORT