Amino Acids Interpretation (AAI) Scheme

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2023 Second Round Interim Report *(DOC5149)*

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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.

1. Results Submission

The deadline for submission of the 2023 second round results was 19th September 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 128 labs (95%) submitted results for the second round.

Note: All results must be submitted in English.

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

49	Marked elevation of tyrosine, mildly elevated glutamic acid, proline, alanine, phenylalanine and ornithine. Arginine was low.	#	#	#	2,0	Tyrosinaemia type 2	#	#	#	2,0	Urine organic acids for tyrosine metabolites to confirm diagnosis and succinylacetone to exclude tyrosinaemia type 1 Enzyme study of TAT Molecular genetic analysis (TAT gene)	#	#	#	2,0

Figure 1: Example of scoring for case 2023.04

[1] **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 2023-4: Tyrosinemia type II (homozygous mutation in *TAT* gene)

3.1.1. Sample Details

The results provided are from seven years old boy with photophobia, eyes pain and visual impairment. The family history is unremarkable, except that the parents are cousins I° grade. The patient did not receive a new-born screening for tyrosinemia in his home country.

The diagnosis of tyrosinemia type II was confirmed by the detection of a homozygous mutation in the *TAT* gene. He received a phenylalanine/tyrosine defined diet after diagnosis. The goal is to keep the tyrosine concentration in the range below 500 µmol/L.

3.1.2. Scoring details

Table 1: Scoring details for case 2023.04

	interpretation		**scores (points)**
findings, abnormalities, maximum 2 points	elevated	tyr	2
diagnosis, maximum 2 points	tyrosinemia type II		2
	tyrosinemia		1
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	organic acids in urine (succinylacetone)		1
	molecular genetic analyses of *TAT*		2
	other tyrosinemia genes (III)		1

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

3.1.3. Comments on overall performance

Overall, the interpretation of the analysis results and the diagnosis were very good. The overall performance was 98%.

3.1.4. Best interpretation (scored with 2 points each)

- **Findings:** Grossly elevated concentration of tyrosine, methionine in the normal range.
- **Diagnosis**: Suspicion of tyrosinemia type II (OMIM 276600). Type I is not very probable as the normal pattern of other AA (methionine) speaks against liver involvement. Besides the that fact no crises are reported.
- **Further tests:** Diagnosis should be verified by analysis of organic acids in urine (detection of succinylacetone) and of the *TAT* gene. A low phenylalanine/tyrosine diet should be initiated.

3.2. Case 2023-5: Remethylation defect (CblC disease)

3.2.1. Sample details

The results provided are from a 55-year-old male patient with pulmonary microangiopathy and renal insufficiency 20 years post renal transplant. Renal insufficiency at 30 years that was not investigated for IEM and has led to a renal transplant.

3.2.2. Scoring details

Table 2: Scoring details for case 2023-5.

	interpretation		scores (points)
findings, abnormalities, maximum 2 points	low (normal)	met	1
	elevated	homocystine	1
diagnosis, maximum 2 points	Primary (IEM) remethylation defect		2
	Secondary (folate, B12, NO) remethylation defect		2
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	organic acids in urine (MMA, methylcitrate)		1
	acylcarnitine profile		
	total homocysteine		1
	folate, vitamin B12 concentration		1
	genes involved in remethylation defects		1
comments	genes involved in remethylation defect: *MTHFR, MMACHC, MMADHC, MTR, MTRR*		

Scores for participating laboratories are in APPENDIX 1 on page 6. Diagnosis of (mild) hyperhomocysteinaemia was scored only with one point.

3.2.3. Comments on overall performance

The overall performance at 94% was good. Nevertheless, the finding of clearly elevated free homocystine is almost certainly indicative of a genetic disorder rather than a secondary hyperhomocysteinaemia. Also, the low / normal methionine level points to a remethylation disorder. Thus, labs not referring to methionine were penalised as were those suggesting only mild/moderate hyperhomocysteinaemia.

3.2.4. Best interpretation (scored with 2 points each)

- **Findings:** The free homocystine was clearly elevated, with a low-normal methionine concentration. Concentrations of some other amino acids were also low to low-normal, i.e., serine, leucine, glutamic acid, arginine, and isoleucine.
- **Diagnosis:** DD for hyperhomocystinaemia with low-normal methionine levels:
  MTHFR deficiency
  MS deficiency
  Defect in Cbl metabolism (Cbl C, D, E, F, G; transcobalamin def; Imerslund syndrome)
  Deficiency of folic acid or vit B12 (nutritional)
  Remark: Homocysteinaemia might also be the result of renal insufficiency
- **Further tests:** Further testing of urine organic acid looking for methylmalonic acid and urine metabolic screen analysis, check total homocysteine in blood, active B12 and folate levels; WES/WGS testing and referral to the metabolic clinic.

3.3. Case 2023-6: Glutaminase deficiency

3.3.1. Sample details

The results provided are from a 3-year-old girl with developmental delay. (Note: In the first request form only developmental delay was noted. In the first clinical letter following symptoms were mentioned: Severe global developmental delay, hypotonia, MRI brain scan shows non-specific delay in maturation of myelination, intermittent tremor, and ataxia. (See van Kuilenburg et al Glutaminase deficiency caused by short tandem repeat expansion in GLS. NEJM 2019)

3.3.2. Scoring details

Table 3: Scoring details for case 2023-6.

	interpretation		scores (points)
findings, abnormalities, maximum 2 points	elevated	gln	2
diagnosis, maximum 2 points	glutaminase deficiency		2
	urea cycle disorder (but arginase def. 0 points)		1
	CAVA		1
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	organic acids		1
	orotic acid		
	molecular genetic analysis glutaminase deficiency		2
	CSF glutamine		1
	enzymatic analysis glutaminase		1

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

3.3.3. Comments on overall performance

This was only moderately good for a rather difficult sample (overall performance 82%). In this case the follow up investigations are important especially in the absence of a correct diagnosis.

3.3.4. Best interpretation (scored with 2 points each)

- **Findings:** Elevated glutamine and mild elevation of several other amino acids including alanine, glycine, proline, threonine, lysine, serine, and arginine
- **Diagnosis:** Very high level of Glutamine with normal ammonia led us to suspect glutaminase deficiency. Pyruvate carboxylase deficiency it is less likely because citrulline and ammonia is normal. If the patient is on glutamine supplementation, exclude mitochondrial disease.
- **Further tests:** Measure organic acids incl. orotic acid in urine, which are normal in published cases of glutaminase deficiency. Also perform genetic analysis to check for a trinucleotide repeat expansion (CGA)n in the glutaminase gene. If negative, consider whole exome sequencing and extended metabolic screening.

3.4. Comments on the whole of the second circulation results 2023

Generally, the overall performance was good although a few labs made inadequate or incorrect interpretation leading to reduced scores. In some cases these were considered to be critical errors.

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

	2023.04				2023.05				2023.06				2023.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Totals
Total Points	254	254	246	**754**	233	241	245	**719**	254	170	203	**627**	**2100**
% proficiency	99%	99%	96%	**98%**	91%	94%	96%	**94%**	99%	66%	79%	**82%**	**91%**

Key

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

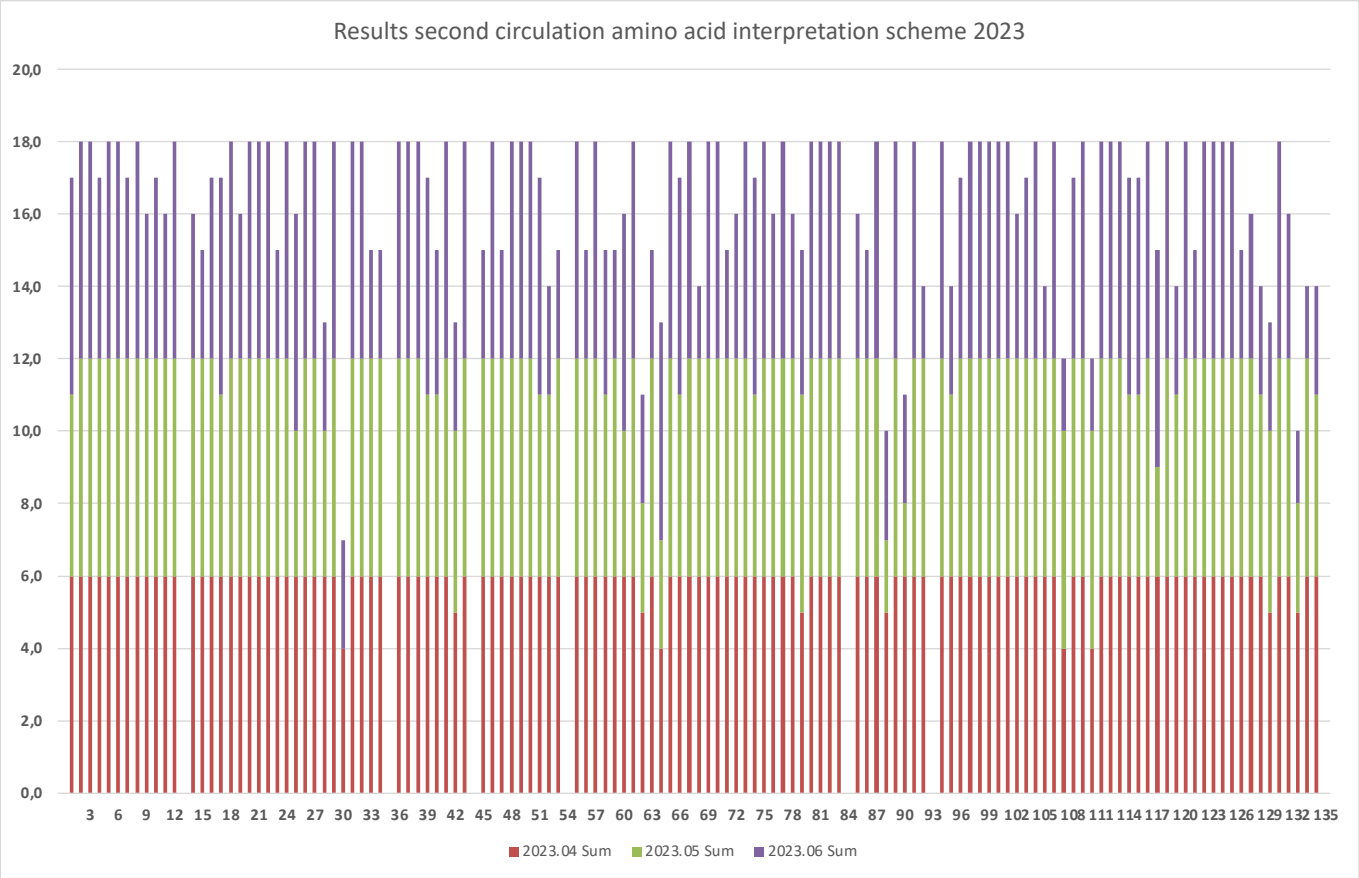

Figure 3: Detailed scores for the second circulation in the Amino Acid Interpretation scheme

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: 19.12.2023

The Scientific Evaluators

Sabine Scholl-Bürgi, Scientific Advisor
Scheme Assessors: Brian Fowler, Rachel Carling, Mary Anne Preece, Daniela Karall, Apolline Imbard, Olivier Braissant, Alistair Horman, Anke Schuhmann

APPENDIX 1. Detailed scores for submitting laboratories

Key

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

Anon. lab number	2023.04				2023.05				2023.06				2023.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
1	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
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
4	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	17.0
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	17.0
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	2.0	2.0	6.0	2.0	0.0	2.0	4.0	16.0
10	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	17.0
11	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
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													
14	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
15	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
16	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	17.0
17	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
18	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
19	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	2.0	4.0	16.0
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
23	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	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	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	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	2.0	2.0	6.0	1.0	1.0	2.0	4.0	2.0	0.0	1.0	3.0	13.0
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	1.0	1.0	4.0	0.0	0.0	0.0	0.0	2.0	0.0	1.0	3.0	7.0
31	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
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	0.0	1.0	3.0	15.0
34	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
35													
36	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
37	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
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	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

Anon. lab number	2023.04				2023.05				2023.06				2023.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
40	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	2.0	0.0	2.0	4.0	15.0
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	2.0	1.0	5.0	2.0	1.0	2.0	5.0	2.0	0.0	1.0	3.0	13.0
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													
45	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
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	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
52	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	2.0	1.0	0.0	3.0	14.0
53	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
54													
55	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
56	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
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	1.0	2.0	2.0	5.0	2.0	1.0	1.0	4.0	15.0
59	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
60	2.0	2.0	2.0	6.0	1.0	1.0	2.0	4.0	2.0	2.0	2.0	6.0	16.0
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	1.0	1.0	1.0	3.0	2.0	0.0	1.0	3.0	11.0
63	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
64	0.0	2.0	2.0	4.0	1.0	2.0	0.0	3.0	2.0	2.0	2.0	6.0	13.0
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	2.0	2.0	6.0	1.0	2.0	2.0	5.0	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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	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	0.0	1.0	3.0	15.0
72	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
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	1.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
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	2.0	6.0	2.0	1.0	1.0	4.0	16.0
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	1.0	1.0	4.0	16.0
79	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
80	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
81	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
82	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
83	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
84													

Anon. lab number	2023.04				2023.05				2023.06				2023.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
85	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
86	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
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	1.0	5.0	1.0	0.0	1.0	2.0	2.0	1.0	0.0	3.0	10.0
89	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
90	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	0.0	1.0	3.0	11.0
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	2.0	2.0	6.0	2.0	0.0	0.0	2.0	14.0
93													
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	2.0	0.0	1.0	3.0	14.0
96	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
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	2.0	6.0	2.0	2.0	2.0	6.0	18.0
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	16.0
103	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	17.0
104	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
105	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	0.0	1.0	1.0	2.0	14.0
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	1.0	1.0	4.0	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	12.0
108	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	17.0
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	0.0	4.0	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	12.0
111	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
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	2.0	6.0	2.0	2.0	2.0	6.0	18.0
114	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
115	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
116	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
117	2.0	2.0	2.0	6.0	1.0	1.0	1.0	3.0	2.0	2.0	2.0	6.0	15.0
118	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
119	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	2.0	0.0	1.0	3.0	14.0
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
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	2.0	6.0	2.0	2.0	2.0	6.0	18.0
126	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	1.0	3.0	15.0
127	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
128	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	2.0	0.0	1.0	3.0	14.0
129	2.0	2.0	1.0	5.0	1.0	2.0	2.0	5.0	2.0	0.0	1.0	3.0	13.0

Anon. lab number	2023.04				2023.05				2023.06				2023.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	16.0
132	2.0	2.0	1.0	5.0	1.0	1.0	1.0	3.0	2.0	0.0	0.0	2.0	10.0
133	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
134	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	2.0	0.0	1.0	3.0	14.0
135													

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

Version Number	Published	Amendments
1	21 December 2023	• 2023 second round interim report published

END OF REPORT