Amino Acids Interpretation (AAI)

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1. Scheme Design

The scheme has been designed and planned by the Scientific Advisor (SA) and Scheme Organisers (SO), listed at the top of this page, both appointed by and according to procedures laid down by the ERNDIM Board.

2. Samples

Cases were provided and selected by the Scientific Advisor and scheme assessors. The cases for this scheme are data only and no physical samples are circulated.

3. Sample distribution

The cases for the first and second rounds were sent to all 148 registered laboratories by email by the Administration Office on 6th May and 18th August 2025 respectively.

4. Receipt of results

Results were submitted to an online form set up by the Administration Office (AO) using the Formdesk website (https://en.formdesk.com/). The submission deadlines for the first round (cases AAI 2025.01, .02 and .03) and second round (samples AAI 2025.04, .05 and .06) were 27th May and 8th September 2025, respectively. Overall, 138/148 (93.2%) registered participants submitted results for both rounds of the 2025. Eight labs (5.4%) only submitted results for one of the rounds (4 for the first round and 4 for the second round). While a separate two laboratories (1.4%) failed to make a return on either submission round.

Note: All results must be submitted in English.

5. Scoring scheme

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.

Scoring schemes were agreed by the scheme assessors in advance of the cases being circulated. Scoring was done by two blinded evaluators each (the evaluators were blinded to both, the ERN number and to the scores of the second

[1] **If this Annual Report is not Version 1 for this scheme year, go to APPENDIX 2 (page 25) for details of the changes made since the last version of this document.**

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.

The maximum score achievable with full submission for all samples is 36. The score required for satisfactory performance will be 20/36 points (56%).

The ERNDIM Scientific Advisory Board (SAB) agreed at their November 2022 meeting that the principle of critical error would apply to the AAI scheme for 2023 onwards. In principle this is a category of error that would be unacceptable to the majority of labs and would have a serious adverse effect on patient management. When a critical error is established for one or more samples, performance is not acceptable in that year, regardless of the number of points assigned. Critical errors are ratified by the ERNDIM Scientific Advisory Board.

For information if any errors in the 2025 participant results would have been considered critical errors this would be noted under the relevant cases in section 6.

a. Appeals

If your laboratory has been assigned poor performance in the 2025 scheme and you wish to appeal against this classification, please use the link given in the Performance Support letter you received to submit your appeal request. The online form should be completed with full details of the reason for your appeal and submitted within one month of receiving your Performance Support Letter. Please note that only appeals submitted using the online response form will be considered.

Further information regarding the Framework for Assessment and Education in Qualitative schemes can be found under the Participant Information tab on the ERNDIM registration website (www.eqa.erndim.org).

6. Results of samples and evaluation of reporting

The diagnoses of the six samples are summarised in Table 1 below.

Table 1: Samples in the 2025 scheme

Sample	Clinical Information	Sex	Age at Diagnosis	Diagnoses
AAI 2025-01	Vomiting and apathy, otherwise normal.	M	18 Months	OTC deficiency.
AAI 2025-02	Strabism, neurological deterioration, dizziness.	M	5 Years	Cystathionine-ß-synthase deficiency.
AAI 2025-03	Psychomotor retardation, behavioural disorder.	M	14 Years	2-Aminoadipic acid semialdehyde synthase deficiency.
AAI 2025-04	Noticeably tired and pale for several weeks, hypochromic microcytic anaemia.	F	1.5 Years	Tyrosinaemia type I
AAI 2025-05	Mild jaundice, positive newborn screening.	F	1 Month	Methionine adenosyl-transferase deficiency I/III
AAI 2025-06	Idiopathic thrombocytopenic purpura.	M	4 Years	Hyperprolinaemia caused by an infusion of Privigen (high in proline content).

Table 2: % proficiencies for the cases in the 2025 scheme

Sample	No of returns	A (%)	D (%)	R (%)	Total (%)
AAI 2025-01	142	82%	83%	94%	87%
AAI 2025-02	142	96%	99%	98%	98%
AAI 2025-03	142	97%	93%	95%	95%
AAI 2025-04	142	100%	83%	81%	88%
AAI 2025-05	142	97%	87%	89%	91%
AAI 2025-06	142	59%	98%	81%	79%

Key

A = Findings, abnormalities
D = Diagnosis
R = Recommendations for further testing

Table 3: Distribution of scores (for labs that submitted results for both rounds)

Score	Score (%)	No of labs	*(% of participating labs)*
0 - 3	0% – 9.9%	0	0.0%
4 – 7	10% – 19%	0	0.0%
8 - 10	20% – 29%	0	0.0%
11 - 14	30% – 39%	0	0.0%
15 - 17	40% – 49%	0	0.0%
18 - 21	50% – 59%	0	0.0%
22 - 24	60% – 69%	3	2.2%
25 - 28	70% – 79%	10	7.2%
29 - 32	80% – 89%	47	34.1%
32 - 36	90% – 99%	73	52.9%
36	100%	5	3.6%
	Total	**138**	**100%**

The full anonymised results for all labs that submitted results are given in APPENDIX 1 on page 15.

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

6.1.1. 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.

Table 4: Sample details for case 2025-1.

amino acids in plasma, done with Jeol AminoTac 500/V				
	µmol/L	reference range		
Phosphoserine	2		<	13
Taurine	150	19	-	130
Phosphoethanolamine	1		<	3
Threonine	126	33	-	130
Serine	160	24	-	178
Asparagine	60	25	-	250
Glutamic Acid	132	6	-	80
Glutamine	1168	20	-	600
Proline	427	51	-	185
Glycine	315	56	-	308
Alanine	1018	99	-	350
Citrulline	9	5	-	24
Valine	175	57	-	270
Cystine	25	10	-	40
Methionine	42	3	-	29
Isoleucine	51	26	-	94
Leucin	102	45	-	155
Tyrosin	73	11	-	120
Phenylalanin	60	23	-	70
Homocystine	0	0	-	0
Ornithine	85	10	-	107
Histidine	130	24	-	112
Lysine	274	45	-	144
Arginine	16	11	-	75

6.1.2. Scoring details

Table 5: 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

Scores for participating laboratories are in APPENDIX 1 on page 15.

6.1.3. 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 may be rare in some regions.
- **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.

Critical Errors: There were three critical errors for this case.

6.1.4. Best interpretation (scored with 2 points each)

- **Findings:** Markedly increased glutamine, glutamic acid, proline, alanine and lysine. Slightly increased methionine. Low-normal levels of citrulline and arginine. Normal ornithine.
- **Diagnosis**: A urea cycle defect would need to be 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:** Urgent plasma ammonia measurement. Urinary orotic acid quantification to distinguish OTC from CPS1/NAGS 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.

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

6.2.1. 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.

Table 6: Sample details for case 2025-2.

amino acids in plasma (ion exchange chromatography with ninhydrin detection)				
	µmol/L	reference range		
Glutamine	532	254	-	823
Alanine	256	152	-	547
Glycine	326	127	-	341
Proline	200	59	-	369
Valine	181	74	-	321
Threonine	155	35	-	226
Lysine	151	48	-	264
Serine	195	69	-	187
Glutamic Acid	97	5	-	150
Leucine	131	49	-	216
Taurine	195	10	-	170
Histidine	81	41	-	121
Ornithine	76	10	-	163
Arginine	44	10	-	140
Tyrosine	50	24	-	115
Phenylalanine	58	26	-	91
Isoleucine	40	22	-	107
Cystine	0	5	-	45
Methionine	778	7	-	47
Aspartic acid	30	1	-	24
Citrulline	30	1	-	46
2-Amino n-butyric acid	23	4		13
n.d. not detected				

Additionally, homocysteine concentration was given (280 µmol/l (< 12 µmol/l)).

6.2.2. Scoring details

Table 7: 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

Scores for participating laboratories are in APPENDIX 1 on page 15.

6.2.3. 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 recommendation’s part, it is important for us to recommend not only molecular genetic analysis (although this of course confirms the diagnosis), but also metabolite diagnostics.

Critical Errors: There were no critical errors for this case.

6.2.4. Best interpretation (scored with 2 points each)

- **Findings:** Strongly elevated homocysteine concentration and strongly elevated methionine concentration in plasma. Cystine is undetectable.
- **Diagnosis:** 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:** 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)

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

6.3.1. Sample details

6.3.2. 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).

Table 8: Sample details for case 2025-3.

amino acids in plasma, done with LC-MS/MS				
	µmol/L	reference range		
Glutamine	447	338	-	658
Alanine	237	201	-	437
Glycine	132	114	-	317
Proline	104	107	-	246
Valine	244	178	-	318
Threonine	92	47	-	247
Lysine	1099	100	-	223
Serine	102	59	-	201
Glutamic Acid	63	17	-	119
Leucine	114	87	-	175
Taurine	70	35	-	152
Histidine	57	51	-	109
Ornithine	12	22	-	109
Arginine	65	40	-	124
Tyrosine	54	37	-	89
Phenylalanine	50	32	-	76
Isoleucine	64	42	-	90
Cysteine	53	43	-	131
Methionine	22	14	-	42
Citrulline	17	13	-	41
Pipecolic acid	26		<	5
n.d. not detected				

Table 9: Sample details for case 2025-3.

amino acids in urines, done with LC-MS/MS				
	µmol/mmol creat	reference range		
Glutamine	114	20	-	76
Alanine	23	15	-	62
Glycine	49	39	-	157
Proline	2		<	8
Valine	7	3	-	13
Threonine	18	7	-	29
Lysine	2134	6	-	48
Serine	44	20	-	47
Glutamic Acid	2		<	12
Leucine	15	2	-	11
Taurine	18	16	-	180
Histidine	84	26	-	153
Ornithine	14		<	4
Arginine	45		<	5
Tyrosine	22	2	-	23
Phenylalanine	11	2	-	19
Isoleucine	2		<	4
Cysteine	92	6	-	34
Methionine	3	2	-	16
Citrulline	14		<	5
n.d. not detected				

6.3.3. Scoring details

Table 10: 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

Scores for participating laboratories are in APPENDIX 1 on page 15.

6.3.4. 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.

Critical Errors: There were no critical errors for this case.

6.3.5. Best interpretation (scored with 2 points each)

- **Findings:** 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:** Hyperlysinemia due to alpha-amino adipic semialdehyde synthase deficiency.
- **Further tests:** 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.

6.4. Case 2025-4: Tyrosinaemia type I

6.4.1. Sample Details

The laboratory results are from a 1.5-year-old girl who has been tired and pale for several weeks. In addition to paleness, clinical and further examination reveals hepatomegaly.

Further investigation reveals significantly elevated tyrosine and methionine concentrations in plasma. Ultimately, the cause of the clinical symptoms and laboratory changes was tyrosinaemia type I, which was confirmed by molecular genetic testing.

In principle, various differential diagnoses can be considered due to the altered amino acid concentrations in plasma:

- Disorders in tyrosine metabolism (i.e. tyrosinaemia type I), which are consistent with the clinical symptoms of anaemia. The elevated methionine concentration can be explained by the onset of liver failure.
- Secondary changes in the context of liver failure that can induce increased methionine and/or tyrosine and/or phenylalanine concentrations.

The elevated methionine concentration could also indicate a metabolic disorder in methionine metabolism. However, neither the clinical symptoms nor the elevated tyrosine concentration is consistent with this.

Table 11: Sample details for case 2025-4.

amino acids in plasma, done with ion exchange chromatography with ninhydrin detection				
	µmol/L	reference range		
Taurine	27	19	-	130
Threonine	186	33	-	130
Serine	273	24	-	178
Asparagine	142	25	-	150
Glutamic Acid	23	6	-	80
Glutamine	666	200	-	600
Proline	517	51	-	185
Glycine	286	56	-	308
Alanine	698	99	-	350
Citrulline	28	5	-	24
Valine	92	57	-	270
Cystine	22	0	-	40
Methionine	631	3	-	29
Cystathionin/Alloisoleucine	3	0	-	0
Isoleucine	31	26	-	94
Leucine	36	45	-	155
Tyrosine	547	11	-	120
Phenylalanine	125	23	-	70
Homocystine	n.d.	0	-	0
Ornithine	57	10	-	107
Lysine	207	45	-	144
Histidine	69	24	-	112
Arginine	56	11	-	75
n.d. not detected				

6.4.2. Scoring details

Table 12: Scoring details for case 2025.04

	interpretation		**scores (points)**
findings, abnormalities, maximum 2 points	elevated	tyr	1
	elevated	met	1
diagnosis, maximum 2 points	tyrosinaemia type I		2
	liver failure (due to other IMD like galactosaemia, mitochondrial disorder, citrin deficiency, etc.)		1
	tyrosinaemia type II		0
further tests, maximum 2 points	alpha-fetoproteine		1
	organic acids (urine)		1
	succinylacetone		1
	homocysteine		1
	5-aminolaevulinic acid/ porphobilinogene synthase acitivity		1
	molecular genetic analysis *FAH* gene		1

Scores for participating laboratories are in APPENDIX 1 on page 15.

6.4.3. Comments on overall performance

Overall proficiency was 88%. The proficiency for abnormalities was 100%. Proficiency in diagnosis and recommendation for further examinations was significantly lower at 83% and 81%. The reason for the point deduction was the focus on a methionine metabolism disorder or the assumption that the changes were secondary due to the atypical presentation. However, no critical error could be detected.

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

- The unspecific clinical symptoms.
- The combined increase in concentration of two amino acids from different metabolic pathways.

Critical Errors: There were no critical errors for this case.

6.4.4. Best interpretation (scored with 2 points each)

- **Findings:** Severe hyperaminoacidaemia: Methionine (21x↑), tyrosine (~4.6x↑), phenylalanine (~1.8x↑). Generalized elevation: alanine, proline, serine, glutamine. Low-normal BCAA. Pattern indicates severe hepatocellular dysfunction.
- **Diagnosis**: The biochemical profile is consistent with tyrosinaemia type I (HT1 - fumarylacetoacetate hydrolase deficiency). Liver dysfunction could also be suspected as it can lead to methioninaemia, tyrosinaemia and phenylalaninaemia and the presence of cystathionine. Microcytic anaemia may be due to elevated succinylacetone, which inhibits heme synthesis.
- **Further tests:** URGENT: Urine/plasma succinylacetone (diagnostic for HT1). Liver function tests, AFP, coagulation studies, ammonia. If positive: immediate NTBC (nitisinone) therapy and tyrosine/phenylalanine-restricted diet. Genetic testing *FAH* gene. Metabolic genetics/hepatology referral. Address anaemia.

6.5. Case 2025-5: Methionine adenosyl-transferase deficiency I/III

6.5.1. Sample details

The results provided were from an asymptomatic girl, born after 40 gestational weeks. Newborn screening was positive with elevated methionine concentration. The sample was taken at age one month. Homocysteine-concentration was slightly increased (40.8 µmol/l), and methionine-concentration was grossly (1087 µmol/l) elevated. Cystine concentration was not decreased. The diagnosis was confirmed by mutation analysis showing homozygous for mutation in MAT1A-gene.
This case was previously used in 2021.

Table 13: Sample details for case 2025-5.

amino acids in plasma, done with ion exchange chromatography with ninhydrin detection				
	µmol/L	reference range		
Taurine	105	10	-	167
Aspartate	6	0	-	31
Threonine	187	46	-	222
Serine	213	92	-	178
Asparagine	99	38	-	121
Glutamate	52	8	-	179
Glutamine	480	402	-	776
Proline	282	97	-	254
Glycine	188	154	-	338
Alanine	319	142	-	421
Citrulline	14	8	-	36
Valine	196	79	-	217
Cystine	51	6	-	43
Methionine	1087	9	-	44
Isoleucine	76	12	-	77
Leucine	132	46	-	147
Tyrosine	114	13	-	91
Phenylalanine	48	25	-	74
Ornithine	96	41	-	129
Lysine	241	69	-	200
Histidine	93	37	-	83
Arginine	107	7	-	128

6.5.2. Scoring details

Table 14: Scoring details for case 2025-5.

	interpretation		scores (points)
findings, abnormalities, maximum 2 points	elevated	met	1
	elevated	hcy	1
	slightly elevated (no additional point)	cys	0
diagnosis, maximum 2 points	MATI/III deficiency		2
	CBS deficiency		1
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	molecular genetic analysis *MATI/III* gene		2
	molecular genetic analysis *CBS* gene		1
	SAM/SAH		2
	Folic acid, vitamin B12, MMA, acylcarnitine profile		1

Scores for participating laboratories are in APPENDIX 1 on page 15.

6.5.3. Comments on overall performance

Overall proficiency was 91% (proficiency for laboratory abnormalities 97%, diagnosis 87% and further recommendation 89%).

- For two points in the assessment of laboratory abnormalities, it was necessary to mention all three relevant amino acids (methionine, homocysteine and cystine).
- The main misdiagnosis was classic homocystinuria, which was given a score of one point. Other diagnoses related to methionine metabolism were also given.

Critical Errors: There were no critical errors for this case.

6.5.4. Best interpretation (scored with 2 points each)

- **Findings:** Markedly increased Met with only mildly increased Tyr, no decreased Cys and moderately increased homocysteine of 40 µmol/L without treatment (< 50 µmol/L).
- **Diagnosis:** The increased Met without high Tyr points to a disorder of the sulfur amino acid metabolism. The HCy of 40 µmol/L argues against CBS deficiency (typically > 50 µmol/L). Also Met level compared to HCy level is too high for CBS deficiency. DD includes MAT I/III, GNMT, SAHH and ADK deficiency.
- **Further tests:** S-adenosylmethionine/S-adenosylhomocysteine in plasma (low), methylmalonic acid in plasma (normal), Folate, B12 vitamin in plasma (normal), mutation analysis in the *MAT1A*-gene.

6.6. Case 2025-6: Hyperprolinaemia caused by an infusion of Privigen (high in proline content).

6.6.1. Sample details

The results are from a patient who received intravenous immunoglobulins for idiopathic thrombocytopenic purpura. Proline is added to the immunoglobulin preparation for stabilisation. A significantly increased proline concentration was observed. The hydroxyproline concentration was normal. During follow-up examination, the proline concentration was normal again.

Table 15: Sample details for case 2025-6.

amino acids in plasma, done with with LC-MS/MS				
	µmol/L	reference range		
Glutamine	676	435	-	721
Alanine	665	182	-	552
Glycine	280	123	-	319
Proline	1683	88	-	290
Valine	196	123	-	210
Threonine	175	102	-	190
Lysine	183	11	-	248
Serine	120	68	-	160
Glutamic Acid	78		<	57
Leucine	134	78	-	160
Taurine	103	6	-	126
Histidine	96	67	-	106
Ornithine	132	27	-	98
Arginine	78	46	-	128
Tyrosine	72	35	-	84
Phenylalanine	75	39	-	74
Isoleucine	57	34	-	84
Cystine	20	35	-	63
Methionine	31	12	-	32
Aspartic acid	7		<	9
Citrulline	40	23	-	61
Hydroxyproline	16		<	41

6.6.2. Scoring details

Table 16: Scoring details for case 2025-6.

	interpretation		scores (points)
findings, abnormalities, maximum 2 points	elevated	pro	1
	normal	h-pro	1
diagnosis, maximum 2 points	hyperprolinaemia		2
	primary causes: P5C DH, Pro DH		2
	secondary causes: medication		2
further tests (if molecular genetic recommended specify the gene)**, maximum 2 points**	medical history (medication)		1
	repetition of amino acid analysis (plasma and/or urine)		1
	Pyrroline-5-carboxylate		1

Scores for participating laboratories are in APPENDIX 1 on page 15.

6.6.3. Comments on overall performance

Overall proficiency in this case was 79%. The concentrations of amino acids were clearly conspicuous.

- For two points in the assessment of laboratory abnormalities, it was necessary to commend on the hydroxyproline concentration (proficiency 59%).
- A total of 25 participants suspected that the increased proline concentration was caused by an exogenous proline intake, i.e. by medication with immunoglobulins.

Critical Errors: There were no critical errors for this case.

6.6.4. Best interpretation (scored with 2 points each)

- **Findings:** Markedly elevated proline. Normal hydroxyproline and alanine. Mildly elevated ornithine and glutamate and low cystine, likely due to delayed processing and breakdown of arginine and glutamine. Otherwise essentially normal.
- **Diagnosis:** Iatrogenic source of proline, possibly from Privigen (IV IgG) treatment that contains proline to treat Idiopatholic Thrombocytopenia Purpura. Otherwise, no obvious inherited primary amino acid metabolism disorder.
- **Further tests:** Contact referring clinician / electronic patient records to check if on IV IgG treatment. Repeat when off treatment to check if proline concentration normalises.

6.7. Comments on the 2025 results

6.7.1. First circulation

The overall proficiency of 93% was above the expected range.

6.7.2. Second circulation

The overall proficiency was 86%

7. Plans for 2026

7.1. Scheme Design:

- The number of participants is limited to 150 with a maximum of one registration per lab.
- 2 submission deadlines on **26th May 2026** and **7th September 2026**, 3 cases per deadline. The full 2026 calendar is published on the ERNDIM website (www.erndim.org) and will also be included in the scheme instructions.
- Online submission of all results will be mandatory, using the Formdesk website as it was for 2025. Only one set of submitted results will be allowed per registration. All reports must be submitted in English.
- Labs that do not submit any results will be classed as non-submitters.
- Labs that submit results for 3 or fewer cases will be classed as partial submitters. These labs will be shown as non-submitters on the certificates of participation.
- As the number of participants in this scheme is limited, due to the manual evaluation of the results, persistent non- and partial submitters may be excluded from participation in future years.
- Educational Participation will not be an option for this scheme.

7.2. Evaluation

- Scientific Advisor and the other scheme assessors to evaluate the results.
- Scoring for the cases will be agreed by the Scientific Advisor and assessors in advance of each circulation.
- As for the 2025 scheme, scoring will be done by two blinded assessors each (blinded to both, the ERN number and to the scores of the second assessor). If the scores are not concordant the Scientific Advisor will score the results as well.

7.3. Poor Performance

- The use of subcontracted (or 'cluster' labs) laboratories is not allowed in this scheme.
- The concept of 'critical error' is applied in the scoring of results in this scheme.
- **For 2026, the SAB has agreed that the score required for satisfactory performance will be increased to 22/36 points (61%).** However, this score will be subject to annual review by the SAB.
- The ERNDIM poor performance policies will apply (i.e., performance support letters will be sent to labs that do not obtain satisfactory performance).

7.4. Reports

- Diagnoses will be circulated to scheme participants approximately 2 weeks after each deadline.
- Interim reports will be published 6-8 weeks after each submission deadline.
- Annual report to be published in Jan 2027.

7.5. Certificates of Participation

- Certificate of Participations will show the AAI scheme under the Qualitative schemes header and will include whether a lab registered for this scheme, if they submitted results, and if their performance was satisfactory.

8. Questions, Suggestions and Complaints

If you have any questions, comments or suggestions for the Scientific Advisor of the scheme, Dr. Sabine Scholl-Bürgi, and/or the ERNDIM Administration Office, please contact us at admin@erndim.org.

Most complaints received by ERNDIM consist of minor misunderstandings, which can usually be resolved via direct contact with the ERNDIM administrative staff. If you wish to file a formal complaint, please email your complaint with details of your issue to admin@erndim.org or contact us through our website at https://www.erndim.org/contact-us/

Date: 12th February 2026

Sabine Scholl-Bürgi, Scientific Advisor
Scheme Assessors: Apolline Imbard (Deputy Scientific Advisor), 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 results

Table 17: First round scores

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

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
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	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

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
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	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

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
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
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

Table 18: Second round scores

Anon. lab number	2025.04				2025.05				2025.06				2025.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
1	2.0	1.0	1.0	4.0	2.0	0.0	0.0	2.0	2.0	2.0	1.0	5.0	11.0
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	1.0	4.0	1.0	2.0	0.0	3.0	13.0
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	1.0	1.0	0.0	2.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	11.0
6													DNS
7													DNS
8	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	13.0
9	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
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	1.0	2.0	1.0	4.0	16.0
12	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
13	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	14.0
14	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
15	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	13.0
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	2.0	2.0	6.0	1.0	2.0	2.0	5.0	1.0	2.0	2.0	5.0	16.0
18	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
19	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

Anon. lab number	2025.04				2025.05				2025.06				2025.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
20	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	1.0	2.0	1.0	4.0	15.0
21	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
22	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	16.0
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	1.0	2.0	2.0	5.0	17.0
25	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	1.0	2.0	1.0	4.0	15.0
26	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
27	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
28	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	13.0
29	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	15.0
30	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	15.0
31	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	15.0
32	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
33	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
34	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	15.0
35	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	13.0
36	2.0	1.0	2.0	5.0	2.0	1.0	2.0	5.0	1.0	2.0	2.0	5.0	15.0
37	2.0	1.0	2.0	5.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	14.0
38	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	1.0	2.0	1.0	4.0	15.0
39	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	1.0	0.0	1.0	2.0	13.0
40	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	1.0	0.0	1.0	2.0	13.0
41	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
42	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	1.0	2.0	2.0	5.0	16.0
43	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
44	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
45	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
46	2.0	1.0	0.0	3.0	2.0	1.0	0.0	3.0	1.0	2.0	1.0	4.0	10.0
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	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	16.0
49	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	1.0	5.0	15.0
50	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
51	2.0	0.0	0.0	2.0	2.0	1.0	2.0	5.0	2.0	2.0	1.0	5.0	12.0
52	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
53	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
54	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	1.0	2.0	2.0	5.0	16.0
55	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	1.0	2.0	1.0	4.0	13.0
56	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
57													DNS
58	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	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	2.0	2.0	6.0	18.0
60	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	13.0
61	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	15.0
62	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
63	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	1.0	2.0	1.0	4.0	15.0
64	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	1.0	2.0	1.0	4.0	15.0

Anon. lab number	2025.04				2025.05				2025.06				2025.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
65	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
66	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
67	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
68	2.0	2.0	2.0	6.0	2.0	2.0	0.0	4.0	2.0	2.0	2.0	6.0	16.0
69	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
70	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	16.0
71	2.0	1.0	0.0	3.0	2.0	1.0	1.0	4.0	1.0	2.0	1.0	4.0	11.0
72	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	15.0
73	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
74	2.0	1.0	0.0	3.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	12.0
75	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
76	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	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	0.0	4.0	16.0
78	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
79	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	1.0	2.0	2.0	5.0	16.0
80	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	1.0	2.0	1.0	4.0	15.0
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	1.0	2.0	2.0	5.0	17.0
83	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	15.0
84	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	1.0	2.0	1.0	4.0	15.0
85	2.0	1.0	2.0	5.0	2.0	1.0	2.0	5.0	1.0	2.0	2.0	5.0	15.0
86	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
87	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	15.0
88	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
89	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
90	2.0	2.0	2.0	6.0	1.0	1.0	1.0	3.0	0.0	2.0	1.0	3.0	12.0
91	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	1.0	2.0	1.0	4.0	13.0
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	2.0	2.0	6.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	15.0
94	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
95	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
96	2.0	1.0	0.0	3.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	14.0
97	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
98	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
99	2.0	1.0	0.0	3.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	12.0
100	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
101													DNS
102	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
103	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
104	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	12.0
105	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
106	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
107	2.0	0.0	0.0	2.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	11.0
108	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
109	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

Anon. lab number	2025.04				2025.05				2025.06				2025.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
110	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	16.0
111	2.0	0.0	1.0	3.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	15.0
112	2.0	0.0	0.0	2.0	2.0	1.0	2.0	5.0	1.0	1.0	1.0	3.0	10.0
113	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	13.0
114	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
115	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
116	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	15.0
117													DNS
118	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	15.0
119	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	16.0
120	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	14.0
121	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
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	1.0	2.0	2.0	5.0	1.0	2.0	2.0	5.0	16.0
124	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	13.0
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	1.0	2.0	1.0	4.0	16.0
127	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
128	2.0	1.0	1.0	4.0	2.0	2.0	1.0	5.0	1.0	2.0	2.0	5.0	14.0
129	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
130	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	15.0
131	2.0	2.0	0.0	4.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	15.0
132	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	1.0	2.0	1.0	4.0	13.0
133	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
134	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
135	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
136	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
137													DNS
138	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
139	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
140	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
141	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
142	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
143	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	15.0
144	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	1.0	2.0	2.0	5.0	16.0
145	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
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	1.0	2.0	2.0	5.0	17.0
148	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

Table 19: Total scores for 2025 scheme

Anon. lab number	First round (2025-01 to -03	Second round (2025-04 to -06)	Total Score	% Max score	
1	14	11	25	69.4%	
2	18	18	36	100.0%	

Anon. lab number	First round (2025-01 to -03	Second round (2025-04 to -06)	Total Score	% Max score	
3	18	13	31	86.1%	
4	18	18	36	100.0%	
5	18	11	29	80.6%	
6	15	0	15	41.7%	Partial submitter
7	0	0	0	0.0%	Non-submitter
8	17	13	30	83.3%	
9	18	16	34	94.4%	
10	18	18	36	100.0%	
11	18	16	34	94.4%	
12	17	16	33	91.7%	
13	17	14	31	86.1%	
14	18	17	35	97.2%	
15	15	13	28	77.8%	
16	17	17	34	94.4%	
17	18	16	34	94.4%	
18	13	17	30	83.3%	
19	17	17	34	94.4%	
20	18	15	33	91.7%	
21	15	14	29	80.6%	
22	15	16	31	86.1%	
23	17	18	35	97.2%	
24	14	17	31	86.1%	
25	15	15	30	83.3%	
26	16	16	32	88.9%	
27	18	17	35	97.2%	
28	15	13	28	77.8%	
29	18	15	33	91.7%	
30	18	15	33	91.7%	
31	18	15	33	91.7%	
32	18	17	35	97.2%	
33	15	16	31	86.1%	
34	17	15	32	88.9%	
35	18	13	31	86.1%	
36	17	15	32	88.9%	
37	15	14	29	80.6%	
38	18	15	33	91.7%	
39	16	13	29	80.6%	
40	18	13	31	86.1%	
41	17	17	34	94.4%	
42	17	16	33	91.7%	
43	18	16	34	94.4%	
44	17	17	34	94.4%	
45	15	17	32	88.9%	
46	14	10	24	66.7%	
47	18	17	35	97.2%	
48	18	16	34	94.4%	

Anon. lab number	First round (2025-01 to -03	Second round (2025-04 to -06)	Total Score	% Max score	
49	17	15	32	88.9%	
50	17	17	34	94.4%	
51	16	12	28	77.8%	
52	18	17	35	97.2%	
53	16	17	33	91.7%	
54	16	16	32	88.9%	
55	16	13	29	80.6%	
56	17	17	34	94.4%	
57	11	0	11	30.6%	CE (sample 1) & Partial submitter
58	17	15	32	88.9%	
59	17	18	35	97.2%	
60	18	13	31	86.1%	
61	18	15	33	91.7%	
62	16	16	32	88.9%	
63	15	15	30	83.3%	
64	16	15	31	86.1%	
65	15	17	32	88.9%	
66	18	16	34	94.4%	
67	18	17	35	97.2%	
68	17	16	33	91.7%	
69	16	16	32	88.9%	
70	17	16	33	91.7%	
71	16	11	27	75.0%	
72	18	15	33	91.7%	
73	18	16	34	94.4%	
74	18	12	30	83.3%	
75	18	16	34	94.4%	
76	18	16	34	94.4%	
77	18	16	34	94.4%	
78	16	17	33	91.7%	
79	11	16	27	75.0%	
80	16	15	31	86.1%	
81	17	18	35	97.2%	
82	18	17	35	97.2%	
83	18	15	33	91.7%	
84	14	15	29	80.6%	
85	18	15	33	91.7%	
86	17	17	34	94.4%	
87	17	15	32	88.9%	
88	17	17	34	94.4%	
89	18	17	35	97.2%	
90	16	12	28	77.8%	
91	0	13	13	36.1%	Partial submitter
92	18	18	36	100.0%	
93	16	15	31	86.1%	

Anon. lab number	First round (2025-01 to -03	Second round (2025-04 to -06)	Total Score	% Max score	
94	17	17	34	94.4%	
95	0	17	17	47.2%	Partial submitter
96	18	14	32	88.9%	
97	18	17	35	97.2%	
98	18	14	32	88.9%	
99	18	12	30	83.3%	
100	18	17	35	97.2%	
101	0	0	0	0.0%	Non-submitter
102	15	17	32	88.9%	
103	18	17	35	97.2%	
104	16	12	28	77.8%	
105	0	17	17	47.2%	Partial submitter
106	18	17	35	97.2%	
107	18	11	29	80.6%	
108	18	17	35	97.2%	
109	18	17	35	97.2%	
110	18	16	34	94.4%	
111	12	15	27	75.0%	
112	15	10	25	69.4%	
113	17	13	30	83.3%	
114	16	17	33	91.7%	
115	18	16	34	94.4%	
116	18	15	33	91.7%	
117	18	0	18	50.0%	Partial submitter
118	18	15	33	91.7%	
119	17	16	33	91.7%	
120	16	14	30	83.3%	
121	10	17	27	75.0%	CE (sample 1)
122	17	18	35	97.2%	
123	17	16	33	91.7%	
124	17	13	30	83.3%	
125	18	18	36	100.0%	
126	18	16	34	94.4%	
127	18	17	35	97.2%	
128	15	14	29	80.6%	
129	18	17	35	97.2%	
130	17	15	32	88.9%	
131	18	15	33	91.7%	
132	17	13	30	83.3%	
133	0	14	14	38.9%	Partial submitter
134	17	17	34	94.4%	
135	18	16	34	94.4%	
136	18	14	32	88.9%	
137	17	0	17	47.2%	Partial submitter
138	12	14	26	72.2%	CE (sample 1)
139	18	17	35	97.2%	

Anon. lab number	First round (2025-01 to -03	Second round (2025-04 to -06)	Total Score	% Max score	
140	17	17	34	94.4%	
141	16	17	33	91.7%	
142	18	16	34	94.4%	
143	18	15	33	91.7%	
144	15	16	31	86.1%	
145	18	17	35	97.2%	
146	17	17	34	94.4%	
147	18	17	35	97.2%	
148	12	17	29	80.6%	

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

Version Number	Published	Amendments
1	12th February 2026	• 2025 annual report published

END OF REPORT