QWAS

Quality in Water Analysis Scheme

Scheme Description

LGC Standards
Proficiency Testing
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Record of issue status and modifications

<table>
<thead>
<tr>
<th>ISSUE</th>
<th>ISSUE DATE</th>
<th>DETAILS</th>
<th>AUTHORISED BY</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>June 2013</td>
<td>Amended details for 417 and 418 to allow separate reporting by cultural and PCR methods.</td>
<td>T.Noblett</td>
</tr>
<tr>
<td>9</td>
<td>Sept 2013</td>
<td>Added microbiological methods. Separated sample 417 and 418 into two separate samples and added ‘Enumeration of sulphite-reducing Clostridia’ to sample 421</td>
<td>T.Noblett</td>
</tr>
<tr>
<td>10</td>
<td>Sept 2014</td>
<td>Added Staphylococcus species to 421. Inclusion of traceability information in Appendix A. Inclusion of subcontracting information in ‘Test Materials’ section.</td>
<td>R.Lathall</td>
</tr>
<tr>
<td>11</td>
<td>Sept 2015</td>
<td>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.</td>
<td>A.S.Eden S.Fairless</td>
</tr>
<tr>
<td>12</td>
<td>Aug 2016</td>
<td>Updated details for Sample 427 regarding setting of assigned value by formulation</td>
<td>A. McCarthy</td>
</tr>
<tr>
<td>13</td>
<td>Sept 2017</td>
<td>Addition of sample 4 – ‘Test using dipslide’ from the Hygiene Scheme. Renamed to sample 428. ‘Enumeration of Legionella species’ added to sample 423.</td>
<td>T. Pullan</td>
</tr>
<tr>
<td>14</td>
<td>May 2018</td>
<td>Amended sample 4 details to be qualitative</td>
<td>T. Pullan</td>
</tr>
<tr>
<td>15</td>
<td>Sept 2018</td>
<td>Replaced method codes with ‘All’. Removed method code information. Updated PCR range to ‘All’.</td>
<td>T. Pullan</td>
</tr>
</tbody>
</table>

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. However, participants may request result submission forms on which to report and return results if they are unable to report through electronic means. This will incur an additional charge.

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 412
**Indicator organisms in potable water**
*Supplied as: 10ml vial (to be resuscitated to final volume of 1 litre)*

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total aerobic count @ 22°C</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>Total aerobic count @ 37°C</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of <em>Escherichia coli</em></td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of coliforms</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of Enterococci</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
</tbody>
</table>

### Sample 413
**Clostridium/Pseudomonas in potable water**
*Supplied as: 10ml vial (to be resuscitated to final volume of 1 litre)*

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of <em>Clostridium perfringens</em></td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of sulphite-reducing Clostridia</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>Detection of sulphite-reducing Clostridia</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 1000</td>
<td>NA</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>NA</td>
</tr>
<tr>
<td>Enumeration of <em>P.aeruginosa</em></td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of sulphite-reducing Clostridia spores ONLY</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu 100 ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
</tbody>
</table>

### Sample 414
**Microorganisms in Process water**
*Supplied as: 10ml vial (to be resuscitated to final volume of 100 ml)*

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total aerobic count</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
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<tr>
<td>Enumeration of <em>Pseudomonas species</em></td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>log&lt;sub&gt;10&lt;/sub&gt; 0.35</td>
<td>cfu ml&lt;sup&gt;-1&lt;/sup&gt;</td>
<td>0</td>
</tr>
</tbody>
</table>
### QWAS Scheme Description

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of yeast and mould (total)</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of yeast</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of mould</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu ml$^{-1}$</td>
<td>0</td>
</tr>
</tbody>
</table>

**Sample 416**  
**Salmonella/E.coli in Effluent sludge**  
**Supplied as:**  
2 x 10g simulated sludge sample

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Detection of <em>Salmonella</em> species</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 10000</td>
<td>NA</td>
<td>cfu 100 ml$^{-1}$</td>
<td>NA</td>
</tr>
<tr>
<td>Enumeration of <em>Escherichia coli</em></td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.50$</td>
<td>cfu ml$^{-1}$</td>
<td>0</td>
</tr>
</tbody>
</table>

**Sample 417**  
**Legionella pneumophila in environmental waters**  
**Supplied as:**  
1 x 10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of <em>Legionella pneumophila</em> by culture</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.50$</td>
<td>cfu L$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Detection of <em>Legionella pneumophila</em></td>
<td>All</td>
<td>QualForm</td>
<td>0 to 100000</td>
<td>NA</td>
<td>cfu L$^{-1}$</td>
<td>NA</td>
</tr>
<tr>
<td>Enumeration of <em>Legionella pneumophila</em> by PCR</td>
<td>PCR</td>
<td>RMean</td>
<td>All</td>
<td>$\log_{10} 0.50$</td>
<td>genomic units L$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Identification of <em>Legionella pneumophila</em></td>
<td>All</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>
### Sample 418
**Legionella species in environmental waters**
*Supplied as:* 1 x 10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of <em>Legionella</em> species by culture</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.50$</td>
<td>cfu L$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Detection of <em>Legionella</em> species</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 100000</td>
<td>NA</td>
<td>cfu L$^{-1}$</td>
<td>NA</td>
</tr>
<tr>
<td>Enumeration of <em>Legionella</em> species by PCR</td>
<td>PCR</td>
<td>RMean</td>
<td>All</td>
<td>$\log_{10} 0.50$</td>
<td>genomic units L$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Identification of <em>Legionella</em> species</td>
<td>All</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

### Sample 419
**Microorganisms in Surface/Waste/Bathing waters**
*Supplied as:* 10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of total coliforms</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of faecal coliforms</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of <em>Escherichia coli</em></td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of enterococci</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Detection of <em>Salmonella</em> species</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 100000</td>
<td>NA</td>
<td>cfu L$^{-1}$</td>
<td>NA</td>
</tr>
</tbody>
</table>
Sample 420  \hspace{1cm} \textbf{Microorganisms in Mineral water}  
\textbf{Supplied as:}  \hspace{1cm} 10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)  

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total aerobic count at 22°C</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Total aerobic count at 37°C</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of \textit{Escherichia coli}</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 250 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of enterococci</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 250 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of \textit{Pseudomonas aeruginosa}</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 250 ml$^{-1}$</td>
<td>0</td>
</tr>
</tbody>
</table>

Sample 421  \hspace{1cm} \textbf{Microorganisms in Surface/Bathing/Recreational water}  
\textbf{Supplied as:}  \hspace{1cm} 10ml vial (to be resuscitated to final volume of 1 litre)  

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of coagulase-positive staphylococci</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of \textit{Staphylococcus} species</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of sulphite-reducing Clostridia</td>
<td>All</td>
<td>RMean</td>
<td>0 to 100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
</tbody>
</table>

Sample 422  \hspace{1cm} \textbf{Microorganisms in Sea Water}  
\textbf{Supplied as:}  \hspace{1cm} 10ml vial (to be resuscitated to final volume of up to 10 x 1 litre)  

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of total coliforms</td>
<td>All</td>
<td>RMean</td>
<td>&lt;100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of faecal coliforms</td>
<td>All</td>
<td>RMean</td>
<td>&lt;100000</td>
<td>$\log_{10} 0.35$</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
</tbody>
</table>
## QWAS Scheme Description

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enumeration of <em>Escherichia coli</em></td>
<td>All</td>
<td>RMean</td>
<td>&lt;100000</td>
<td>log$_{10}$ 0.35</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Enumeration of enterococci</td>
<td>All</td>
<td>RMean</td>
<td>&lt;100000</td>
<td>log$_{10}$ 0.35</td>
<td>cfu 100 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Detection of <em>Salmonella</em> species</td>
<td>All</td>
<td>QualForm</td>
<td>&lt;10000</td>
<td>NA</td>
<td>cfu L$^{-1}$</td>
<td>NA</td>
</tr>
</tbody>
</table>

### Sample 423

**Legionella in Potable Water (Presence/absence)**

**Supplied as:**
10ml vial (to be resuscitated to final volume of 10 x 1 litre)

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Detection of <em>Legionella</em> species at low levels</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 1000</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>Enumeration of <em>Legionella</em> species by culture</td>
<td>All</td>
<td>RMean</td>
<td>0 to 1000</td>
<td>log$_{10}$ 0.50</td>
<td>cfu L$^{-1}$</td>
<td>0</td>
</tr>
</tbody>
</table>

### Sample 424

**Microorganisms in Mineral water (Presence/absence)**

**Supplied as:**
10ml vial (to be resuscitated to final volume of 1 litre)

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Detection of coagulase-positive staphylococci</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 1000</td>
<td>NA</td>
<td>cfu 250 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Detection of sulphite-reducing <em>Clostridia</em></td>
<td>All</td>
<td>QualForm</td>
<td>0 to 1000</td>
<td>NA</td>
<td>cfu 50 ml$^{-1}$</td>
<td>0</td>
</tr>
<tr>
<td>Detection of spores of sulphite-reducing <em>Clostridia</em></td>
<td>All</td>
<td>QualForm</td>
<td>0 to 1000</td>
<td>NA</td>
<td>cfu 50 ml$^{-1}$</td>
<td>0</td>
</tr>
</tbody>
</table>
QWAS Scheme Description

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

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Detection of <em>Escherichia coli</em></td>
<td>All</td>
<td>QualForm</td>
<td>0 to 100</td>
<td>NA</td>
<td>cfu 100 ml⁻¹</td>
<td>NA</td>
</tr>
<tr>
<td>Detection of coliforms</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 100</td>
<td>NA</td>
<td>cfu 100 ml⁻¹</td>
<td>NA</td>
</tr>
<tr>
<td>Detection of enterococci</td>
<td>All</td>
<td>QualForm</td>
<td>0 to 100</td>
<td>NA</td>
<td>cfu 100 ml⁻¹</td>
<td>NA</td>
</tr>
</tbody>
</table>

**Sample 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.

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Identification of unknown organism</td>
<td>All</td>
<td>Formulation</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

**Sample 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.

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Counting of colonies and calculation of number of microorganisms</td>
<td>Visual count only</td>
<td>Formulation</td>
<td>0 to 300</td>
<td>Greater of robust SD or log 0.05</td>
<td>cfu/ml</td>
<td>NA</td>
</tr>
</tbody>
</table>

**Sample 428**  
**Hygiene testing using dip slides**  
**Supplied as:**  
Lyophilised tablet/s to be added to sterile water

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Method</th>
<th>AV</th>
<th>Range</th>
<th>SDPA</th>
<th>Units</th>
<th>DP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total viable count</td>
<td>Dip slide</td>
<td>Qual Form</td>
<td>0 to 100,000</td>
<td>N/A</td>
<td>cfu/dipslide or cfu/cm²</td>
<td>N/A</td>
</tr>
<tr>
<td>Enumeration of coliforms</td>
<td>Dip slide</td>
<td>Qual Form</td>
<td>0 to 100,000</td>
<td>N/A</td>
<td>cfu/dipslide or cfu/cm²</td>
<td>N/A</td>
</tr>
</tbody>
</table>

*Not currently included in LGC’s UKAS Scope of Accreditation*