FEPTU
Food & Environmental Proficiency Testing Unit
Operated by UK Health Security Agency

# Summary of Results

## External Quality Assessment of Water Microbiology

## Wastewater Scheme

**Distribution Number: WW001 Sample Numbers: WW001A & WW001B**

| | |
|---|---|
| Distribution Date: | **28 July 2025** |
| Results Due: | **29 August 2025** |
| Report Date: | **24 September 25** |
| Samples prepared and quality control tested by: | **Divya George**<br>**Afifa Halim**<br>**Nafeesa Hussain**<br>**Cansev Katar**<br>**Sabine Naujokat**<br>**Zak Prior**<br>**Jake Videlefsky** |
| Data analysed by: | **Nita Patel**<br>**Zak Prior** |
| Report compiled by: | **Nita Patel**<br>**Zak Prior** |
| Authorised by: | **Nita Patel** |



**UK Health Security Agency**
**Food and Environmental Proficiency Testing Unit (FEPTU)**
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**Overview:**
Wastewater harbors a complex and dynamic bacterial community. By elucidating the roles of both harmful and beneficial microbes, we can optimise wastewater treatment strategies for cleaner water and improved public health. The implementation of rigorous quality control measures, exemplified by using proficiency testing samples, ensures the accuracy and reliability of wastewater analysis, a cornerstone of effective environmental protection.

**FEPTU Quality Control:**
To demonstrate homogeneity of the sample, a minimum of 10 freeze-dried vials, selected randomly from a batch, are tested in duplicate for selected parameters requiring enumeration or detection.

To demonstrate stability of the sample, a minimum of six freeze-dried vials, selected randomly from a batch, are examined throughout the distribution period for enumeration/detection parameters.

UKHSA uses methods stipulated in the Standing Committee of Analysts series of documents for methods stipulated in the Microbiology of Recreational and Environmental Waters: Microbiology Working Group – Standing Committee of Analysts

The FEPTU results are used for guidance in the preliminary intended results.

**Guidelines and general advice:**

If you experience difficulties with any of the examinations, please refer to the Scheme Guide
Scheme Guide - Food and Environmental Proficiency Testing Unit

**Please contact FEPTU staff for advice and information:**

| | | |
|---|---|---|
| **Repeat samples** | Carmen Gomes or Kermin Daruwalla | **Tel: +44 (0)20 8327 7119** |
| **Data analysis** | Zak Prior | |
| **Microbiological advice** | Zak Prior or Nita Patel | **E-mail: foodeqa@ukhsa.gov.uk** |
| **General comments and complaints** | Zak Prior or Nita Patel | |
| **Scheme Advisor** | N/A | |
| **Scheme Co-ordinator** | Nita Patel | |

**Accreditation:**

This non-accredited distribution was produced using the principles and practices within ISO/IEC 17043:2023.

| | |
|---|---|
| Total sent samples | 18 |
| Non returns | 2 |

## Sample: WW001A

**Contents:** *Escherichia coli* ($4.5x10^5$) (wild strain), *Pantoea agglomerans* ($1.0x10^4$) (wild strain), *Enterococcus faecium* ($6.8x10^6$) (wild strain), *Pseudomonas aeruginosa* ($1.0x10^3$) (wild strain) SARS-CoV-2 Omicron B.1.1.529 (quantification: undetermined by FEPTU)

**Expected results:**

All counts are expressed as colony forming units (cfu) per 100 mL (or genome copies per 100mL for SARS-CoV-2) unless otherwise stated

**Guide to Scoring and Statistics:**

Please note that there are not enough data results (<10) to calculate robust statistics and scores. Whilst this data has been presented as a guide to provide some indication of your performance, they should be interpreted with caution. Your results can be found on pages 5 and 6 of this report and to note the z-scores have been calculated using the wider fixed standard deviation 0.55.

| Parameter | Coliform | *Escherichia coli* | Enterococci | *Salmonella* spp. | SARS-CoV-2 |
|---|---|---|---|---|---|
| FEPTU median | $4.1x10^5$ ($5.61 \log_{10}$) | $4.1x10^5$ ($5.61 \log_{10}$) | $6.0x10^6$ ($6.78 \log_{10}$) | Not detected | Detected |
| No. results returned | 5 | 8 | 8 | 4 | 7 (6 quantification) |
| Assigned value (Participants median all results) | $1.95x10^6$ ($6.29 \log_{10}$) | $1.02x10^6$ ($6.01 \log_{10}$) | $6.40x10^6$ ($6.81 \log_{10}$) | Not detected | $9.47x10^5$ ($5.98 \log_{10}$) |
| Minimum and maximum values | $5.50x10^5$ – $2.41x10^6$ | $5.00x10^5$ – $1.53x10^6$ | $4.20x10^6$ – $6.80x10^6$ | | $7.40x10^4$ – $7.50x10^6$ |
| Expected range | $6.17x10^5$ – $6.17x10^6$ | $2.93x10^5$ – $3.54x10^6$ | $2.02x10^6$ – $2.02x10^7$ | | $2.36x10^4$ – $3.79x10^7$ |
| Standard deviation* ($\log_{10}$) | 0.11 | 0.27 | 0.03 | | 0.80 |
| Uncertainty of assigned value ($U(Xpt)= \log_{10}$) | 0.07 | 0.13 | 0.01 | | 0.41 |
| Total number of censored values (greater than) | 1 | 1 | 3 | | 0 |
| False Positives | N/A | N/A | N/A | 0 | N/A |
| False Negatives | 0 | 0 | 0 | N/A | 0 |
| Not examined | 11 | 8 | 8 | 12 | 9 |

*Robust *S** based on median absolute deviation about the participants' median *(MADe)* and is based on logged data

## Sample: WW001B

**Contents:** *Citrobacter braakii* ($2.1x10^2$) (wild strain), *Enterococcus faecalis* ($6.0x10^3$) (wild strain), *Salmonella* Wentworth 11;$z_{10}$;1,2 ($4.9x10^3$ per vial) (wild strain) and SARS-CoV-2 Beta B.1.351 (quantification: undetermined by FEPTU)

**Expected results:**

All counts are expressed as colony forming units (cfu) per 100 mL (or genome copies per 100mL for SARS-CoV-2) unless otherwise stated

**Guide to Scoring and Statistics:**

Please note that there are not enough data results (<10) to calculate robust statistics and scores. Whilst this data has been presented as a guide to provide some indication of your performance, they should be interpreted with caution. Your results can be found on pages 5 and 6 of this report and to note the z-scores have been calculated using the wider fixed standard deviation 0.55.

| Parameter | Coliform | *Escherichia coli* | Enterococci | *Salmonella* spp. | SARS-CoV-2 |
|---|---|---|---|---|---|
| FEPTU median | $2,4x10^2$ ($2.38 \log_{10}$) | 0 | $5.9x10^3$ ($3.77 \log_{10}$) | Detected | Detected |
| No. results returned | 5 | 8 | 8 | 4 | 7 (6 quantification) |
| Assigned value (Participants median all results) | $6.49x10^2$ ($2.81 \log_{10}$) | - | $8.44x10^3$ ($3.93 \log_{10}$) | Detected | $3.22x10^6$ ($6.51 \log_{10}$) |
| Minimum and maximum values | $1.40x10^2$ – $3.00x10^3$ | - | $6.40x10^3$ – $1.30x10^4$ | | $6.69x10^4$ – $2.06x10^7$ |
| Expected range | $1.32x10^2$ – $3.17x10^3$ | - | $2.67x10^3$ – $2.67x10^4$ | | $2.05x10^5$ – $5.17x10^7$ |
| Standard deviation* ($\log_{10}$) | 0.34 | - | 0.09 | | 0.60 |
| Uncertainty of assigned value ($U(Xpt)= \log_{10}$) | 0.19 | - | 0.04 | | 0.31 |
| Total number of censored values (greater than) | 0 | - | 0 | | 0 |
| False Positives | N/A | 0 | N/A | 0 | N/A |
| False Negatives | 0 | N/A | 0 | N/A | 0 |
| Not examined | 11 | 8 | 8 | 12 | 9 |

*Robust *S** based on median absolute deviation about the participants' median *(MADe)* and is based on logged data

**Summary of all the participant's results for WW001A and WW001B for *Escherichia coli***

| Lab | Results WW001A | UKHSA score | Z-score | Results WW001B | UKHSA score | Z-score |
|---|---|---|---|---|---|---|
| | 1553100 | 2 | 0.33 | 0 | 2 | N/A |
| | 500000 | 2 | -0.56 | 0 | 2 | N/A |
| | 540000 | 2 | -0.50 | 0 | 2 | N/A |
| | 1080000 | 2 | 0.05 | 0 | 2 | N/A |
| | 1413600 | 2 | 0.26 | <1 | 2 | N/A |
| | >100000 | 2 | N/A | 0 | 2 | N/A |
| | 1020000 | 2 | 0.00 | 0 | 2 | N/A |
| | 531818 | 2 | -0.51 | 0 | 2 | N/A |

**Summary of all the participant's results for WW001A and WW001B for coliform**

| Lab | Results WW001A | UKHSA score | Z-score | Results WW001B | UKHSA score | Z-score |
|---|---|---|---|---|---|---|
| | 1732900 | 2 | -0.09 | 649 | 2 | 0.00 |
| | 2200000 | 2 | 0.09 | 3000 | 2 | 1.21 |
| | 550000 | 0 | -1.00 | 140 | 2 | -1.21 |
| | 2419600 | 2 | 0.17 | 1022 | 2 | 0.36 |
| | >100000 | 2 | N/A | 380 | 2 | -0.42 |

**Summary of all the participant's results for WW001A and WW001B for Enterococci**

| Lab | Results WW001A | UKHSA score | Z-score | Results WW001B | UKHSA score | Z-score |
|---|---|---|---|---|---|---|
| | 6800000 | 2 | 0.05 | 8500 | 2 | 0.00 |
| | 6400000 | 2 | 0.00 | 13000 | 2 | 0.34 |
| | 6600000 | 2 | 0.02 | 6700 | 2 | -0.18 |
| | >1000000 | 2 | N/A | 8400 | 2 | 0.00 |
| | TNTC | N/A | N/A | 9804 | 2 | 0.12 |
| | >100000 | 2 | N/A | 6400 | 2 | -0.22 |
| | 4200000 | 2 | -0.33 | 7500 | 2 | -0.09 |
| | 6150000 | 2 | -0.03 | 9350 | 2 | 0.08 |

**Summary of all the participant's results for WW001A and WW001B for *Salmonella* spp.**

| Lab | Results WW001A | UKHSA score | Z-score | Results WW001B | UKHSA score | Z-score |
|---|---|---|---|---|---|---|
| | Not detected | 2 | 0 | Detected | 2 | 0 |
| | Not detected | 2 | 0 | Detected | 2 | 0 |
| | Not detected | 2 | 0 | Detected | 2 | 0 |
| | Not detected | 2 | 0 | Detected | 2 | 0 |

**Summary of all the participant's results for WW001A for SARS-CoV-2**

| Lab | Results WW001A | UKHSA score | Z-score | Quantification results WW001A | UKHSA score | Z-score |
|---|---|---|---|---|---|---|
| | Detected | 2 | 0 | 7.40E+04 | 2 | -2.01 |
| | Detected | 2 | 0 | 5.11E+06 | 2 | 1.33 |
| | Detected | 2 | 0 | 7.50E+06 | 2 | 1.63 |
| | Detected | 2 | 0 | 4.24E+05 | 2 | -0.64 |
| | Detected | 2 | 0 | 6.28E+05 | 2 | -0.32 |
| | Detected | 2 | 0 | | | |
| | Detected | 2 | 0 | 1.43E+06 | 2 | 0.32 |

**Summary of all the participant's results for WW001B for SARS-CoV-2**

| Lab | Results WW001B | UKHSA score | Z-score | Quantification results WW001B | UKHSA score | Z-score |
|---|---|---|---|---|---|---|
| | Detected | 2 | 0 | 6.69E+04 | 1 | -3.06 |
| | Detected | 2 | 0 | 1.49E+07 | 2 | 1.21 |
| | Detected | 2 | 0 | 2.06E+07 | 2 | 1.47 |
| | Detected | 2 | 0 | 2.29E+06 | 2 | -0.27 |
| | Detected | 2 | 0 | 2.79E+06 | 2 | -0.11 |
| | Detected | 2 | 0 | | | |
| | Detected | 2 | 0 | 3.72E+06 | 2 | 0.11 |

## General comments

Scoring of this scheme:

The expected range for the quantification/enumeration results reported have been calculated using the median absolute deviation from the median (*MADe***) values in whole numbers, which are determined from the median result reported by participants' and take into account the following criteria:

(1) median ± 2 *MADeS**
(2) median ± 3 *MADeS**
(3) median ± 0.5 $\log_{10}$ units

If the ranges in (1) and/or (2) are less than the value of the median ± 0.5 $\log_{10}$ units then the expected range is extended as described in (3).

**The median absolute deviation from the median value is a robust estimate of the standard deviation (*S**). It is only possible to calculate a precise estimate of the *S** if more than 20 participants report a value.

| | Score |
|---|---|
| Expected range within the range according to criteria (1) | 2 |
| Outlying results (1) within the range of criteria (2) but not within criteria (1) | 1 |
| Outlying results (2) outside the range of criteria (2) | 0 |

Statistical evaluation

Participants are advised that for a robust statistical evaluation at least 20 reported results are required for a parameter. When statistical calculation is based on 10 – 19 results, they should be interpreted with caution as they may be overly influenced by outlying results. This is the reason why the standard deviation of the enumeration results reported can be wide.

Information of importance

Please refer to this website to obtain the latest information for your proficiency testing: https://www.feptu.org.uk/ or use the following links for more specific detail:

1. Report format explained: Annotated report

2. Performance rating: Performance-over-time and Scheme guide (section 16.0)

3. Scoring and statistics used: Scoring information and stats

4. Homogeneity and stability: Scheme guide (section 9.0)

5. Complaints and appeal process: Scheme guide (section 20.0 and 21.0)

For further information about the operation of the service including confidentiality and terms of participation, please refer to the Scheme Guide: Scheme guide

## Questionnaire analysis

Please note that not all participants provided the relevant information.

FEPTU are aware that processes are different and therefore have not attempted to categorise the information into specific groups for comparing data.

The data shown below is for information only and does not attempt to compare the performance of the various methods used by laboratories in this PT distribution. Not all laboratories provided information to all the questions.

The below table provides information on the published methods followed and the number of users for coliform, *Escherichia coli*, Enterococci and *Salmonella* spp. examinations.

| Coliform | | *Escherichia coli* | | Enterococci | | *Salmonella* spp. | |
|---|---|---|---|---|---|---|---|
| ISO 9308-2:2012 | 3 | ISO 9308-2:2012 | 1 | ISO 7899-1:1998 | 1 | ISO 19250:2010 | 1 |
| SCA: Microbiology of recreational and Environmental Waters Part 3 | 2 | ISO 9308-1:2014 | 1 | ISO 7899-2:2000 | 2 | SCA: Microbiology of recreational and Environmental Waters Part 8 | 3 |
| | | SCA: Microbiology of recreational and Environmental Waters Part 3 | 5 | SCA: Microbiology of recreational and Environmental Waters Part 4 | 4 | | |
| | | | | Enterolert-E | 1 | | |

SCA: Standing committee of analysts: Microbiology Working Group – Standing Committee of Analysts

The below table provides information on the type of methods used and the number of users for coliform, *Escherichia coli*, Enterococci and *Salmonella* spp. examinations.

| Method type | Coliform | *Escherichia coli* | Enterococci | *Salmonella* spp. |
|---|---|---|---|---|
| Membrane filtration | 3 | 6 | 7 | |
| Most probable numbers | 2 | 1 | | |
| Membrane filtration followed by enrichment - XLD | | | | 4 |

The following method analysis is for the SARS-CoV-2 examination as provided by five laboratories:

Standard guideline followed:

| |
|---|
| The Lab followed the indications from the OMS and the Portuguese Health General-Directorate Center for Disease Control and Prevention |
| In-house method |
| RT-qPCR for detection of SARS-CoV-2 in wastewater V.2 dx.d |

| |
|---|
| In-house validated method: https://doi.org/10.1128/msystems.00353-21 |
| In house methodology developed as part of the Northern Ireland wastewater surveillance programme. |

The volume examined varied with 15mL, 20mL, 80mL, 100mL and 200mL.

The volume concentrated varied with 0.5mL, 1.2mL, 15mL and 100mL.

The concentration methods used is shown in the table below:

| | |
|---|---|
| Samples are centrifuged for 10 minutes at 10000xg to remove solid wastes. $1x10^5$ copies of IBV is added (used as an extraction control). A first filtration is performed using a 0,45 µm filter. The filtrate is submitted to a new filtration using a 1 µm filter. The filter is removed and placed in a 15 mL tube that contains a 2 mL saline solution. For RNA extraction the lab used 200 µL of the suspension. | Microfiltration |
| Filtration concentration using Vivaspin units, (Vivaspin® 20 10 kDa MWCO filtration units). | Ultrafiltration |
| 20mLs of sample is centrifuged then 15mLs of supernatant is placed in an Amicon filter and centrifuged again. 180µL of the concentrate extracted. 20µL of the PRRSV internal control is added to the 180µL concentrate prior to extraction. | Ultrafiltration |
| Size-exclusion Filter centrifugation Briefly, following removal of solids by centrifugation at 2,000‰Ã—‰g, raw sewage was filtered through a 0.45-um filter (Nalgene 100-ml Rapid-Flow) and concentrated down to 1.2 ml using Vivaspin 20 centrifugal concentrators with a 10 kDa molecular weight cutoff and following manufacturer's instructions. | Ultrafiltration |
| Concentrated using InnovaPrep CP Select Concentrating Pipette (https://www.innovaprep.com/products/cp-select).<br>Ultrafilter tips (150 kDa MWCO), purged using an elution buffer containing 0.075% Tween 20 in 25<br>mM Tris. | Ultrafiltration |

The primers used is shown below:

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|---|
| Primers used: N1FW and N1RV, as well as IBVFW and IBVRV |
| ¢ Forward primer (N1-F): GACCCCAAAATCAGCGAAAT (50 µM stock)<br>¢ Reverse primer (N1-R): TCTGGTTACTGCCAGTTGAATCTG (50 µM stock)<br>¢ Probe (N1-P): ACCCCGCATTACGTTTGGTGGACC with FAM-MGB (5 µM stock) |
| Primer name Sequence (5'-3')<br>2019-nCoV_N1 - Forward Primer GAC CCC AAA ATC AGC GAA AT<br>2019-nCoV_N1 - Reverse Primer TCT GGT TAC TGC CAG TTG AAT CTG<br>2019-nCoV_N1 - Probe FAM-ACC CCG CAT TAC GTT TGG TGG ACC-BHQ1<br>PRRSV1 - Forward Primer CAG GAC TTC GGA GCC TCG T<br>PRRSV1 - Reverse Primer AGC AAC TGG CAC AGT TGA TTG A<br>PRRSV1 - Probe /5Cy5/ACG AGC TGT /TAO/TAA ACG AGG A/3IAbRQSp/ |

| |
|---|
| in house |
| Commercial kit - Qiagen SARS-CoV-2 N1+N2 Assay Kit (https://www.qiagen.com/us/products/discovery-and-translational-research/pcr-qpcr-dpcr/qpcr-assays-and-instruments/sars-cov-2-assay-kit). |

Information on the RNA details is shown below:

| RNA extraction reagents | RNA extraction equipment | RNA volume |
|---|---|---|
| Kits used for RNA extraction: GeneJET RNA Purification Kit; RTP® Pathogen Kit | Centrifuges, filtration equipment, micropipettes. The amplification was performed in a CFX Real Time equipment. | 5 µL |
| Maxwell® RSC GMO authentication kit cartridges<br><br>Promega Lysis Buffer MC501 | Maxwell® RSC 48 Instrument | 5µl |
| MagMAX Viral/Pathogen II (MVP II) Nucleic Acid Isolation Kit | Kingfisher Flex instrument with 96 well head. | 5µL |
| MagMax Viral RNA extraction kit | Kingfisher Duo | 5uL out of 90uL extracted |
| Roche MagNA Pure 96 DNA and Viral NA Large Volume Kit | Roche MagNA Pure 96 Instrument | Three PCR reps of 3µL and three of 6µL |

Details on the mastermix is shown below:

| |
|---|
| Mastermix: NZYSpeedy One-step RT-qPCR Probe Master Mix (NZYTech - 10 µL; 1 µL primer; 4 µL H2O; Total - 15 µL reaction volume |
| For each 20µl reaction = - 7.08 µl nuclease-free water<br>- 5.00 µl TaqMan Virus Fast one-step qRT-PCR mix<br>- 1.00 µl BSA (from RNA Ultrasense kit)<br>- 0.32 µl MgSO„ (from RNA Ultrasense kit)<br>- 0.20 µl N1-F primer (50 µM stock) †' Final: 0.5 µM<br>- 0.40 µl N1-R primer (50 µM stock) †' Final: 1.0 µM<br>- 1.00 µl N1-P probe (5 µM stock) †' Final: 0.25 µM<br>Total master mix volume per reaction: 15µl + 5µl of sample RNA |
| Reagent<br><br>Luna Warm Start RT Enzyme Mix 10 µL<br>Primer Warm Start RT Enzyme Mix 1 µL<br>Primer/Probe Mix 1.5 µL<br>BSA (20µg/µL) 0.1 µL<br>Water 2.4 µL<br><br>Primer and probe stocks are at 100µM |
| For Primary Reaction (Invitrogen SuperScript III One-Step RT-PCR System with Platinum Taq High Fidelity DNA Polymerase)<br>2xReaction Mix:12.5uL |

| |
|---|
| Enzyme: 1uL<br>Sense primer: 0.5uL<br>Antisense primer: 0.5uL<br>Nuclease free Water: 5.5uL<br><br>Nested Reaction<br>Dream Taq Master Mix: 12.5uL<br>Sense primer: 1uL<br>Antisense primer: 1uL<br>Nuclease free Water: 8.5uL |
| Applied Biosystems AgPath One-Step RT PCR reagent<br>(https://www.thermofisher.com/order/catalog/product/AM1005).<br><br>Per reaction: 12.5 µL of 2x RT-PCR buffer, 1 µL of 25x Enzyme mix, 0.25 µL of BSA, DEPC - 4.25 µL per sample for 6 µL RNA input, 7.25 µL per sample for 3 µL RNA input. |

The cycle run details is shown below:

| |
|---|
| 50ºC - for 20 sec<br>95ºC - 3.00 m<br>95ºC - 10 sec<br>58ºC - 45 sec<br>x40 |
| Reverse Transcription: 50°C for 30 min (1 cycle)<br>Initial Denaturation: 95°C for 20 s (1 cycle)<br>PCR Cycling (45 cycles):<br>Denaturation: 95°C for 3 s<br>Annealing/Extension: 60°C for 45 s (with data collection) |
| Temperature Time Cycles<br>55°C 10 min 1<br>95°C 1 min<br>95°C 10 sec 40<br>55°C 30 sec |
| For Primary Reaction<br>50°C for 30 minutes<br>94°C for 2 minutes<br>40 cycles 94°C for 15 seconds<br>50°C for 30 seconds<br>68°C for 1 minute<br>68°C for 5 minutes<br>10°C Hold<br><br>For Nested Reaction<br>94°C for 2 minutes<br>40 cycles 94°C for 15 seconds<br>50°C for 30 seconds<br>68°C for 30 seconds<br>68°C for 5 minutes<br>10°C Hold |
| 1x cycle of reverse transcription at 50oC for 10 mins, 1x cycle of RT denaturation at 95oC for 10 mins, 45x cycles of denaturation at 95oC for 10 secs and combined annealing and extension at 60oC for 30 secs. |

The amplification platform used along the lower limit of detection (LOD) and quantification (LOQ) is shown in the table below:

| Amplification platform | LOD | LOQ |
|---|---|---|
| Real Time PCR CFX | 100 copies/100 mL | 100 copies/100 mL |
| Stratagene Mx3005P | Not established | Not established |
| ABi 7500 | 1,316 gc/L (based on original SEPA data) | 11,368 gc/L (based on original SEPA data) |
| Mastercycler Nexus X2 | Information not accessible at the moment | Information not accessible at the moment |
| Roche LightCycler 480 II. | 2 gene copies per reaction. | 3.5 gene copies per reaction. |

Details about other viruses tested is shown below:

| |
|---|
| Norovirus GI and norovirus GII in wastewater |
| Poliovirus, non polio enteroviruses, influenzavirus - Hepatitis E and Norovirus and work in progress |
| Rotavirus, Norovirus (GI,GII,GIV,GIX), Hepatitis A virus (HAV), Hepatitis E virus (HEV), Enterovirus A71, Enterovirus D68, Sapovirus, Aichivirus, Astrovirus. |
| Influenza, Norovirus, RSV, EV-D68, Polio, HAdV-F41. |

1/5 of the laboratories stated they already participate in a SARS-CoV-2 proficiency testing scheme.

Conclusions on this PT exercise is:

- Due to the low number of data sets reported for each examination, the performance of a laboratory must be interpreted with caution.
- The low number of data sets used for statistical calculations can result in wider expected range, standard deviation and uncertainty.
- The variability of how laboratories examine wastewater for SARS-CoV-2 is clear from the analysis undertaken on the methods, this is expected as there is no approved published method for laboratories to follow.
- In general the overall performance of laboratories in this PT exercise is very good with >95% of the results being correct.

The next distribution for the wastewater scheme is scheduled for 16 February 2026.

The organisers would like to thank the participants for providing additional methodology information and to David Walker at Cefas for providing expert comments and for supporting this scheme.

End of report