



QWAS

Quality in Water Analysis Scheme

Scheme Description

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Record of issue status and modifications

| ISSUE | ISSUE DATE | DETAILS | AUTHORISED BY |
|-------|------------|---|--|
| 10 | Sept 2014 | Added Staphylococcus species to 421. Inclusion of traceability information in Appendix A. Inclusion of subcontracting information in 'Test Materials' section. | R.Lathall |
| 11 | Sept 2015 | Corrected SPDA for 416 to 0.5 Included samples previously included in QMIS, i.e. identification test, paper exercise. Methods updated Removed Hard copy report information | A.S.Eden S.Fairless A.McCarthy |
| 12 | Aug 2016 | Updated details for Sample 427 regarding setting of assigned value by formulation | T.Noblett |
| 13 | Sept 2017 | Addition of sample 4 – 'Test using dipslide' from the Hygiene Scheme. Renamed to sample 428. 'Enumeration of <i>Legionella</i> species' added to sample 423. | T. Pullan |
| 14 | Sept 2018 | Amended sample 4 details to be qualitative Replaced method codes with 'All' Removed method code information Updated PCR range to 'All' | T. Pullan |
| 15 | Aug 2019 | Removed (Presence/Absence) from the title of sample 423 Included direct count analyte to samples 417 & 418 | A McCarthy R.Smith |
| 16 | Nov 2019 | Added 'Enumeration of <i>Pseudomonas aeruginosa</i> ' to sample 414 | A.S.Eden |
| 17 | Feb 2020 | Unit amended for sample 417 & 418 Enumeration of <i>Legionella</i> species by culture (direct count) Updated UKAS Logo | R.Smith A McCarthy |
| 18 | June 2020 | Unit amended for sample 427. Added yeast and mould to sample 413. | R.Smith T.Noblett |
| 19 | Sept 2020 | Test material 429 TVC in dialysis water added. Test material 430 SARS-CoV-2 in waste water added. | R.Smith |
| 20 | Feb 2021 | Format of 430 amended | R.Smith |
| 21 | July 2021 | Updated email address and UKAS logo Test materials 417 and 418 sample description changed from environmental to industrial waters Structure of 430 updated | A Collins M.Bell |
| 22 | Sept 2022 | Removed sample 428 (Dipslide) Added 'C.perfringens' and 'TVC' as new parameters for sample 421. Added sample 431 | M.Bell |

Notes:

Where this document has been translated, the English version shall remain the definitive version

Scheme Aims and Organisation

The primary aim of the Quality in Water Analysis Scheme (QWAS) is to enable laboratories performing the microbiological analysis of water to monitor their performance and compare it with that of their peers. QWAS also aims to provide information to participants on technical issues and methodologies relating to microbiological testing of water and related materials.

The QWAS scheme year operates from January to December. Further information about QWAS, including test material availability, round despatch dates and reporting deadlines, are available on the current QWAS application form.

Test Materials

Details of test materials available in QWAS are given in Appendix A. The test parameters are continually reviewed to ensure they meet the needs of current laboratory testing and regulatory requirements.

Test material batches are tested for homogeneity for at least one test parameter where deemed appropriate. Details of homogeneity tests performed and results are given in the QWAS Scheme Reports.

Some aspects of the scheme, such as test material production, homogeneity testing and stability assessment, can from time to time be subcontracted. When subcontracting occurs, it is placed with a competent subcontractor and LGC is responsible for this work. The planning of the scheme, the evaluation of performance and the authorisation of the final report will never be subcontracted.

Statistical Analysis

Information on the statistics used in QWAS can be found in the General Protocol and in the Scheme Report. Methods for determining assigned values and the values for SDPA used for individual samples are given in Appendix A.

Methods

Methods are listed in PORTAL. Please select the most appropriate method from the list. If none of the methods are appropriate, then please report your method as 'Other' and record a brief description in the Comments Section in PORTAL.

Results and Reports

QWAS results are returned through our electronic reporting software, PORTAL, full instructions for which are provided by email.

QWAS reports will be available on the website within 10 working days of round closure. Participants will be emailed a link to the report when it is available.

APPENDIX A - Description of abbreviations used

Assigned Value (AV)

The assigned value may be derived in the following ways:

- From the robust mean (median) of participant results (RMean). This is the median of participant results after the removal of test results that are inappropriate for statistical evaluation, e.g. miscalculations, transpositions and other gross errors. Generally, the assigned value will be set using results from all methods, unless the measurement is considered method-dependant, in which case the assigned value will be set by method and indicated in the report tables. For some analytes, where there is a recognised reference method for that type of measurement, this may be used as the assigned value for a particular analyte i.e. it would be applied to results obtained by any method.

Traceability: Assigned values which are derived from the participant results, or a sub-set of the results are not traceable to an international measurement standard. The uncertainty of assigned values derived in this way is estimated from the participant results, according to ISO 13528.

- From a formulation value (Form). This denotes the use of an assigned value derived from sample preparation details, where known and exact quantities of analyte have been used to prepare the sample.

Traceability: Assigned values calculated from the formulation of the test sample are traceable, via an unbroken metrological traceability chain, to an international measurement standard. The measurement uncertainty of the assigned value is calculated using the contributions from each calibration in the traceability chain.

- From a qualitative formulation (Qual Form). This applies to qualitative tests where the assigned value is simply based on the presence/absence of the analyte in the test material.

Traceability: Assigned values calculated from the qualitative formulation of the test sample are traceable to a certified reference standard or a microbiological reference strain.

- From expert labs (Expert). The assigned value for the analyte is provided by an 'expert' laboratory.

Traceability: Assigned values provided by an 'expert' laboratory may be traceable to an international measurement standard, according to the laboratory and the method used. The uncertainty of measurement for an assigned value produced in this way will be provided by the laboratory undertaking the analysis. Details of traceability and the associated uncertainty will be provided in the report for the scheme/round.

Range

This indicates the concentration range at which the analyte may be present in the test material.

SDPA

SDPA represents the 'standard deviation for proficiency assessment' which is used to assess participant performance for the measurement of each analyte. This may be a fixed value (as stated), a percentage (%) of the assigned value or based on the robust standard deviation of the participant measurement results, either across all methods or by method depending on whether the measurement made is method dependent (see assigned value).

Units

This indicates the units used for the assessment of data. These are the units in which participants should report their results. For some analytes in some schemes participants may have a choice of which units to report their results, however, the units stipulated in this scheme description are the default units to which any results reported using allowable alternative results will be converted to.

DP

This indicates the number of decimal places to which participants should report their measurement results.

APPENDIX A

Sample PT-WT-412

Indicator organisms in potable water

Supplied as:

10ml vial (to be resuscitated to final volume of 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|--|--------|-------|-----------|------------------------|--------------------------|----|
| Total aerobic count @ 22°C Total aerobic count @ 37°C | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu ml ⁻¹ | 0 |
| Enumeration of <i>Escherichia coli</i> | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of coliforms | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of Enterococci | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |

Sample PT-WT-413

Environmental organisms in potable water

Supplied as:

10ml vial (to be resuscitated to final volume of 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|---|--------|----------|-----------|------------------------|--------------------------|----|
| Enumeration of <i>Clostridium perfringens</i> | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of sulphite-reducing Clostridia | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Detection of sulphite-reducing Clostridia | All | QualForm | 0 to 1000 | NA | cfu 100 ml ⁻¹ | NA |
| Enumeration of sulphite-reducing Clostridia spores ONLY | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of <i>P.aeruginosa</i> | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of yeast; mould; yeast and mould (combined) | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |

QWAS Scheme Description

Sample PT-WT-414

Microorganisms in Process water

Supplied as:

10ml vial (to be resuscitated to final volume of 100 ml)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|---|--------|-------|-------------|------------------------|----------------------|----|
| Total aerobic count | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu ml ⁻¹ | 0 |
| Enumeration of <i>Pseudomonas</i> species | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu ml ⁻¹ | 0 |
| Enumeration of <i>Pseudomonas aeruginosa</i> | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu ml ⁻¹ | 0 |
| Enumeration of yeast; mould; yeast and mould (combined) | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu ml ⁻¹ | 0 |

Sample PT-WT-416

Salmonella/E.coli in Effluent sludge

Supplied as:

2 x 10g simulated sludge sample

| Analyte | Method | AV | Range | SDPA | Units | DP |
|--|--------|----------|-------------|------------------------|--------------------------|----|
| Detection of <i>Salmonella</i> species | All | QualForm | 0 to 10000 | NA | cfu 100 ml ⁻¹ | NA |
| Enumeration of <i>Escherichia coli</i> | All | RMean | 0 to 100000 | log ₁₀ 0.50 | cfu ml ⁻¹ | 0 |

Sample PT-WT-417

***Legionella pneumophila* in Industrial waters**

Supplied as:

1 x 10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|---|--------|----------|-------------|------------------------|---------------------|----|
| Enumeration of <i>Legionella pneumophila</i> by culture (membrane filtration) | All | RMean | 0 to 100000 | log ₁₀ 0.50 | cfu L ⁻¹ | 0 |
| Enumeration of <i>Legionella pneumophila</i> by culture (direct count) | All | RMean | 0 to 100000 | log ₁₀ 0.50 | cfu L ⁻¹ | 0 |
| Detection of <i>Legionella pneumophila</i> | All | QualForm | 0 to 100000 | NA | cfu L ⁻¹ | NA |

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| Analyte | Method | AV | Range | SDPA | Units | DP |
|---|--------|-------|-------|------------------------|-------------------------------|----|
| Enumeration of <i>Legionella pneumophila</i> by PCR | PCR | RMean | All | log ₁₀ 0.50 | genomic units L ⁻¹ | 0 |
| Identification of <i>Legionella pneumophila</i> | All | NA | NA | NA | NA | NA |

Sample PT-WT-418

Legionella species in Industrial waters

Supplied as:

1 x 10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|---|--------|----------|-------------|------------------------|-------------------------------|----|
| Enumeration of <i>Legionella</i> species by culture (membrane filtration) | All | RMean | 0 to 100000 | log ₁₀ 0.50 | cfu L ⁻¹ | 0 |
| Enumeration of <i>Legionella</i> species by culture (direct count) | All | RMean | 0 to 100000 | log ₁₀ 0.50 | cfu L ⁻¹ | 0 |
| Detection of <i>Legionella</i> species | All | QualForm | 0 to 100000 | NA | cfu L ⁻¹ | NA |
| Enumeration of <i>Legionella</i> species by PCR | PCR | RMean | All | log ₁₀ 0.50 | genomic units L ⁻¹ | 0 |
| Identification of <i>Legionella</i> species | All | NA | NA | NA | NA | NA |

Sample PT-WT-419

Microorganisms in Surface/Waste/Bathing waters

Supplied as:

10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|---------------------------------|--------|-------|-------------|------------------------|--------------------------|----|
| Enumeration of total coliforms | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of faecal coliforms | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |

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| Analyte | Method | AV | Range | SDPA | Units | DP |
|--|--------|----------|-------------|------------------------|--------------------------|----|
| Enumeration of <i>Escherichia coli</i> | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of enterococci | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Detection of <i>Salmonella</i> species | All | QualForm | 0 to 10000 | NA | cfu L ⁻¹ | NA |

Sample PT-WT-420

Microorganisms in Mineral water

Supplied as:

10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|--|--------|-------|-----------|------------------------|--------------------------|----|
| Total aerobic count at 22°C Total aerobic count at 37°C | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu ml ⁻¹ | 0 |
| Enumeration of <i>Escherichia coli</i> | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 250 ml ⁻¹ | 0 |
| Enumeration of enterococci | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 250 ml ⁻¹ | 0 |
| Enumeration of <i>Pseudomonas aeruginosa</i> | All | RMean | 0 to 1000 | log ₁₀ 0.35 | cfu 250 ml ⁻¹ | 0 |

Sample PT-WT-421

Microorganisms in Surface/Bathing/Recreational water

Supplied as:

10ml vial (to be resuscitated to final volume of 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|---|--------|-------|-------------|------------------------|--------------------------|----|
| Enumeration of coagulase-positive staphylococci Enumeration of <i>Staphylococcus</i> species | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of sulphite-reducing Clostridia | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |

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|---|-----|-------|-------------|------------------------|--------------------------|---|
| Enumeration of <i>Clostridium perfringens</i> | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Total aerobic count | All | RMean | 0 to 100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |

Sample PT-WT-422

Microorganisms in Sea Water

Supplied as:

10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|--|--------|----------|---------|------------------------|--------------------------|----|
| Enumeration of total coliforms | All | RMean | <100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of faecal coliforms | All | RMean | <100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of <i>Escherichia coli</i> | All | RMean | <100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Enumeration of enterococci | All | RMean | <100000 | log ₁₀ 0.35 | cfu 100 ml ⁻¹ | 0 |
| Detection of <i>Salmonella</i> species | All | QualForm | <10000 | NA | cfu L ⁻¹ | NA |

Sample PT-WT-423

Legionella in Potable Water

Supplied as:

10ml vial (to be resuscitated to final volume of 10 x 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|--|--------|----------|-----------|------------------------|---------------------|----|
| Detection of <i>Legionella</i> species at low levels | All | QualForm | 0 to 1000 | NA | NA | NA |
| Enumeration of <i>Legionella</i> species by culture | All | RMean | 0 to 1000 | log ₁₀ 0.50 | cfu L ⁻¹ | 0 |

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Sample PT-WT-424 **Microorganisms in Mineral water (Presence/absence)**
Supplied as: 10ml vial (to be resuscitated to final volume of 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|---|--------|----------|-----------|------|--------------------------|----|
| Detection of coagulase-positive staphylococci | All | QualForm | 0 to 1000 | NA | cfu 250 ml ⁻¹ | 0 |
| Detection of sulphite-reducing Clostridia | All | QualForm | 0 to 1000 | NA | cfu 50 ml ⁻¹ | 0 |
| Detection of spores of sulphite-reducing Clostridia | All | QualForm | 0 to 1000 | NA | cfu 50 ml ⁻¹ | 0 |

Sample PT-WT- 425 **Indicator organisms in potable water (Presence/absence)**
Supplied as: 10ml vial (to be resuscitated to a final volume of 1 litre)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|--------------------------------------|--------|----------|----------|------|--------------------------|----|
| Detection of <i>Escherichia coli</i> | All | QualForm | 0 to 100 | NA | cfu 100 ml ⁻¹ | NA |
| Detection of coliforms | All | QualForm | 0 to 100 | NA | cfu 100 ml ⁻¹ | NA |
| Detection of enterococci | All | QualForm | 0 to 100 | NA | cfu 100 ml ⁻¹ | NA |

Sample PT-WT-426 **Identification Test (non-pathogen)**
Supplied as: Participants will be provided with a vial of freeze-dried material containing a single organism which will need to be cultured on non-selective agar before test. The sample may contain biosafety level 1 or 2 organisms typically found in water.
 The organism should be identified to the correct family, genus or species level.

| Analyte | Method | AV | Range | SDPA | Units | DP |
|------------------------------------|--------|-------------|-------|------|-------|----|
| Identification of unknown organism | All | Formulation | NA | NA | NA | NA |

Sample PT-WT-427 **Paper exercise**
Supplied as: Participants will be provided with a photograph and a scenario in order to count the number of colonies and calculate the number of microorganisms in the original sample.

| Analyte | Method | AV | Range | SDPA | Units | DP |
|--|-------------------|-------------|----------|----------------------------------|---------|----|
| Counting of colonies and calculation of number of microorganisms | Visual count only | Formulation | 0 to 300 | Greater of robust SD or log 0.05 | Various | NA |

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Sample PT-WT-429

Total viable count in dialysis water

Supplied as:

10ml vial (to be resuscitated to a final volume of 100ml)

| Analyte | Method | AV | Range | SDPA | Units | DP |
|-------------------------------|--------|-------|----------|------------------------|----------------------|----|
| Total aerobic count @ 17-23°C | All | RMean | 0 to 100 | log ₁₀ 0.35 | Cfu ml ⁻¹ | 0 |

Sample PT-WT-430*

SARS-CoV-2 in waste water

Supplied as:

2 x 1.5 ml vial (A & B) of non-infectious, SARS-CoV-2 virus (whole genome)

2 x tablet (simulated waste water)

| Analyte | Method | Range | AV | SDPA | Units | DP |
|------------------------------|-----------|-------------------------|-------------|-----------|-------------------------|----|
| Detection of SARS-CoV-2 | Molecular | Positive/Negative | Qual Form | NA | NA | NA |
| Quantification of SARS-CoV-2 | Molecular | 0 to 10000 virus copies | Formulation | Robust SD | Copies ml ⁻¹ | NA |

Sample PT-WT-431*

Somatic Coliphages (φX174) in water

Supplied as:

2 x vial (A & B)

2 x 2ml PBS for resuscitation

| Analyte | Method | Range | AV | SDPA | Units | DP |
|--------------------------------------|--------|-------------------|-------------|-----------|--------------------------|----|
| Detection of Somatic coliphages | All | Positive/Negative | Qual Form | NA | NA | NA |
| Quantification of Somatic coliphages | All | 0 to 1000 | Formulation | Robust SD | PFU 100 ml ⁻¹ | NA |

* Test material currently not included in LGC's UKAS Scope of Accreditation.