Amino Acids Interpretation (AAI)

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Annual Report 2023 *[DOC5126]*

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Please Note:

- This annual report is intended for participants of the ERNDIM AAI EQA scheme. The contents should not be used for any publication without permission of the Scientific Advisor.
- The fact that your laboratory participates in ERNDIM schemes 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. 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 135 registered laboratories by email by the Administration Office on 9th May and 29th August 2023 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 2023.01, .02 and .03) and second round (samples AAI 2023.04, .05 and .06) were 30th May and 19th September 2023 respectively. Overall, 127/135 (94.1%) registered participants submitted results for both rounds of the 2023. Five labs (3.7%) only submitted results for one of the rounds (4 for just the first round and 1 for just the second round). While a separate three laboratories (2.2%) 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 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 2023 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.**

a. Appeals

If your laboratory has been assigned poor performance in the 2023 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.

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 2023 scheme

Sample	Clinical Information	Sex	Age at Diagnosis	Diagnoses
AAI 2023-01	Two days old, resuscitation for ventricular fibrillation, antibiotic therapy for suspected sepsis	M	2 days	Carbamylphosphat synthetase deficiency (CPS deficiency), detection of two pathogenic nonsense mutations
AAI 2023-02	Cholestatic jaundice with normally coloured stools, hepatomegaly, global hypotonia and eye-tracking difficulties, micrognathia, high-arched palate, unique transverse palmer crease	M	2.5 months	Adenosine kinase deficiency
AAI 2023-03	Ten days old, cerebral seizures, somnolence, shrill screaming, weight loss	F	10 days	Classical MSUD
AAI 2023-04	Seven years old, photophobia, eyes pain, visual impairment	M	7 years	Tyrosinemia type II (homozygous mutation in *TAT* gene)
AAI 2023-05	Pulmonary microangiopathy and renal insufficiency in a patient 20 years post renal transplant	M	55 years	Remethylation defect (CblC disease)
AAI 2023-06	Developmental delay	F	3 years	Glutaminase deficiency

Table 2: % proficiencies for the cases in the 2023 scheme

Sample	No of returns	A (%)	D (%)	R (%)	Total (%)
AAI 2023-01	131	98%	90%	95%	**95%**
AAI 2023-02	131	99%	84%	81%	**88%**
AAI 2023-03	131	99%	100%	92%	**97%**
AAI 2023-04	128	99%	99%	96%	**98%**
AAI 2023-05	128	91%	94%	96%	**94%**
AAI 2023-06	128	99%	66%	79%	**82%**

Key

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

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

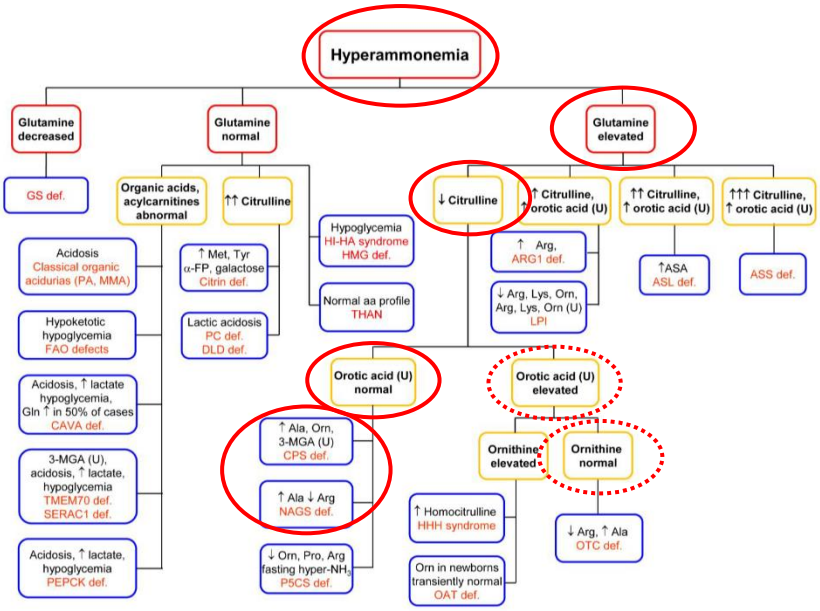
Total Score	No of labs	*(% of participating labs)*
0%	0	*0.0%*
0 – 9.9%	0	*0.0%*
10 – 19.9%	0	*0.0%*
20 – 29.9%	0	*0.0%*
30 – 39.9%	0	*0.0%*
40 – 49.9%	0	*0.0%*
50 – 59.9%	1	*0.8%*
60 – 69.9%	3	*2.4%*
70 – 79.9%	5	*3.9%*
80 – 89.9%	33	*26.0%*
90 – 99.9%	44	*34.6%*
100%	41	*32.3%*
Total	**127**	***100%***

The full anonymised results for all labs that submitted results are given in APPENDIX 1 on page 10.

6.1. Case 2023-1: Carbamylphosphat synthetase deficiency (CPS deficiency)

6.1.1. Sample Details

The results provided were from a boy on the 2nd day of life, who has to be resuscitated for a short time during ventricular fibrillation. As sepsis was suspected, empirical antibiotic therapy was started. Because infection parameters were negative a metabolic work up was performed, which showed a hyperammonemia with ammonia concentrations up to max. 2700 µmol/l. Plasma amino acid profile revealed beside elevated glutamine and alanine, low citrulline concentration. No orotic acid excretion detectable (not reported here). Carbamylphosphat synthetase deficiency (CPS deficiency) was confirmed by the detection of two pathogenic nonsense mutations.



1. Investigations in plasma if not stated otherwise; U: urine; 3-MGA: 3-methylglutaconic aciduria (Rokicki et al. 2017) I

Figure 2: Application of the diagnostic algorithm on case 1, as concentration of orotic acid was not reported OTC, NAGS or CPS deficiency would be possible (see: UCD GUIDELINE – 1st REVISION 2018 (awmf.org))

6.1.2. Scoring details

Table 4: Scoring details for case 2023-1.

	Interpretation		Score (points)
Findings, abnormalities [A, maximum 2 points]	elevated	gln, ala	1
	low	cit	1
Diagnosis [D, maximum 2 points]	proximal urea cycle deficiency		2
	urea cycle deficiency		1
	CPS deficiency		1
	OTC deficiency		1
	NAGS deficiency		1
	CAVA deficiency		1
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**	orotic acid, organic acids in urine		1
	molecular genetic analyses of *UCD* genes		1
	enzymatic analyses of UCD enzymes		1

Scores for participating laboratories are in APPENDIX 1 on page 10.

6.1.3. Comments on overall performance

Overall proficiency was 95%. The proficiency for diagnosis was lowest at 90%, the most common "misdiagnosis" was carbonic anhydrase VA (CA-VA) deficiency.

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

6.1.4. Best interpretation (scored with 2 points each)

- **Findings:** There is a very strong hyperammonaemia with an elevated glutamine, glutamate, alanine, proline and lysine. Citrulline is non-detectable and arginine is low. Argininosuccinate is not reported (Lab. 37).
- **Diagnosis**: Ornithine transcarbamylase (OTC), carbamoyl phosphate synthetase (CPS), or N-acetyl glutamate synthase (NAGS) deficiency. Elevated lysine may be secondary to shortage of alpha-ketoglutarate (Lab. 116).
- **Further tests:** Determination of orotic acid. If orotic acid is high: enzymatic activity in liver and mutational analysis of *OTC* gene. If orotic acid is low: mutational analysis of *CPS1* and *NAGS* gene. Organic acids in urine (Lab. 40).

6.2. Case 2023-2: Adenosine kinase deficiency

6.2.1. Sample details

The results of the amino acid analysis in plasma were obtained from a 2.5-month-old boy who presented with cholestatic jaundice with normal coloured stools, hepatomegaly, global muscular hypotonia and eye movement disorders. He also had dysmorphic features such as micrognathia, high arched palate and unique transverse palmar folds. Adenosine kinase deficiency has been shown to be the cause of the clinical symptoms and biochemical changes.

6.2.2. Scoring details

Table 5: Scoring details for case 2023-2.

	Interpretation		Score (points)
Findings, abnormalities [A, maximum 2 points]	elevated	met	1
	elevated	tyr, thr	1
	normal	cit	
	elevated (unspecific)	lys	
Diagnosis [D, maximum 2 points]	Hepatic dysfunction leading to increased met and tyr		1
	Adenosine kinase deficiency		2
	Tyrosinaemia type I		1
	MAT I/III		

	Interpretation	Score (points)
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**	homocysteine	1
	SAH/SAM	1
	organic acids	1
	molecular genetic analysis (*ADK*, *MAT1/III*)	1

Scores for participating laboratories are in APPENDIX 1 on page 10.

6.2.3. Comments on overall performance

The overall proficiency is relatively low at 88%, whereas the description of the laboratory results was correct in almost 99% of the participants. Almost all laboratories recognised the abnormalities with significantly elevated methionine and tyrosine concentrations. Proficiency in interpreting the results was low at 84%. The proficiency of the recommendation was also low (81%). This may be due to the fact that the constellation of findings allowed two directions of interpretation (with different recommendations), first a liver disease, then methionine degradation disorders including an adenosine kinase deficiency.

Critical Errors: One critical error was agreed for one lab. The participant interpreted the changes as a result of a liver dysfunction. The recommendations for further examinations did not take an inborn disorder of metabolism into consideration.

6.2.4. Best interpretation (scored with 2 points each)

- **Findings:** Markedly increased tyrosine, methionine and moderately increased threonine and slightly increased lysine, ornithine, arginine (Lab. 121).
- **Diagnosis:** Results together with clinical suggest adenosine kinase deficiency. Need to exclude tyrosinaemia type-1 as a cause of liver dysfunction. Consider congenital disorders of glycosylation (Lab. 20).
- **Further tests**: Analyse SAM, SAH in blood, analyse homocysteine in blood, analyse succinylacetone in blood, confirm diagnosis with genetic testing (Lab. 2).

6.3. Case 2023-3: Classical MSUD

6.3.1. Sample details

The results of the amino acid analysis in plasma were obtained from ten days old girl with cerebral seizures, somnolence, shrill screaming and weight loss (ammonia 160 µmol/L). Based on the results of the analysis of plasma amino acids and organic acids, the diagnosis of MSUD was made and confirmed by molecular genetics.

6.3.2. Scoring details

Table 6: Scoring details for case 2023-3.

	Interpretation		Score (points)
Findings, abnormalities [A, maximum 2 points]	elevated	leu, ile, val	1
	elevated	allo ile	1
	low	ala	1
Diagnosis [D, maximum 2 points]	MSUD		2
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**	organic acids in urine		1
	molecular genetic analyses of *BCKDC*		1
	enzymatic analyses of BCKDC		1

Scores for participating laboratories are in APPENDIX 1 on page 10.

6.3.3. Comments on overall performance

The overall performance was very good with 97%. All participants made the right diagnosis! This was due to the clear and well-known abnormalities in the plasma aminogram. Some of the recommendations for further examinations only included the recommendation to carry out a genetic examination. There was no mention of which gene should be examined, nor was there any mention of other examinations such as the analysis of organic acids. For this reason, some participants lost points, but overall the performance was also high with 92%.

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

6.3.4. Best interpretation (scored with 2 points each)

- **Findings:** Markedly elevated branched-chain amino acids (leucine, valine, isoleucine) including alloisoleucine. Low alanine, borderline low glutamine (Lab. 124).

- **Diagnosis:** Increased branched chain amino acids with pathognomonic increase of allo-isoleucine are diagnostic for Maple Syrup Urine Disease (MSUD). Clinical information is consistent with this diagnosis. (Lab. 4)
- **Further tests:** Urine organic acid profile analysis. Analysis of the genes encoding subunits of the BCKD complex. (If necessary, enzymatic assay of complex activity in cultured fibroblasts.) (Lab. 5)

6.4. Case 2023-4: Tyrosinemia type II (homozygous mutation in *TAT* gene)

6.4.1. Sample Details

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

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

6.4.2. Scoring details

Table 7: Scoring details for case 2023.04

	Interpretation		**Score (points)**
Findings, abnormalities [A, maximum 2 points]	elevated	tyr	2
Diagnosis [D, maximum 2 points]	Tyrosinaemia type II		2
	Tyrosinaemia		1
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**)	organic acids in urine (succinlyacetone)		1
	molecular genetic analysis of *TAT* gene		2
	other tyrosinaemia genes (III)		1

Scores for participating laboratories are in APPENDIX 1 on page 10.

6.4.3. Comments on overall performance

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

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

6.4.4. Best interpretation (scored with 2 points each)

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

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

6.5.1. Sample details

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

6.5.2. Scoring details

Table 8: Scoring details for case 2023-5.

	Interpretation		**Score (points)**
Findings, abnormalities [A, maximum 2 points]	low (normal)	met	1
	elevated	homocystine	1

	Interpretation	Score (points)
Diagnosis [D, maximum 2 points]	primary remethylation defect	2
	secondary (folate, B12, NO) remethylation defect	2
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**	organic acids in urine (MMA, methylcitrate)	1
	acylcarnitine profile	
	total homocysteine	1
	folate, vitamin B12 concentration	1
	genes involved in remethylation defects	1
Comments	Genes involved in remethylation defect: *MTHFR, MMACHC, MMADHC, MTR, MTRR*	

Scores for participating laboratories are in APPENDIX 1 on page 10. Diagnosis of (mild) hyperhomocysteinaemia was scored only with one point.

6.5.3. Comments on overall performance

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

Critical Errors: Four critical errors were agreed for suggesting mild hyperhomocysteinaemia, a normal profile, or wrong diagnosis, without a further recommendation to clarify the findings.

6.5.4. Best interpretation (scored with 2 points each)

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

6.6. Case 2023-6: Glutaminase deficiency

6.6.1. Sample details

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

6.6.2. Scoring details

Table 9: Scoring details for case 2023-6.

	Interpretation		Score (points)
Findings, abnormalities [A, maximum 2 points]	elevated	gln	2
Diagnosis [D, maximum 2 points]	glutaminase deficiency		2
	urea cycle disorder (but argninase def. 0 points)		1
	CAVA		1

	Interpretation	Score (points)
Further tests (if molecular genetics recommended, specify the gene) **[R, maximum 2 points]**)	organic acids	1
	orotic acid	
	molecular genetic analysis glutaminase deficiency	2
	CSF glutamine	1
	enzymatic analysis glutaminase	1

Scores for participating laboratories are in APPENDIX 1 on page 10.

6.6.3. Comments on overall performance

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

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

6.6.4. Best interpretation (scored with 2 points each)

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

6.7. Comments on the 2023 results

6.7.1. First circulation

The overall performance was good (93%). Some of the recommendations for further examinations only included the recommendation to carry out a genetic examination. There was no mention of which gene should be examined, nor was there any mention of other examinations such as the analysis of organic acids. For this reason, some participants lost points.

6.7.2. Second circulation

Generally, the overall performance was good (91%) although a few labs made inadequate or incorrect interpretation leading to reduced scores. In some cases these were considered to be critical errors.

7. Plans for 2024

7.1. Scheme Design:

- The number of participants is limited to 150 with a maximum of one registration per lab.
- 2 submission deadlines on **28th May 2024** and **9th September 2024**, 3 cases per deadline. The full 2024 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 for 2024. 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 2023 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 Scientific Advisory Board (SAB) agreed at their November 2023 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.
- 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 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, if they submitted results, and if their performance was satisfactory.

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: 3rd May 2024

The Scientific Evaluators

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

APPENDIX 1. Detailed scores for submitting laboratories

Key

A = Findings, abnormalities

D = Diagnosis

R = Recommendations for further testing

DNS = Did not submit results

Table 10: First round scores

Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
1	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
2	2.0	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	0.0	3.0	2.0	2.0	2.0	**6.0**	**15.0**
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	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
7	2.0	1.0	2.0	5.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	**6.0**	**16.0**
8	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
9	2.0	2.0	2.0	6.0	2.0	1.0	2.0	5.0	2.0	2.0	2.0	**6.0**	**17.0**
10	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**
11	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**
12	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**
13	1.0	1.0	1.0	3.0	2.0	2.0	1.0	5.0	2.0	2.0	0.0	**4.0**	**12.0**
14	2.0	2.0	1.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	0.0	**4.0**	**13.0**
15	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**
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	1.0	1.0	4.0	2.0	0.0	0.0	2.0	2.0	2.0	2.0	**6.0**	**12.0**
18	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**
19	2.0	2.0	2.0	6.0	1.0	0.0	2.0	3.0	2.0	2.0	2.0	**6.0**	**15.0**
20	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
21	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
22	2.0	2.0	2.0	6.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	**6.0**	**16.0**
23	2.0	2.0	1.0	5.0	2.0	1.0	1.0	4.0	2.0	2.0	2.0	**6.0**	**15.0**
24	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
25	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	1.0	**5.0**	**16.0**
26	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
27	2.0	2.0	2.0	6.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**18.0**
28	2.0	1.0	2.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**17.0**
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	1.0	2.0	5.0	2.0	2.0	2.0	**6.0**	**17.0**
31	2.0	1.0	1.0	4.0	2.0	1.0	2.0	5.0	2.0	2.0	1.0	**5.0**	**14.0**
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	2.0	1.0	5.0	2.0	2.0	2.0	6.0	2.0	2.0	2.0	**6.0**	**17.0**
35	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**
36	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**
37	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**

Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .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	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**
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	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
42	2.0	1.0	2.0	**5.0**	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**16.0**
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													**DNS**
45	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**
46	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
47	2.0	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	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
49	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
50	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
51	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
52	2.0	1.0	2.0	**5.0**	2.0	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	**15.0**
53	2.0	2.0	2.0	**6.0**	1.0	2.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	**16.0**
54	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**
55	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**
56	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**
57	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
58	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
59	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**
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	2.0	2.0	1.0	**5.0**	2.0	1.0	1.0	**4.0**	2.0	2.0	0.0	**4.0**	**13.0**
63	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**
64	2.0	1.0	2.0	**5.0**	2.0	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	**15.0**
65	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
66	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**17.0**
67	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
68	2.0	1.0	2.0	**5.0**	2.0	0.0	1.0	**3.0**	2.0	2.0	2.0	**6.0**	**14.0**
69	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
70	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
71	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
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	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
77	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
78	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
79	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**
80	2.0	2.0	2.0	**6.0**	2.0	1.0	0.0	**3.0**	2.0	2.0	2.0	**6.0**	**15.0**
81	2.0	1.0	2.0	**5.0**	2.0	0.0	0.0	**2.0**	2.0	2.0	2.0	**6.0**	**13.0**
82													**DNS**

Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .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	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
84													**DNS**
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	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**
87	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
88	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	0.0	**4.0**	**16.0**
89	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**
90	2.0	1.0	2.0	**5.0**	2.0	0.0	0.0	**2.0**	2.0	2.0	1.0	**5.0**	**12.0**
91	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
92	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	1.0	2.0	1.0	**4.0**	**14.0**
93													**DNS**
94	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
95	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	1.0	2.0	2.0	**5.0**	**16.0**
96	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**
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	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
100	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
101	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
102	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**17.0**
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	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**
105	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**
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	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
108	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**
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	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**
112	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
113	2.0	2.0	2.0	**6.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
114	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**
115	2.0	1.0	1.0	**4.0**	2.0	2.0	0.0	**4.0**	2.0	2.0	2.0	**6.0**	**14.0**
116	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**
117	1.0	1.0	1.0	**3.0**	2.0	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	**13.0**
118	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**
119	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**
120	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
121	2.0	1.0	1.0	**4.0**	2.0	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	**14.0**
122	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
123	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
124	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
125	2.0	2.0	2.0	**6.0**	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
126	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**
127	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**

Anon. lab number	2023.01				2023.02				2023.03				2023.01 - .03
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
128	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**
129	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**
130	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
131	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	1.0	**5.0**	**16.0**
132	1.0	1.0	1.0	**3.0**	2.0	1.0	0.0	**3.0**	2.0	2.0	0.0	**4.0**	**10.0**
133	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**
134	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**
135	2.0	2.0	2.0	**6.0**	2.0	1.0	0.0	**3.0**	2.0	2.0	1.0	**5.0**	**14.0**

Table 11: Second round scores

Anon. lab number	2023.04				2023.05				2023.06				2023.04 - .06
	A	D	R	Sum	A	D	R	Sum	A	D	R	Sum	Total Score
1	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
2	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
3	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
4	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	**17.0**
5	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
6	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
7	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	**17.0**
8	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
9	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	2.0	**4.0**	**16.0**
10	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	**17.0**
11	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
12	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
13													**DNS**
14	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
15	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
16	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	**17.0**
17	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
18	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
19	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	2.0	**4.0**	**16.0**
20	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
21	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
22	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
23	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
24	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
25	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	**16.0**
26	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
27	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
28	2.0	2.0	2.0	**6.0**	1.0	1.0	2.0	**4.0**	2.0	0.0	1.0	**3.0**	**13.0**
29	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
30	2.0	1.0	1.0	**4.0**	0.0	0.0	0.0	**0.0**	2.0	0.0	1.0	**3.0**	**7.0**
31	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
32	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
33	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**

34	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
35													**DNS**
36	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
37	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
38	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
39	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
40	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	0.0	2.0	**4.0**	**15.0**
41	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
42	2.0	2.0	1.0	**5.0**	2.0	1.0	2.0	**5.0**	2.0	0.0	1.0	**3.0**	**13.0**
43	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
44													**DNS**
45	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
46	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
47	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
48	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
49	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
50	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
51	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
52	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	1.0	0.0	**3.0**	**14.0**
53	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
54													**DNS**
55	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
56	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
57	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
58	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	1.0	1.0	**4.0**	**15.0**
59	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
60	2.0	2.0	2.0	**6.0**	1.0	1.0	2.0	**4.0**	2.0	2.0	2.0	**6.0**	**16.0**
61	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
62	2.0	2.0	1.0	**5.0**	1.0	1.0	1.0	**3.0**	2.0	0.0	1.0	**3.0**	**11.0**
63	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
64	0.0	2.0	2.0	**4.0**	1.0	2.0	0.0	**3.0**	2.0	2.0	2.0	**6.0**	**13.0**
65	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
66	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
67	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
68	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	**14.0**
69	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
70	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
71	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
72	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
73	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
74	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
75	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
76	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
77	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
78	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
79	2.0	2.0	1.0	**5.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**15.0**
80	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**

81	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
82	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
83	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
84													**DNS**
85	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
86	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
87	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
88	2.0	2.0	1.0	**5.0**	1.0	0.0	1.0	**2.0**	2.0	1.0	0.0	**3.0**	**10.0**
89	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
90	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	2.0	0.0	1.0	**3.0**	**11.0**
91	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
92	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	**14.0**
93													**DNS**
94	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
95	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	2.0	0.0	1.0	**3.0**	**14.0**
96	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	1.0	**5.0**	**17.0**
97	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
98	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
99	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
100	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
101	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
102	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
103	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	**17.0**
104	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
105	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	0.0	1.0	1.0	**2.0**	**14.0**
106	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
107	2.0	1.0	1.0	**4.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	**12.0**
108	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	2.0	**5.0**	**17.0**
109	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
110	2.0	2.0	0.0	**4.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	**12.0**
111	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
112	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
113	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
114	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
115	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	2.0	2.0	**6.0**	**17.0**
116	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
117	2.0	2.0	2.0	**6.0**	1.0	1.0	1.0	**3.0**	2.0	2.0	2.0	**6.0**	**15.0**
118	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
119	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	0.0	1.0	**3.0**	**14.0**
120	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
121	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
122	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
123	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
124	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
125	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
126	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	1.0	**3.0**	**15.0**
127	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**

128	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	0.0	1.0	**3.0**	**14.0**
129	2.0	2.0	1.0	**5.0**	1.0	2.0	2.0	**5.0**	2.0	0.0	1.0	**3.0**	**13.0**
130	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	**18.0**
131	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	1.0	1.0	**4.0**	**16.0**
132	2.0	2.0	1.0	**5.0**	1.0	1.0	1.0	**3.0**	2.0	0.0	0.0	**2.0**	**10.0**
133	2.0	2.0	2.0	**6.0**	2.0	2.0	2.0	**6.0**	2.0	0.0	0.0	**2.0**	**14.0**
134	2.0	2.0	2.0	**6.0**	1.0	2.0	2.0	**5.0**	2.0	0.0	1.0	**3.0**	**14.0**
135													**DNS**

Table 12: Total scores for 2023 scheme

Anon. lab number	First round (2023-01 to -03	Second round (2023-04 to -06)	Total Score	% Max score*	
1	18.0	17.0	35.0	97.2%	
2	18.0	18.0	36.0	100.0%	
3	15.0	18.0	33.0	91.7%	
4	18.0	17.0	35.0	97.2%	
5	18.0	18.0	36.0	100.0%	
6	18.0	18.0	36.0	100.0%	
7	16.0	17.0	33.0	91.7%	
8	18.0	18.0	36.0	100.0%	
9	17.0	16.0	33.0	91.7%	
10	16.0	17.0	33.0	91.7%	
11	16.0	16.0	32.0	88.9%	
12	17.0	18.0	35.0	97.2%	
13	12.0		12.0		Partial submitter
14	13.0	16.0	29.0	80.6%	
15	17.0	15.0	32.0	88.9%	
16	17.0	17.0	34.0	94.4%	
17	12.0	17.0	29.0	80.6%	
18	17.0	18.0	35.0	97.2%	
19	15.0	16.0	31.0	86.1%	
20	18.0	18.0	36.0	100.0%	
21	18.0	18.0	36.0	100.0%	
22	16.0	18.0	34.0	94.4%	
23	15.0	15.0	30.0	83.3%	
24	18.0	18.0	36.0	100.0%	
25	16.0	16.0	32.0	88.9%	
26	18.0	18.0	36.0	100.0%	
27	18.0	18.0	36.0	100.0%	
28	17.0	13.0	30.0	83.3%	
29	18.0	18.0	36.0	100.0%	
30	17.0	7.0	24.0	66.7%	Poor Performer: Critical Error (2023.05)
31	14.0	18.0	32.0	88.9%	
32	18.0	18.0	36.0	100.0%	
33	18.0	15.0	33.0	91.7%	
34	17.0	15.0	32.0	88.9%	
35	16.0		16.0	44.4%	Partial submitter
36	16.0	18.0	34.0	94.4%	

Anon. lab number	First round (2023-01 to -03	Second round (2023-04 to -06)	Total Score	% Max score*	
37	17.0	18.0	35.0	97.2%	
38	18.0	18.0	36.0	100.0%	
39	17.0	17.0	34.0	94.4%	
40	18.0	15.0	33.0	91.7%	
41	18.0	18.0	36.0	100.0%	
42	16.0	13.0	29.0	80.6%	
43	18.0	18.0	36.0	100.0%	
44					Non-submitter
45	14.0	15.0	29.0	80.6%	
46	18.0	18.0	36.0	100.0%	
47	17.0	15.0	32.0	88.9%	
48	18.0	18.0	36.0	100.0%	
49	17.0	18.0	35.0	97.2%	
50	18.0	18.0	36.0	100.0%	
51	18.0	17.0	35.0	97.2%	
52	15.0	14.0	29.0	80.6%	
53	16.0	15.0	31.0	86.1%	
54	17.0		17.0		Partial submitter
55	17.0	18.0	35.0	97.2%	
56	18.0	15.0	33.0	91.7%	
57	18.0	18.0	36.0	100.0%	
58	18.0	15.0	33.0	91.7%	
59	17.0	15.0	32.0	88.9%	
60	18.0	16.0	34.0	94.4%	
61	18.0	18.0	36.0	100.0%	
62	13.0	11.0	24.0	66.7%	
63	17.0	15.0	32.0	88.9%	
64	15.0	13.0	28.0	77.8%	
65	18.0	18.0	36.0	100.0%	
66	17.0	17.0	34.0	94.4%	
67	18.0	18.0	36.0	100.0%	
68	14.0	14.0	28.0	77.8%	
69	18.0	18.0	36.0	100.0%	
70	18.0	18.0	36.0	100.0%	
71	18.0	15.0	33.0	91.7%	
72	18.0	16.0	34.0	94.4%	
73	18.0	18.0	36.0	100.0%	
74	18.0	17.0	35.0	97.2%	
75	18.0	18.0	36.0	100.0%	
76	17.0	16.0	33.0	91.7%	
77	18.0	18.0	36.0	100.0%	
78	18.0	16.0	34.0	94.4%	
79	17.0	15.0	32.0	88.9%	
80	15.0	18.0	33.0	91.7%	Poor Performer: Critical Error (2023.02)
81	13.0	18.0	31.0	86.1%	
82		18.0	18.0		Partial submitter

Anon. lab number	First round (2023-01 to -03	Second round (2023-04 to -06)	Total Score	% Max score*	
83	17.0	18.0	35.0	97.2%	
84					Non-submitter
85	18.0	16.0	34.0	94.4%	
86	17.0	15.0	32.0	88.9%	
87	18.0	18.0	36.0	100.0%	
88	16.0	10.0	26.0	72.2%	Poor Performer: Critical Error (2023.05)
89	17.0	18.0	35.0	97.2%	
90	12.0	11.0	23.0	63.9%	Poor Performer: Critical Error (2023.05)
91	18.0	18.0	36.0	100.0%	
92	14.0	14.0	28.0	77.8%	
93					Non-submitter
94	18.0	18.0	36.0	100.0%	
95	16.0	14.0	30.0	83.3%	
96	16.0	17.0	33.0	91.7%	
97	18.0	18.0	36.0	100.0%	
98	18.0	18.0	36.0	100.0%	
99	17.0	18.0	35.0	97.2%	
100	18.0	18.0	36.0	100.0%	
101	18.0	18.0	36.0	100.0%	
102	17.0	16.0	33.0	91.7%	
103	18.0	17.0	35.0	97.2%	
104	17.0	18.0	35.0	97.2%	
105	17.0	14.0	31.0	86.1%	
106	18.0	18.0	36.0	100.0%	
107	17.0	12.0	29.0	80.6%	
108	16.0	17.0	33.0	91.7%	
109	18.0	18.0	36.0	100.0%	
110	18.0	12.0	30.0	83.3%	
111	17.0	18.0	35.0	97.2%	
112	18.0	18.0	36.0	100.0%	
113	17.0	18.0	35.0	97.2%	
114	17.0	17.0	34.0	94.4%	
115	14.0	17.0	31.0	86.1%	
116	17.0	18.0	35.0	97.2%	
117	13.0	15.0	28.0	77.8%	
118	17.0	18.0	35.0	97.2%	
119	18.0	14.0	32.0	88.9%	
120	18.0	18.0	36.0	100.0%	
121	14.0	15.0	29.0	80.6%	
122	18.0	18.0	36.0	100.0%	
123	18.0	18.0	36.0	100.0%	
124	18.0	18.0	36.0	100.0%	
125	17.0	18.0	35.0	97.2%	
126	17.0	15.0	32.0	88.9%	
127	17.0	16.0	33.0	91.7%	

Anon. lab number	First round (2023-01 to -03	Second round (2023-04 to -06)	Total Score	% Max score*	
128	17.0	14.0	31.0	86.1%	
129	16.0	13.0	29.0	80.6%	
130	18.0	18.0	36.0	100.0%	
131	16.0	16.0	32.0	88.9%	
132	10.0	10.0	20.0	55.6%	Poor Performer: Score & Critical Error (2023.05)
133	17.0	14.0	31.0	86.1%	
134	18.0	14.0	32.0	88.9%	
135	14.0		14.0		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	03 May 2024	• 2023 annual report published

END OF REPORT