

Amino Acids Interpretation (AAI) PILOT

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Please Note:

- This annual report is intended for participants of the ERNDIM AAI Pilot scheme. The contents should not be used for any publication without permission of the Scientific Advisor.
- The fact that your laboratory participates in this pilot scheme is not confidential, however, the raw data and
 performance scores are confidential and will only be shared within ERNDIM for the purpose of evaluating your
 laboratories performance, unless ERNDIM is required to disclose performance data by a relevant government
 agency. For details please see the ERNDIM Privacy Policy on <u>www.erndim.org</u>.

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. Shipment

The cases for the first and second rounds were sent to all 105 registered laboratories by email by the Administration Office on 14th February and 9th May 2022 respectively.

4. Receipt of results

Results were submitted to an online form set up by the Administration Office (AO) using the Formdesk website (<u>https://en.formdesk.com/</u>). The submission deadlines for the first round (cases AAI 2022.01, .02 and .03) and second round (samples AAI 2022.04, .05 and .06) were 7th March 2022 and 30th May 2022 respectively. Overall, 89/105 (84.8%) registered participants submitted results for both rounds of the 2022 pilot. Eleven labs (10.5%) only submitted results for one of the rounds (9 for just the first round and 2 for just the second round). While a separate three laboratories (2.9%) failed to make a return on either submission round; and a further two labs withdrew from the scheme.

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 evaluators 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 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 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. For information if any errors in the 2022 participant results would have been considered critical errors this would be noted under the relevant cases in section 6.

¹ If this Annual Report is not Version 1 for this scheme year, go to APPENDIX 2 (page 15) for details of the changes made since the last version of this document.

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 2022 scheme

Sample	Clinical Information	Sex	Age at Diagnosis	Diagnoses
AAI 2022-01	Positive new-born screening (slightly decreased activity of GALT), galactose 20 mg/dL	М	10 days	Classical galactosemia with liver failure.
AAI 2022-02	Splenomegaly (chronic EBV-infection and other infections), intermittent mild pancytopenia, mental retardation, dysmorphism since early childhood	М	14 years	Prolidase deficiency
AAI 2022-03	Muscular hypotonia ("floppy infant"), dystrophia, dysmorphism	М	6 months	Hypotonia-cystinuria syndrome
AAI 2022-04	Developmental delay	F	2 years	BCAT deficiency
AAI 2022-05	Congenital heart disease, positive newborn screening (raised methionine and homocysteine)	F	19 days	No metabolic disorder, low vitamin B12 concentration
AAI 2022-06	After an infection (gastroenteritis) sepsis-like disease with petechial efflorescence	М	7 months	Ethylmalonic encephalopathy

Table 2: % proficiencies for the cases in the 2022 scheme

Sample	No of returns	A (%)	D (%)	R (%)	Total (%)
AAI 2022-01	99	88%	78%	73%	80%
AAI 2022-02	99	76%	60%	55%	63%
AAI 2022-03	99	100%	82%	72%	85%
AAI 2022-04	91	70%	51%	84%	68%
AAI 2022-05	91	99%	55%	63%	72%
AAI 2022-06	91	99%	89%	87%	92%

Key

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

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

Total Score	No of labs	(% of participating labs)
0%	0	0%
0 – 9.9%	0	0%
20 - 29.9%	0	0%
30 - 39.9%	2	2.2%
40 - 49.9%	2	2.2%
50 - 59.9%	8	9.0%
60 – 69.9%	16	18.0%
70 – 79.9%	18	20.2%
80 - 89.9%	23	25.8%
90 - 99.9%	18	20.2%
100%	2	2.2%
Total	89	100%

The full anonymised results for all labs that submitted results are given in APPENDIX 1 on page 9.

ERNDIM



6.1. Details for Cases 2022.01 – 2022.06

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

6.1.1.1. Sample Details

The results provided were from a boy with positive new-born screening due to slightly elevated galactose concentration (21.8 mg/dL, cut off 20 mg/dL). New-born screening was taken at the third day of life. A control was requested from the new-born screening laboratory. Amino acid concentrations were determined at the age of 11 days when the patient came to the emergency department due to vomiting, hyperbilirubinemia, and weight loss. Plasma amino acids showed as well as other elevated amino acids, elevated tyrosine (822 μ mol/L) and phenylalanine (165 μ mol/L) and low isoleucine concentrations (7 μ mol/L). Additionally, activities of liver enzymes were elevated, and coagulation parameters were altered.

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

6.1.1.2. Scoring details

 Table 4: Scoring details for case 2022-1.

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

Scores for participating laboratories are in APPENDIX 1 on page 9.

6.1.1.3. Comments on overall performance

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

Potential Critical Errors: none.

6.1.1.4. Best interpretation (scored with 2 points each)

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

6.1.2. Case 2022-2: Prolidase deficiency

6.1.2.1. Sample details

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

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







6.1.2.2. Scoring details

Table 5: Scoring details for case 2022-2.

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

Scores for <u>participating</u> laboratories are in APPENDIX 1 on page 9.

6.1.2.3. Comments on overall performance

Performance was 60% for overall proficiency. This case was difficult for some of the participants as they don't use "classical" amino acid analysis (HPLC with ninhydrin detection).

The SAB agreed that this case would have been classed as Educational if the 2022 AAI had been running as a full EQA scheme.

Potential Critical Errors: none.

6.1.2.4. Best interpretation (scored with 2 points each)

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

6.1.3. Case 2021-3: Hypotonia-cystinuria syndrome

6.1.3.1. Sample details

The sample was from a 6-month-old male who had muscular hypotonia ("floppy infant"), dystrophia and dysmorphism. Parents were consanguineous (cousins I°). The extended examination showed reduced tubular



reabsorption of dibasic amino acids (COLA = cysteine, ornithine, lysine, and arginine). Later, it could be shown that the patient had hypotonia-cystinuria syndrome with homozygous microdeletion of part of the *SLC3A1* and *PREPL* genes on chromosome 2p21. Patients with hypotonia-cystinuria syndrome show cystinuria, hypotonia, growth retardation, facial dysmorphism, mental retardation and later obesity (see Jaeken et al 2006).

6.1.3.2. Scoring details

Table 6: Scoring details for case 2022-3.

	Interpretation	Score (points)	
Findings, abnormalities [A, maximum 2 points]	Elevated	2	
Diagnosis [D, maximum 2	Cystinuria	1	
points]	Hypotonia-cystine	2	
Further tests (if molecular	Molecular genetic	1	
genetics recommended, specify the gene) [R, maximum 2 points]	WES, GCH array		2

Scores for <u>participating</u> laboratories are in APPENDIX 1 on page 9.

6.1.3.3. Comments on overall performance

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

Potential Critical Errors: none.

6.1.3.4. Best interpretation (scored with 2 points each)

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

6.1.4. Case 2022-4: BCAT (branched-chain amino acid transaminase) deficiency.

6.1.4.1. Sample Details

The results provided were from a 2-year-old girl with developmental delay. For further details please see Kneer et al. Expanding the genetic and phenotypic spectrum of branched-chain amino acid transferase 2 deficiency. J Inherit Metab Dis. 2019 Sep;42(5):809-17 (subject 2).

6.1.4.2. Scoring details

 Table 7: Scoring details for case 2022-4.

	Interpretation	Score (points)	
Findings, abnormalities [A,	Elevated	Val > leu > ile	2
maximum 2 points]	Elevated	Val, leu, ile	1
	BCAT deficiency		2
Diagnosis [D, maximum 2	Ketosis	1	
points]	Valine metabolism	1	
	MSUD	0	
	Molecular genetic t	2	
Further tests (if molecular genetics recommended, specify	Amino acids in plas alloisoleucine	1	
the gene) [R, maximum 2 points]	Organic acids urine	1	
	Ketone bodies	1	

Scores for participating laboratories are in APPENDIX 1 on page 9.

6.1.4.3. Comments on overall performance

Overall proficiency was 68%. Especially, the diagnosis (D, proficiency 51%) and subsequently the recommendation for further tests (R, proficiency 84%) was difficult to make because BCAT deficiency is very rare and the amino acid pattern is similar to that of "more common" maple syrup disease. Therefore, this case may also lead to a better diagnosis in the future.

Potential Critical Errors: none.



6.1.4.4. Best interpretation (scored with 2 points each)

- **Findings:** Increased valine, leucine, isoleucine, with valine >> leucine
- **Diagnosis**: Possible branched chain aminotransferase (BCAT) deficiency. Maple syrup urine disease unlikely but not excluded.
- **Further tests:** Urine organic acids, plasma alloisoleucine, molecular genetic analysis (*BCAT2, BCKDHA, BCKDHB and DBT*), refer to metabolic team.

6.1.5. Case 2022-5: No specific inborn disorder of metabolism

6.1.5.1. Sample details

The results were from a sample from a 19-day old girl who had as an in-patient new-born screening methionine and homocysteine above cut off value. Venous plasma was deproteinised promptly upon receipt. Patient had congenital heart disease with some liver dysfunction and low vitamin B₁₂ concentration (192 ng/L (259-823)) normal folate (7.2 μ g/L (3.5-14.5)) and increased homocysteine.

6.1.5.2. Scoring details

Table 8: Scoring details for case 2022-5.

	Interpretation	Score (points)	
Findings, abnormalities [A,	Elevated	Homocysteine	2
maximum 2 points]	Normal	Met	1
	No metabolic diso	rder	1
Diagnosis [D, maximum 2 points]	Vitamin B ₁₂ deficie	1	
pointe]	Folate deficiency/	1	
	Vitamin B ₁₂ conce	1	
Further tests (if molecular	Folate concentrati	1	
genetics recommended, specify	Repeat homocyste	1	
the gene) [R, maximum 2 points]	MMA (plasma or u	1	
	Urine organic acid	1	

Scores for participating laboratories are in APPENDIX 1 on page 9.

6.1.5.3. Comments on overall performance

Performance was 72% for overall proficiency. Performance for diagnosis and further testing was particularly low.

This case was difficult because the patient does not have a metabolic disorder but only low vitamin B12 concentration. This was for the participants difficult to discuss AND for the evaluators to score.

Potential Critical Errors: none.

6.1.5.4. Best interpretation (scored with 2 points each)

- Findings: Elevated total homocysteine, methionine high normal.
- **Diagnosis:** Hyperhomocysteinemia probably due to low maternal folate and vitamin B₁₂ concentrations.
- **Further tests:** Request vitamin B₁₂ and folate and urine organic acids including a methylmalonic acid quantitation. Consider *MTHFR* genotyping.

6.1.6. Case 2022-6: Ethylmalonic encephalopathy

6.1.6.1. Sample details

The sample was from a 6-month-old male who developed after an infection (gastroenteritis) sepsis-like disease with petechial efflorescence. The diagnosis of an infection could not be confirmed. He had persistent lactataemia, muscular hypotonia and a halt in physical and mental development.

6.1.6.2. Scoring details

Table 9: Scoring details for case 2022-6.

	Interpretation	Interpretation					
	Elevated	proline	1				
Findings, abnormalities [A, maximum 2 points]	Elevated	alanine	1				
	Elevated	alanine/lysine	1				
Diagnosis [D, maximum 2	Mitochondrial diso	2					
points]	Ethylmalonic ence	2					



	Interpretation	Score (points)
Further tests (if molecular	organic acids urine	2
genetics recommended, specify	acylcarnitine profile	2
the gene) [R, maximum 2	genetic testing mitochondrial disorder	2
pointsj)	genetic testing ETHE1	2

Scores for participating laboratories are in APPENDIX 1 on page 9.

6.1.6.3. Comments on overall performance

Overall proficiency was 92%.

Potential Critical Errors: none.

6.1.6.4. Best interpretation (scored with 2 points each)

- **Findings:** Strongly raised alanine and moderately raised proline. Alanine/lysine ratio > 3 suggests true hyperalaninaemia.
- **Diagnosis:** Alanine and proline likely elevated secondary to lactic acidosis. Clinical history and results may suggest ETHE1 deficiency or other mitochondrial disease.
- Further tests: Molecular genetic analysis of *ETHE1*. Functional analysis of respiratory chain complexes.

6.2. Comments on the 2022 results

- The amino acid interpretation scheme is a pilot scheme with 105 participants.
- We tried to include cases where changes in amino acid concentrations can be primary or secondary to the underlying inborn disorder of metabolism.
- In case 2 (prolidase deficiency) a chromatogram was provided for HPLC with ninhydrin detection. Some of the participants don't use this method. It has to be discussed how to proceed in the future with this situation. However, the 2023 results submission form will include a question asking you to submit your analysis method.
- As well as testing the participants competence for more routine disorders, this scheme also aims to give them the opportunity of expanding their knowledge. Therefore, we included prolidase deficiency and hypotonia-cystinuria syndrome in the first circulation. Additionally, we included the concept of "best interpretation".
- For the second round, the amino acid concentrations of two patients with very rare and unusual inborn errors of metabolism and one patient with a vitamin deficiency were selected.
- The overall performance in all three second round cases was below 80% (80% was considered to be a good result).

7. Plan for the scheme to run as a full EQA scheme in 2023

7.1. Scheme Design:

- Limit number of participants to 135 (this is an increase compared to 2022 as the intention is to recruit an additional assessor) with a maximum one registration per lab.
- 2 submission deadlines on 30th May 2023 and 19th September 2023, 3 cases per deadline. The full 2023 calendar will be published on the ERNDIM website (<u>www.erndim.org</u>) in early January 2023 and will also be included in the scheme instructions.
- Online submission of all results will be mandatory, using the Formdesk website as for 2022. Only one set of submitted results will be allowed per registration.
- 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 plus 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 2022 pilot, 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 were 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 Scientific Advisory Board (SAB) agreed at their November 2022 meeting that the principle of critical error will apply to this scheme and the score required for satisfactory performance will be 20/36 points (56%). However, this score will be subject to annual review by the SAB.
- 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 2024.

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 (Y/N), if they submitted results (Y/N), and if their performance was satisfactory (Y/N).

7.6. Scheme price

• The scheme price will be 150 Euro per registration.

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: 28th April 2023

The Scientific Evaluators

S. Celle - Buy

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



APPENDIX 1. Detailed scores for submitting laboratories

<u>Key</u>

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

Anon. lab		202	22.01		2022.02			2022.03				First round	
number	Α	D	R	Sum	Α	D	R	Sum	Α	D	R	Sum	total score
1	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
2	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	16.0
3	2.0	1.0	1.0	4.0	1.0	2.0	2.0	5.0	2.0	1.0	0.0	3.0	12.0
4	2.0	2.0	2.0	6.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	13.0
5	1.0	1.0	1.0	3.0	2.0	2.0	0.0	4.0	2.0	2.0	2.0	6.0	13.0
6	2.0	2.0	2.0	6.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	13.0
7	2.0	2.0	2.0	6.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	13.0
8	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	0.0	0.0	2.0	13.0
9	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	0.0	4.0	16.0
10	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	14.0
11	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
12	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
13	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	14.0
14	2.0	1.0	2.0	5.0	0.0	0.0	0.0	0.0	2.0	2.0	2.0	6.0	11.0
15	2.0	1.0	2.0	5.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	16.0
16	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
17	1.0	2.0	1.0	4.0	0.0	0.0	0.0	0.0	2.0	2.0	1.0	5.0	9.0
18	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	1.0	1.0	4.0	12.0
19	1.0	1.0	1.0	3.0	2.0	2.0	1.0	5.0	2.0	2.0	1.0	5.0	13.0
20	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
21	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
22	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
23	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
24	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
25	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	15.0
26	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
27	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	15.0
28	2.0	2.0	1.0	5.0	2.0	2.0	1.0	5.0	2.0	0.0	0.0	2.0	12.0
29	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
30	1.0	2.0	2.0	5.0	2.0	2.0	1.0	5.0	2.0	0.0	0.0	2.0	12.0
31	1.0	2.0	1.0	4.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	15.0
32	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
33	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	16.0
34	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
35	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	16.0
36	1.0	1.0	1.0	3.0	2.0	2.0	1.0	5.0	2.0	1.0	1.0	4.0	12.0
37	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	15.0

Table 10: First round scores (for labs that submitted results)



Anon. lab		202	22.01			202	22.02			202	22.03		First round
number	Α	D	R	Sum	Α	D	R	Sum	Α	D	R	Sum	total score
38	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
39	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	13.0
40	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
41	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
42	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	1.0	5.0	16.0
43	1.0	1.0	2.0	4.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	16.0
44	1.0	2.0	1.0	4.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	15.0
45	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
46	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
47	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
48	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
49	2.0	1.0	1.0	4.0	1.0	0.0	0.0	1.0	2.0	1.0	0.0	3.0	8.0
50	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
51	2.0	1.0	1.0	4.0	0.0	0.0	0.0	0.0	2.0	1.0	0.0	3.0	7.0
52	1.0	1.0	1.0	3.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	11.0
53	1.0	1.0	1.0	3.0	1.0	0.0	0.0	1.0	2.0	1.0	1.0	4.0	8.0
54	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
55	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
56	2.0	2.0	1.0	5.0	1.0	0.0	1.0	2.0	2.0	2.0	2.0	6.0	13.0
57	2.0	2.0	1.0	5.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	16.0
58	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
59	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
60	2.0	1.0	2.0	5.0	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	16.0
61	2.0	2.0	2.0	6.0	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	17.0
62	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
63	2.0	2.0	2.0	6.0	1.0	0.0	0.0	1.0	2.0	1.0	1.0	4.0	11.0
64	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
65	2.0	2.0	1.0	5.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	12.0
66	2.0	2.0	1.0	5.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	12.0
67	1.0	2.0	2.0	5.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	13.0
68	2.0	1.0	1.0	4.0	1.0	0.0	0.0	1.0	2.0	1.0	0.0	3.0	8.0
69	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	15.0
70	2.0	1.0	1.0	4.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	15.0
71	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	0.0	0.0	2.0	10.0
72	2.0	1.0	1.0	4.0	1.0	0.0	2.0	3.0	2.0	2.0	2.0	6.0	13.0
73	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	15.0
74	2.0	1.0	1.0	4.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	11.0
75	1.0	1.0	2.0	4.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	11.0
76	2.0	2.0	1.0	5.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	12.0
77	2.0	1.0	1.0	4.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	11.0
78	1.0	1.0	1.0	3.0	0.0	0.0	0.0	0.0	2.0	2.0	2.0	6.0	9.0
79	2.0	2.0	1.0	5.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	13.0
80	2.0	2.0	1.0	5.0	1.0	0.0	0.0	1.0	2.0	1.0	0.0	3.0	9.0
81	2.0	1.0	1.0	4.0	1.0	0.0	0.0	1.0	2.0	2.0	0.0	4.0	9.0
82	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	17.0
83	2.0	1.0	1.0	4.0	0.0	0.0	0.0	0.0	2.0	2.0	2.0	6.0	10.0



Anon. lab		202	22.01			202	22.02			202	22.03		First round
number	Α	D	R	Sum	Α	D	R	Sum	Α	D	R	Sum	total score
84	1.0	1.0	2.0	4.0	0.0	0.0	0.0	0.0	2.0	1.0	1.0	4.0	8.0
85	2.0	0.0	1.0	3.0	0.0	0.0	0.0	0.0	2.0	2.0	1.0	5.0	8.0
86	2.0	1.0	1.0	4.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	11.0
87	2.0	1.0	1.0	4.0	0.0	0.0	0.0	0.0	2.0	1.0	0.0	3.0	7.0
88	1.0	2.0	1.0	4.0	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	13.0
89	1.0	1.0	1.0	3.0	0.0	0.0	0.0	0.0	2.0	1.0	0.0	3.0	6.0
90	2.0	0.0	0.0	2.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	9.0
91	2.0	2.0	0.0	4.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	11.0
92	1.0	2.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	16.0
93	2.0	1.0	1.0	4.0	0.0	0.0	0.0	0.0	2.0	1.0	0.0	3.0	7.0
94	1.0	2.0	1.0	4.0	1.0	0.0	0.0	1.0	2.0	1.0	0.0	3.0	8.0
95	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	16.0
96	2.0	1.0	0.0	3.0	1.0	0.0	1.0	2.0	2.0	1.0	0.0	3.0	8.0
97	1.0	1.0	1.0	3.0	1.0	0.0	0.0	1.0	2.0	2.0	2.0	6.0	10.0
98	1.0	1.0	1.0	3.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	15.0
99	1.0	2.0	2.0	5.0	0.0	0.0	0.0	0.0	2.0	2.0	2.0	6.0	11.0

Table 11: Second round scores (for labs that submitted results)

Anon. lab	2022.04			2022.05				2022.06				Second round	
number	Α	D	R	Sum	Α	D	R	Sum	Α	D	R	Sum	total score
1	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
2	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	14.0
3	2.0	0.0	1.0	3.0	2.0	0.0	0.0	2.0	2.0	2.0	0.0	4.0	9.0
4	2.0	0.0	2.0	4.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	12.0
5	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
6	1.0	2.0	2.0	5.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	13.0
7	1.0	0.0	1.0	2.0	2.0	0.0	0.0	2.0	2.0	1.0	0.0	3.0	7.0
8	1.0	2.0	2.0	5.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	13.0
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	1.0	0.0	2.0	3.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	11.0
11	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
12	1.0	1.0	2.0	4.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	15.0
14	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
15	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	14.0
16	1.0	0.0	2.0	3.0	2.0	0.0	2.0	4.0	2.0	2.0	2.0	6.0	13.0
17	1.0	0.0	2.0	3.0	2.0	1.0	1.0	4.0	2.0	2.0	1.0	5.0	12.0
18	1.0	0.0	2.0	3.0	2.0	2.0	2.0	6.0	2.0	0.0	2.0	4.0	13.0
19	2.0	2.0	1.0	5.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	16.0
20	1.0	0.0	2.0	3.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	11.0
21	1.0	2.0	1.0	4.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	15.0
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	1.0	0.0	2.0	3.0	2.0	0.0	2.0	4.0	2.0	2.0	2.0	6.0	13.0
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	1.0	1.7	4.7	2.0	2.0	2.0	6.0	16.7



Anon. lab		202	22.04			202	22.05			202	22.06		Second round
number	Α	D	R	Sum	Α	D	R	Sum	Α	D	R	Sum	total score
28	1.0	2.0	1.0	4.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	14.0
29	1.0	0.0	2.0	3.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	13.0
30	1.0	0.0	2.0	3.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	11.0
31	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
32	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
33	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
34	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	14.0
35	2.0	1.0	1.0	4.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	12.0
36	2.0	2.0	2.0	6.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	17.0
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	0.0	2.0	4.0	2.0	2.0	2.0	6.0	16.0
39	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
40	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
42	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
43	1.0	0.0	1.0	2.0	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	11.0
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	0.0	1.0	2.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	10.0
46	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
47	1.0	1.0	2.0	4.0	2.0	0.0	2.0	4.0	2.0	2.0	2.0	6.0	14.0
48	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
49	1.0	1.0	2.0	4.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	15.0
50	2.0	0.0	2.0	4.0	2.0	0.0	0.0	2.0	2.0	2.0	0.0	4.0	10.0
51	1.0	0.0	1.0	2.0	2.0	0.0	2.0	4.0	2.0	2.0	0.0	4.0	10.0
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	1.0	2.0	5.0	2.0	2.0	2.0	6.0	16.0
55	2.0	2.0	2.0	6.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	14.0
56	1.0	2.0	2.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	15.0
57	1.0	2.0	0.0	3.0	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	12.0
58	1.0	0.0	2.0	3.0	1.7	0.0	1.0	2.7	2.0	1.0	0.0	3.0	8.7
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	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	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	18.0
63	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
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	0.0	1.0	2.0	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	11.0
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	1.0	2.0	5.0	2.0	1.0	2.0	5.0	2.0	0.0	2.0	4.0	14.0
69	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
70	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
71	2.0	0.0	2.0	4.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	12.0
72	1.0	2.0	2.0	5.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	16.0
73	1.0	0.0	1.0	2.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	14.0
74	1.0	0.0	2.0	3.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	14.0
75	1.0	2.0	2.0	5.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	16.0
76	1.0	2.0	2.0	5.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	13.0



Anon. lab		202	22.04			202	22.05		2022.06				Second round
number	Α	D	R	Sum	Α	D	R	Sum	Α	D	R	Sum	total score
77	1.0	0.0	2.0	3.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	11.0
78	2.0	0.0	0.0	2.0	2.0	2.0	1.0	5.0	2.0	2.0	0.0	4.0	11.0
79	1.0	0.0	2.0	3.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	6.0	11.0
80	1.0	0.0	2.0	3.0	2.0	2.0	0.0	4.0	2.0	2.0	2.0	6.0	13.0
81	1.0	2.0	2.0	5.0	0.0	0.0	1.0	1.0	0.0	0.0	2.0	2.0	8.0
82	2.0	2.0	0.0	4.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	14.0
83	1.0	0.0	1.0	2.0	2.0	2.0	1.0	5.0	2.0	2.0	2.0	6.0	13.0
85	1.0	2.0	2.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	15.0
87	1.0	0.0	1.0	2.0	2.0	0.0	0.0	2.0	2.0	0.0	0.0	2.0	6.0
88	1.0	0.0	1.0	2.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	14.0
89	1.0	0.0	0.0	1.0	2.0	0.0	0.0	2.0	2.0	0.0	0.0	2.0	5.0
90	1.0	1.0	1.0	3.0	2.0	0.0	1.0	3.0	2.0	1.0	2.0	5.0	11.0
94	1.0	0.0	1.0	2.0	2.0	0.0	2.0	4.0	2.0	1.0	2.0	5.0	11.0
95	2.0	1.0	1.0	4.0	2.0	1.0	0.0	3.0	2.0	2.0	2.0	6.0	13.0
96	1.0	0.0	1.0	2.0	2.0	2.0	2.0	6.0	2.0	1.0	0.0	3.0	11.0
97	1.0	0.0	1.0	2.0	2.0	1.0	2.0	5.0	2.0	0.0	0.0	2.0	9.0
99	1.0	0.0	2.0	3.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	6.0	13.0
100	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
101	1.0	1.0	1.0	3.0	2.0	1.0	1.0	4.0	2.0	0.0	2.0	4.0	11.0

Table 12: Total scores for 2022 pilot scheme (for labs that submitted results)

Anon. lab number	First round (2022-01 to -03	Second round (2022-04 to -06)	Total Score	% Max score*	
1	18	17	35	97%	
2	16	14	30	83%	
3	12	9	21	58%	
4	13	12	25	69%	
5	13	15	28	78%	
6	13	13	26	72%	
7	13	7	20	56%	
8	13	13	26	72%	
9	16	18	34	94%	
10	14	11	25	69%	
11	18	17	35	97%	
12	18	15	33	92%	
13	14		14		Partial submitter
14	11	16	27	75%	
15	16	14	30	83%	
16	18	13	31	86%	
17	9	12	21	58%	
18	12	13	25	69%	
19	13	16	29	81%	
20	17	11	28	78%	
21	17	15	32	89%	
22	17	18	35	97%	
23	18	13	31	86%	



Anon. lab number	First round (2022-01 to -03	Second round (2022-04 to -06)	Total Score	% Max score*	
24	18	18	36	100%	
25	15	16	31	86%	
26	17	18	35	97%	
27	15	16.7	31.7	88%	
28	12	14	26	72%	
29	17	13	30	83%	
30	12	11	23	64%	
31	15	17	32	89%	
32	17	18	35	97%	
33	16	18	34	94%	
34	18	14	32	89%	
35	16	12	28	78%	
36	12	17	29	81%	
37	15	18	33	92%	
38	17	16	33	92%	
39	13	15	28	78%	
40	18	17	35	97%	
41	17		17		Partial submitter
42	16	18	34	94%	
43	16	11	27	75%	
44	15	17	32	89%	
45	18	10	28	78%	
46	17	17	34	94%	
47	18	14	32	89%	
48	18	16	34	94%	
49	8	15	23	64%	
50	17	10	27	75%	
51	7	10	17	47%	
52	11	18	29	81%	
53	8	16	24	67%	
54	18	16	34	94%	
55	17	14	31	86%	
56	13	15	28	78%	
57	16	12	28	78%	
58	17	8.7	25.7	71%	
59	17	18	35	97%	
60	16	18	34	94%	
61	17		17		Partial submitter
62	18	18	36	100%	
63	11	15	26	72%	
64	17	16	33	92%	
65	12	11	23	64%	
66	12	18	30	83%	
67	13	14	27	75%	
68	8		8		
69	15	17	32	89%	

Anon. lab number	First round (2022-01 to -03	Second round (2022-04 to -06)	Total Score	% Max score*	
70	15	16	31	86%	
71	10	12	22	61%	
72	13	16	29	81%	
73	15	14	29	81%	
74	11	14	25	69%	
75	11	16	27	75%	
76	12	13	25	69%	
77	11	11	22	61%	
78	9	11	20	56%	
79	13	11	24	67%	
80	9	13	22	61%	
81	9	8	17	47%	
82	17	14	31	86%	
83	10	13	23	64%	
84	8		8		Partial submitter
85	8	15	23	64%	
86	11		11		Partial submitter
87	7	6	13	36%	
88	13	14	27	75%	
89	6	5	11	31%	
90	9	11	20	56%	
91	11		11		Partial submitter
92	16		16		Partial submitter
93	7		7		Partial submitter
94	8	11	19	53%	
95	16	13	29	81%	
96	8	11	19	53%	
97	10	9	19	53%	
98	15		15		Partial submitter
99	11	13	24	67%	
100		15	15		Partial submitter
101		11	11		Partial submitter

* = % Max Score (36 points) is shown only for labs that submitted results for both submission rounds

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

Version Number	Published	Amendments
1	28 April 2023	2022 Pilot annual report published

END OF REPORT

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