Amino Acids Interpretation (AAI) Scheme

Scheme Organisers
Administration Office
c c/o EMQN CIC Office, Third Floor, ICE Building
3 Exchange Quay, Salford, M5 3ED, United Kingdom
Tel: +44 161 757 4952
Fax: +44 161 850 1145
Email: 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

2025 First Round Interim Report *(DOC5136)*

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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 2025 first round results was 27th May 2025. Participants were able to view the cases and submit their results using the ERNDIM Formdesk website.

148 laboratories registered for the 2025 AAI scheme, of these 142 labs (96%) 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.

Case 1 abnormalities	1	2	7	2025.01 abnormalities	Case 1 diagnosis	1	2	7	2025.01 diagnosis	Case 1 further testing recommendations (Is the missing recommendation for ammonia determination a critical error? YES, if not UCD is suspected)	1	2	7	2025.01 recommendations
Each 1 point: elevated gln and/or ala, **low normal** arg and/or cit and/or orn, **maximum 2 points**					**OTC deficiency 2 points,** proximal urea cycle disorder 2 points, urea cycle disorder 1 point, mitochondrial dysfunction/disorder 1 point, CA-VA 1 point, **maximum 2 points**					**each 1 point (maximum 2 points):** ammonia, urea in plasma, orotic acid or organic acids in urine, uracil in urine, molecular genetic analysis of *OTC* gene/UCD genes				
Elevated concentration of Glutamine,Glutamic acid,Proline, Alanine. Citrulline, Arginine level in the low normal range.	2	2	2	2	Possible urea cycle disorder. The elevated glutamine and alanine and the low-normal levels of citrulline and arginine may reflect impaired flux through the urea cycle, possibly involving partial enzyme deficiency such as in NAGS deficiency, OTC deficiency, or other proximal defects	2	2	2	2	1. Plasma **ammonia** measurement (venous blood, processed immediately) 2. Liver function panel including urea, AST/ALT, lactate and pyruvate 3. Urine organic acid analysis (GC-MS) 4. Genetic testing: NGS panel targeting urea cycle	2	2	2	2

Figure 1: Example of scoring for case 2025-1.

[1] **If this Report is not Version 1 for this scheme year, go to APPENDIX 2 (page 10) for details of the changes made since the last version of this document.**

3. Results of samples and evaluation of reporting

3.1. Case 2025-1: Ornithine transcarbamylase deficiency (OTC deficiency)

3.1.1. Sample Details

The results are from an 18-months-old boy who was admitted to the emergency department due to vomiting and apathy. No previous illness was known. The medical history revealed that the boy had had recurrent episodes of clouding of consciousness for four months. The ammonia concentration was slightly elevated (137 µmol/L). The diagnosis was confirmed by molecular genetics (detection of a hemizygous mutation in the *OTC* gene). The therapy consists of a protein-defined diet with substitution of essential amino acids.

3.1.2. Scoring details

Table 1: Scoring details for case 2025-1.

	interpretation		scores (points)
findings, abnormalities, maximum 2 points	elevated	gln, ala	1
	elevated	glu, pro, gly, met	0
	(low) normal	arg, cit, orn	1
diagnosis, maximum 2 points	ornithine transcarbamylase deficiency		2
	proximal urea cycle disorder		2
	urea cycle disorder		1
	mitochondrial dysfunction/disorder		1
	carbonic anhydrase VA deficiency		1
	lysinuric protein intolerance		0
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	orotic acid in urine (organic acids in urine)		1
	uracil in urine		1
	ammonia in plasma, urea in plasma/serum		1
	genetic analysis of *OTC* gene (UCD genes)		1
comments	The clinical symptoms reported are very sparse, as is often the case in everyday clinical practice.		
critical error	If the participant does not recommend the ammonia determination and does not have a suspected diagnosis of an urea cycle defect, this is considered a critical error.		

Scores for participating laboratories are in APPENDIX 1 on page 7.

3.1.3. Comments on overall performance

Overall proficiency was 87%. The proficiency for abnormalities was lowest at 83%. The most common reason for a point deduction was the lack of indication that the concentrations of arginine and/or citrulline and/or ornithine were low normal.

This is a difficult case from everyday life, some points made the diagnosis difficult:

- The age of the child, as non-neonatal OTC deficiency is very rare.
- **It is also important to describe the low concentrations!** Therefore, in some cases there was only one point.
- **An increased glutamine concentration should in any case lead to the determination of ammonia**. Therefore, it was discussed whether the missing recommendation to determine the ammonia concentration is seen as a critical error. In the event that the diagnosis of a urea cycle defect was made, the lack of recommendation to determine the ammonia concentration was not considered a critical error.
- The specified quotients may be helpful in daily life.

3.1.4. Best interpretation (scored with 2 points each)

- **Findings (*47):** Markedly increased glutamine, glutamic acid, proline, alanine and lysine. Slightly increased methionine. Low-normal levels of citrulline and arginine. Normal ornithine.
- **Diagnosis (*2)**: A urea cycle defect would need to excluded: OTC (male patient), CPS1/NAGS, CAVA. Orn:Cit=9.5, Cit:Arg=0.6 (ref. <0.36), Cit:Phe=0.15 (ref <0.1), Gln:Cit=130 (ref. <104).
- **Further tests (*135):** Urgent plasma ammonia measurement. Urinary orotic acid quantification to distinguish OTC from CPS1 deficiency. Sequence *OTC* gene; consider full urea cycle gene panel if negative. Initiate ammonia-lowering therapy (eg. sodium benzoate, arginine), protein restriction, IV glucose, and dialysis if needed.

3.2. Case 2025-2: ´Classical` homocystinuria due to a cystathionine-ß-synthase deficiency

3.2.1. Sample details

This sample is from a 5-year-old boy, who was referred to the general paediatric consultation due to new onset of strabism, neurological deterioration and dizziness.

Based on the results of the plasma amino acid concentrations and the increased concentration of homocysteine, a classic homocystinuria was suspected. This diagnosis was confirmed by molecular genetic analysis of *CBS* gene. Treatment with vitamin B6 reduced the homocysteine concentration to below 50 µmol/l. The patient therefore received treatment with vitamin B6, folic acid and vitamin B12. Nutritional therapy or betaine is not administered.

3.2.2. Scoring details

Table 2: Scoring details for case 2025-2.

	interpretation		scores (points)
findings, abnormalities, maximum 2 points	elevated	met, hcys	1
	decreased	cys	1
diagnosis, maximum 2 points	"classical" homocystinuria due to CBS deficiency		2
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	MMA, folic acid, vitamin B12, SAM/SAH (each 1 point)		1
	molecular genetic analysis of *CBS* gene		1
comments	This constellation of findings appears quite clear and indicative of a 'classic' homocystinuria.		
critical error	A critical error is when the participant overlooks the constellation of conspicuous findings and assesses the result as normal.		

Scores for participating laboratories are in APPENDIX 1 on page 7.

3.2.3. Comments on overall performance

Overall proficiency was 98%. The case was very clear, so there was a high overall proficiency.

- For two points in the assessment of laboratory abnormalities, it was necessary to also describe the low cystine concentration. Eleven participants therefore had one point deducted.
- The term 'classical' was not necessary to receive two points in the diagnosis section.
- **Recommendations for therapy could not be assessed (although they are very important),** as this scheme is a diagnostic scheme.
- In the further testing recommendations part, it is important for us to recommend not only molecular genetic analysis (although this of course confirms the diagnosis), but also metabolite diagnostics.

3.2.4. Best interpretation (scored with 2 points each)

- **Findings (*52):** Strongly elevated homocysteine concentration and strongly elevated methionine concentration in plasma. Cystine is undetectable.
- **Diagnosis (*52):** The combination of strongly elevated tHcy and Met points to cystathionine beta-synthase deficiency (classical homocystinuria). Low cystine in plasma also fits with this diagnosis. Based on the extent of the tHcy elevation SAHH, MATI/III, GNMT, and ADK deficiency are unlikely.
- **Further tests (*134):** The diagnosis CBS deficiency should be confirmed by the identification of biallelic pathogenic variants in the CBS gene. We would request to repeat AAs in plasma, B12, folate, complete blood count, kidney function, methylmalonic acid (in plasma or urine).

3.3. Case 2025-3: 2-Aminoadipic acid semialdehyde synthase (AASS) deficiency

3.3.1. Sample details

The results are from a 14 year-old boy with psychomotor retardation and behavioural disorder, without other symptoms. The patient was confirmed to have a 2-aminoadipic acid semialdehyde synthase deficiency (detection of homozygous pathogenic variant in *AASS* gene).

3.3.2. Scoring details

Table 3: Scoring details for case 2025-3.

	interpretation		scores (points)
findings, abnormalities, maximum 2 points	elevated (plasma/urine)	lys	1
	elevated (plasma)	pipicolic acid	1
	elevated (urine)	cys, orn, arg, cit	no add. points
		-	
diagnosis, maximum 2 points	hyperlysinemia due to 2-AASS deficiency		2
	hyperlysinemia (without further specification)		1
	lysinuric protein intolerance		0
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	saccharopine		1
	2-aminoadipic acid semialdehyde		1
	molecular genetic analysis of *AASS* gene		2
	lactic acid, ammonia (sec. hyperlysinemia)		1
comments	2-Aminoadipic acid semialdehyde synthase deficiency as form of primary hyperlysinemia is considered as a non-disease. Primary hyperlysinaemia must be differentiated from secondary forms, including pyruvate carboxylase deficiency and mitochondrial NADP(H) due to *NADK2* mutations.		
critical error	none		

Scores for participating laboratories are in APPENDIX 1 on page 7.

3.3.3. Comments on overall performance

Overall proficiency in this case was 95 %. The concentrations of amino acids were clearly conspicuous.

- For two points in the assessment of laboratory abnormalities, it was also necessary to assess the increased pipecolic acid concentration. Nine participants were therefore deducted one point.

3.3.4. Best interpretation (scored with 2 points each)

- **Findings (*59):** The plasma AA profile shows significantly elevated levels of lysine and pipecolic acid. In the urine sample, the concentration of lysine remains significantly elevated, with an increase in the levels of cysteine and arginine. Slight increase in ornithine, citrulline and leucine.
- **Diagnosis (*31):** Hyperlysinemia due to alpha-amino adipic semialdehyde synthase deficiency.

- **Further tests (*99):** Analysis of saccharopine in urine, analysis of NH_3 (because lysine inhibits arginase and leads to diminished ornithine urea cycle could theoretically be affected), molecular genetic analysis of *AASS* gene

3.4. Comments on the whole of the first circulation results 2025

We hope that we have once again succeeded in presenting three interesting and instructive cases to the participants this year. The aim should be to describe the laboratory changes, the diagnosis and the further recommendations in such a way that it is also easy to understand for the doctors looking after the patient. In this year's cases, it was also important to describe the low concentrations of certain amino acids (cases 1 and 2) or the presence of particular metabolites (case 3).

The overall competence was good with 93%.

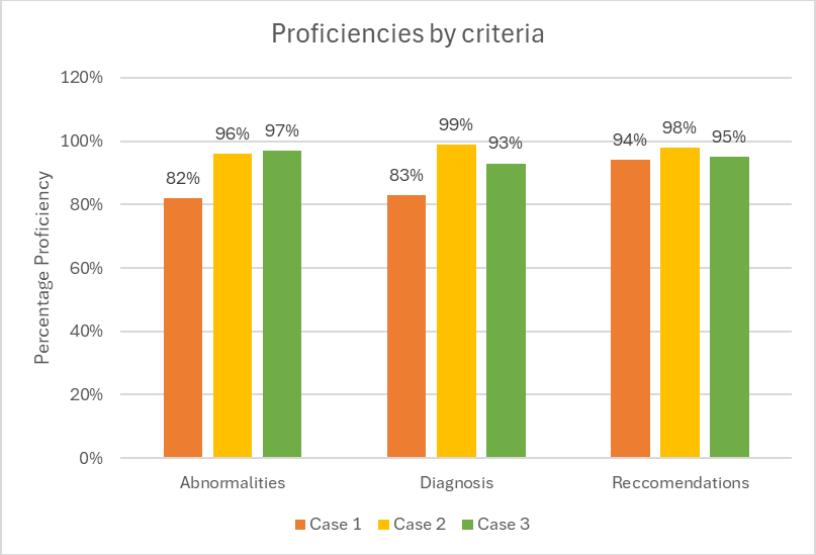

Figure 2: Proficiencies by criteria.

The common methods used by the participants for amino acid analysis are LC-MS/MS with a share of 43% and HPLC with ninhydrin detection with a share of 38%.

Table 4: Laboratory methods for the analysis of amino acids used by the participants (141/148 participants completed this question)

Method	No of responses
LC-MS/MS	61
Ion-exchange chrom Ninhydrin 1/2 Int. Std	46
Reverse phase HPLC/UPLC with non MS detection	14
LC-MS	9
Ion-exchange chrom Ninhydrin 0 Int. Std	6
GC-FID and/or Reverse phase HPLC with Fluorimetric detection	1
HPLC-FLD Detection	1
Ion exchange and reverse phase HPLC	1
Ion-exchange chrom Ninhydrin 1 Int. Std	1
Ultraperformance liquid chromatography/Ultraviolet detection	1
Total	**141**

Table 5: Overall scores for the first circulation in the Amino Acid Interpretation scheme

	2025.01				2025.02				2025.03				2025.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Totals
Total Points	234	236	268	738	273	282	279	834	275	264	269	808	2380
% proficiency	82%	83%	94%	87%	96%	99%	98%	98%	97%	93%	95%	95%	93%

Key

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

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: 4th August 2025

The Scientific Evaluators

Sabine Scholl-Bürgi, Scientific Advisor
Scheme Assessors: Apolline Imbard, Olivier Braissant, Rachel Carling, Alistair Horman, Daniela Karall, and Anke Schumann

APPENDIX 1. Detailed scores for submitting laboratories

Key

A = Findings, Abnormalities
D = Diagnosis
R = Recommendations for further testing
DNS = did not submit any results

Anon. lab number	2025.01				2025.02				2025.03				2025.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
1	1.0	1.0	2.0	4.0	2.0	2.0	0.0	4.0	2.0	2.0	2.0	6.0	14.0
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	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	1.0	2.0	1.0	4.0	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	15.0
7													DNS
8	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
9	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
10	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
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	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
13	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
14	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
15	1.0	1.0	2.0	4.0	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	15.0
16	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
17	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
18	1.0	2.0	2.0	5.0	1.0	2.0	2.0	5.0	1.0	1.0	1.0	3.0	13.0
19	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
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	1.0	1.0	2.0	4.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	15.0
22	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
23	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
24	1.0	1.0	2.0	4.0	2.0	2.0	2.0	6.0	1.0	1.0	2.0	4.0	14.0
25	1.0	1.0	2.0	4.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	15.0
26	2.0	0.0	2.0	4.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	16.0
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	1.0	1.0	2.0	4.0	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	15.0
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
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	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
34	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
35	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
36	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
37	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	2.0	2.0	0.0	4.0	15.0
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

Anon. lab number	2025.01				2025.02				2025.03				2025.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
39	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
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	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
42	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
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	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
45	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	15.0
46	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	0.0	1.0	2.0	14.0
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	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
50	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
51	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
52	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
53	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
54	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	16.0
55	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
56	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
57	1.0	0.0	0.0	1.0	2.0	2.0	0.0	4.0	2.0	2.0	2.0	6.0	11.0
58	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
59	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
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	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
63	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
64	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
65	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
66	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
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	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
69	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
70	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
71	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	16.0
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	2.0	6.0	2.0	2.0	2.0	6.0	18.0
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	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	16.0
79	1.0	0.0	2.0	3.0	2.0	0.0	1.0	3.0	2.0	1.0	2.0	5.0	11.0
80	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
81	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
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

Anon. lab number	2025.01				2025.02				2025.03				2025.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
84	1.0	1.0	1.0	3.0	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	14.0
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	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
87	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
88	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
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	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
91													DNS
92	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
93	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
94	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
95													DNS
96	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
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													DNS
102	1.0	0.0	2.0	3.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	15.0
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	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
105													DNS
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	2.0	6.0	2.0	2.0	2.0	6.0	18.0
108	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
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	1.0	1.0	2.0	4.0	2.0	2.0	2.0	6.0	1.0	0.0	1.0	2.0	12.0
112	1.0	2.0	1.0	4.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	15.0
113	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
114	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
115	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
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	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
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	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
120	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
121	1.0	0.0	1.0	2.0	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	10.0
122	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
123	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
124	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
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	2.0	2.0	6.0	18.0
127	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
128	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

Anon. lab number	2025.01				2025.02				2025.03				2025.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
129	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
130	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
131	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
132	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
133													DNS
134	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
135	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
136	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
137	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
138	1.0	0.0	1.0	2.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	12.0
139	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
140	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
141	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	16.0
142	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
143	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
144	1.0	1.0	2.0	4.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	15.0
145	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
146	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
147	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
148	2.0	2.0	1.0	5.0	1.0	2.0	2.0	5.0	2.0	0.0	0.0	2.0	12.0

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

Version Number	Published	Amendments
1	04 August 2025	• 2025 first round interim report published

END OF REPORT