Proficiency Testing

# Drinking Water Microbiology

## March 2016

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*Proficiency testing*

# Drinking water Microbiology

March 2016

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1457
ISO/IEC 17043

**Parameters included**

**Coliform bacteria** and ***Escherichia coli*** with membrane filter method (MF)

**Coliform bacteria** and ***Escherichia coli***, (rapid methods with MPN)

***Clostridium perfringens*** with MF

**Actinomycetes** with MF

**Moulds** with MF

**Yeasts** with MF

**Culturable microorganisms** (total count) 3 days incubation at **22 °C**

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# Abbreviations and explanations

### *Microbiological media*

| | |
|---|---|
| ACTA | Actinomycete Isolation Agar (according to SS 028212) |
| CCA | Chromocult Coliform Agar® (Merck; according to EN ISO 9308-1:2014) |
| Colilert | Colilert® Quanti-Tray® (IDEXX Inc.; according to EN ISO 9308-2:2014) |
| LES | m-Endo Agar LES (according to SS 028167) |
| LTTC | m-Lactose TTC Agar with Tergitol (acc. to EN-ISO 9308-1:2000) |
| m-FC | m-FC Agar (according to SS 028167) |
| PAB/TSC/SFP | Tryptose Sulfite Cycloserine Agar (acc. to ISO/CD 6461-2:2002) |
| RBCC | Rose Bengal Agar with both chlortetracycline and chloramphenicol (according to SS 028192) |
| YeA | Yeast extract Agar (according to EN ISO 6222:1999) |

### *Other abbreviations*

| | |
|---|---|
| MF | Membrane filter (method) |
| MPN | "Most Probable Number" (quantification based on statistical distributions) |
| ISO | "International Organization for Standardization" and their standards |
| EN | European standard from "Comité Européen de Normalisation" (CEN) |
| NMKL | "Nordisk Metodikkomité for næringsmidler" and their standards |
| DS, NS, SFS, SS | National standards from Denmark, Norway, Finland and Sweden |

### *Legend to method comparison tables*

| | |
|---|---|
| N | total number of laboratories that reported methods and numerical results |
| n | number of results except false results and outliers |
| Mv | mean value (with outliers and false results *excluded*) |
| Med | median value (with outliers and false results *included*) |
| CV | coefficient of variation = relative standard deviation in percentage of the mean, calculated from square root transformed results |
| F | number of false positive or false negative results |
| < | number of low outliers |
| > | number of high outliers |
| 🟨 | total number of results for the parameter |
| 601 | remarkably low result |
| 278 | remarkably high result or CV or many deviating results |

### *Explanations to histograms with accepted and deviating results*

| | |
|---|---|
| ▨ | result without remark |
| ☐ | false negative result |
| ■ | outlier |
| ↓ 34 | average without deviating results |

# Contents

# General information on results evaluation

The histograms and calculation of outliers are described on page 29 under "Processing of numerical results" with further reference to the scheme protocol (1).

The proficiency testing program organised by the National Food Agency is accredited against EN ISO/IEC 17043. This standard prescribes that results should be grouped based on the method used. Therefore it is mandatory for participants to inform about method data. Method data where differences are present or could be expected are here reported for each parameter.

The method information gathered is sometimes difficult to interpret. Sometimes there is no consistency between the standard referred to and the information given regarding various method details. Results from laboratories with ambiguous details are either excluded or placed in the group "Other/Unknown" in the tables, together with results from methods used only by individual laboratories. Thus, to get as appropriate evaluation as possible of the results, it is important that correct standards and method details are reported.

Outliers and false results are not included in the calculation of mean value and measure of dispersion for the various method groups. The numbers of low and high outliers, as well as false results, are instead explicitly given in tables together with the group means etc. The measure of dispersion is not shown for groups with 4 or fewer results. However, all results are shown in the method histogram when possible.

# Results of the PT round

## General outcome

Test items were sent to 95 laboratories, 38 in Sweden, 47 in other Nordic countries (Faeroe Islands, Greenland and Åland included), 3 more from EU, 2 from the rest of Europe and 5 from countries outside Europe. Results were reported from 92 laboratories.

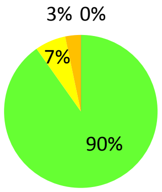
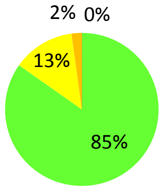
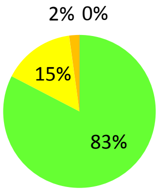
The percentages of false results and outliers are compiled in **table 1**. These deviating results are excluded in most calculations.

Microorganisms and parameters of analyses are also compiled in table 1. For the MF analyses the parameters *suspected* coliform bacteria and thermotolerant coliform bacteria could be reported as well. The results from suspected colonies are only used for interpretations and discussions.

All reported results are compiled in **annex A** and results for each laboratory are also shown on our website after logging in (www2.slv.se/absint).

Standardized z-scores for all evaluated results are given in **annex B** and photographs with examples of colony appearance on various media are presented in **annex C**.

**Table 1** *Microorganisms in each mixture and percentages of deviating results (F%: false positive or false negative, X%: outliers); parameters with grey rows are not assessed*

| **Mixture** | **A** | | | **B** | | | **C** | | |
|---|---|---|---|---|---|---|---|---|---|
| **Percentage of laboratories with**<br>🟩 0 deviating results<br>🟨 1 deviating result<br>🟧 2 deviating results<br>🟥 >2 deviating results |  | | |  | | |  | | |
| No. of evaluable results | 555 | | | 552 | | | 554 | | |
| No. of deviating results * | 12 (2 %) | | | 16 (3 %) | | | 18 (3 %) | | |
| **Microorganisms** | *Saccharomyces cerevisiae*<br>*Cladosporium cladosporoides*<br>*Streptomyces sp.* | | | *Enterobacter cloacae*<br>*Hafnia alvei*<br>*Clostridium bifermentans*<br>*Staphylococcus maltophilia*<br>*Rhodotorula minuta*<br>*Pleurophoma sp.* | | | *Escherichia coli*<br>*Klebsiella pneumoniae*<br>*Clostridium perfringens*<br>*Cladosporium cladosporoides*<br>*Staphylococcus saprophyticus* | | |
| **Analysis** | **Target** | **F%** | **X%** | **Target** | **F%** | **X%** | **Target** | **F%** | **X%** |
| Coliform bacteria (MF) | – | 3 | – | *E. cloacae*<br>*{H. alvei}* | 1 | 3 | *E. coli*<br>*K. pneumoniae* | 1 | – |
| Susp. thermotolerant coliform bact. (MF) | – | – | – | *E. cloacae* | – | – | *E. coli*<br>*K. pneumoniae* | – | – |
| *E. coli* (MF) | – | 5 | – | *[E. cloacae]* | 1 | – | *E. coli*<br>*[K. pneumon.]* | 0 | – |
| Coliform bacteria (rapid method) | – | 0 | – | *E. cloacae*<br>*{H. alvei}* | 0 | 8 | *E. coli*<br>*K. pneumoniae* | 0 | – |
| *E. coli* (rapid meth.) | – | 0 | – | – | 0 | 7 | *E. coli* | 0 | – |
| Presumptive *C. perfringens* (MF) | – | 11 | – | *C. biferment.* | 0 | 4 | *C. perfringens* | 2 | 4 |
| *Clostridium perfringens* (MF) | – | 3 | – | – | 0 | – | *C. perfringens* | 3 | 11 |
| Actinomycetes (MF) 25 °C | *Streptomyces sp.* | 6 | 6 | – | 3 | – | – | 3 | – |
| Moulds (MF) | *C. cladospor.* | 0 | 0 | *(Pleurophoma sp.)* | 2 | – | *C. cladospor.* | 0 | – |
| Yeasts (MF) 22 °C | *S. cerevisiae* | 0 | 0 | *R. minuta–* | 5 | – | – | 0 | – |
| Culturable micro-organisms (total count), 2 days 36 °C | *Streptomyces sp.*<br>*(S. cerevisiae)*<br>*(C. cladospor.)* | 0 | 10 | *S. maltophilia*<br>*(E. coli)*<br>*(H. alvei)*<br>*(Rh. minuta)* | 1 | 5 | *S. saprophyticus*<br>*(C. cladospor.)*<br>*(E. coli )*<br>*(K. pneumoniae)* | 2 | 4 |

* In total 27 of 95 laboratories (28%) reported at least one deviating result

– Organism missing or numerical result irrelevant

( ) The organism contributes with only very few colonies

[ ] The organism is presumptively false positive on the primary growth medium

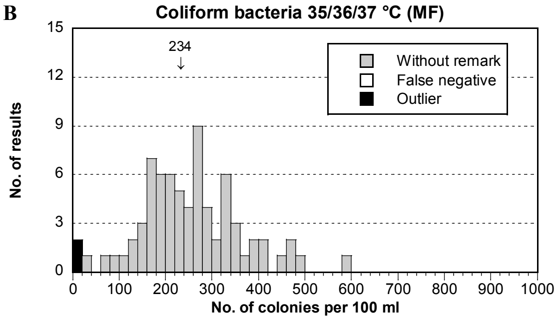
{ } The organism may give different results depending on method or definition used

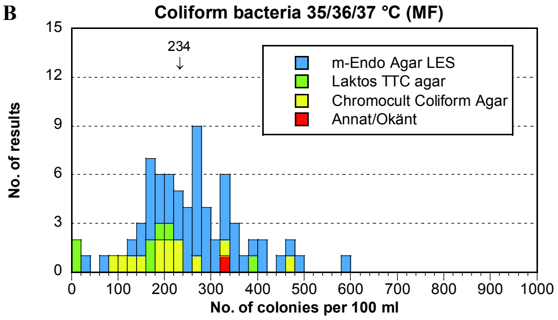
# Coliform bacteria (MF)

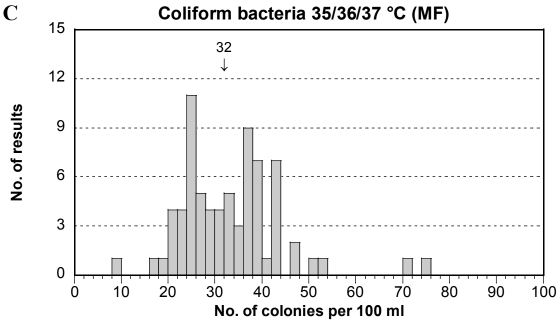
In two cases the primary medium reported was not the one prescribed in the standard referred to. Here we have assumed the medium to be correct. The medium Endo Agar reported by some participants is here included in m-Endo Agar LES (LES).

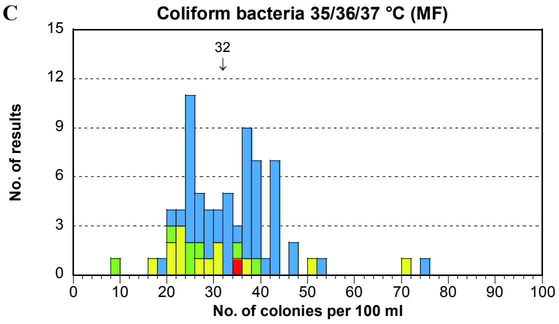
From the table it is clear that LES was used by far more laboratories than other media. The proportion that used CCA is higher than before simultaneously as it has decreased for LTTC. This is reasonable since CCA has replaced LTTC in the latest edition of EN ISO 9308-1 from 2014. There is an indication that LES gave a somewhat higher mean result compared to both LTTC and CCA in both mixture B and C. The medium giving the lowest average is varying.

| Medium | N | A | | | | | | B | | | | | | C | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total** | 73 | 72 | **0** | – | 1 | – | – | 71 | **244** | 21 | 0 | 2 | 0 | 73 | **32** | 16 | 2 | 0 | 0 |
| m-Endo Agar LES | 52 | 52 | **0** | – | 0 | – | – | 52 | **256** | 21 | 0 | 0 | 0 | 52 | **34** | 14 | 2 | 0 | 0 |
| Laktos TTC Agar | 7 | 6 | **0** | – | 1 | – | – | 5 | **215** | 19 | 0 | 0 | 0 | 7 | **24** | 22 | 0 | 0 | 0 |
| Chromocult C Agar | 13 | 13 | **0** | – | 0 | – | – | 13 | **206** | 23 | 0 | 2 | 0 | 13 | **29** | 22 | 0 | 0 | 0 |
| Other/Unknown | 1 | 1 | **0** | – | 0 | – | – | 1 | **320** | – | 0 | 0 | 0 | 1 | **35** | – | 0 | 0 | 0 |









## Mixture A

- There were no coliform bacteria in the mixture but one false positive result.

### Mixture B

- Two strains of coliform bacteria were included. *Enterobacter cloacae* appears with typical colonies, metallic sheen on LES, light yellow on LTTC and pink ones on CCA at 37 °C. *Hafnia alvei* appears with more or less red colonies on LES and pinkish ones on LTTC. On CCA are they pale pink to the colour of apricot.
- The colonies of *H. alvei* have probably not been reckoned as from coliform bacteria due to the colour. This is evident by a comparison with the rapid method for coliform bacteria (p. 12) where higher counts were generally obtained.
- The distribution of the results was less dispersed with the MF method compared with the rapid methods (see page 13). Two low outliers were present with the MF method, in both cases with CCA.

### Mixture C

- One strain of *Escherichia coli* was present together with a strain of *Klebsiella pneumoniae* as coliform bacteria. Both appear with, for coliform bacteria, typical colonies on the MF media at 37 °C, a metallic sheen on LES and yellowish on LTTC. The colonies of *E. coli* were violet blue on CCA and those of *K. pneumoniae* pink to red. There was no problem with this analysis.
- There were no deviating results.

## Suspected thermotolerant coliform bacteria (MF)

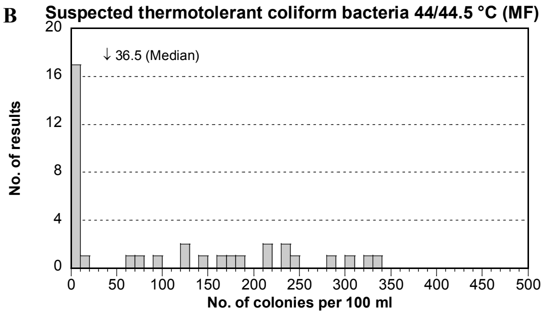
The two most used growth media were m-FC and LTTC. The incubation temperature was 44 or 44.5 °C. Here, results were separated based on the method standards most commonly used, to get a further division beyond the media. They are EN ISO 9308-1:2000 with LTTC and three standards with m-FC from the Nordic countries, namely SS 028167 from Sweden, SFS 4088 from Finland and NS 4792 from Norway. The methods were sometimes used slightly modified.

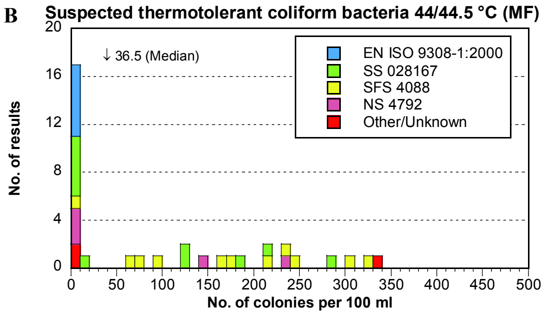
The Swedish standard states incubation at 44 °C but one laboratory reported 44.5 °C. The temperature 44 °C is also stated in EN ISO 9308-1:2000. One of five laboratories using Norwegian standard incubated at 44 °C, the other four used 44.5 °C. All laboratories using Finnish standard has incubated at 44 °C. Results related to the methods are here described under the respective mixture.

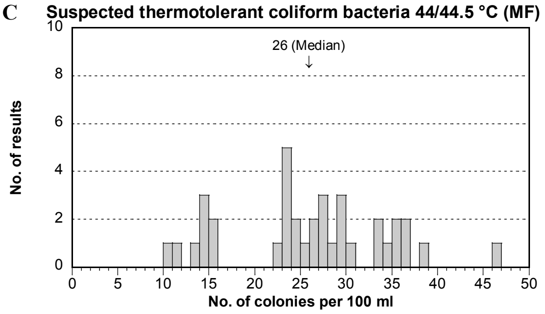
| **Standard, Method** | **Tot** | **A** | | | | | | **B** | | | | | | **C** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | n | n | **Med** | CV | F | < | > | n | **Med** | CV | F | < | > | n | **Med** | CV | F | < | > |
| **Total** | 36 | 34 | **0** | – | – | – | – | 36 | **37** | – | – | – | – | 36 | **26** | – | – | – | – |
| EN ISO 9308-1 | 6 | 5 | **0** | – | – | – | – | 6 | **0** | – | – | – | – | 6 | **26** | – | – | – | – |
| SS 028167 | 11 | 10 | **0** | – | – | – | – | 11 | **13** | – | – | – | – | 11 | **24** | – | – | – | – |
| SFS 4088 | 11 | 11 | **0** | – | – | – | – | 11 | **175** | – | – | – | – | 11 | **29** | – | – | – | – |
| NS 4792 | 5 | 5 | **0** | – | – | – | – | 5 | **0** | – | – | – | – | 5 | **27** | – | – | – | – |
| Other/Unknown | 3 | 3 | **0** | – | – | – | – | 3 | **0** | – | – | – | – | 3 | **23** | – | – | – | – |

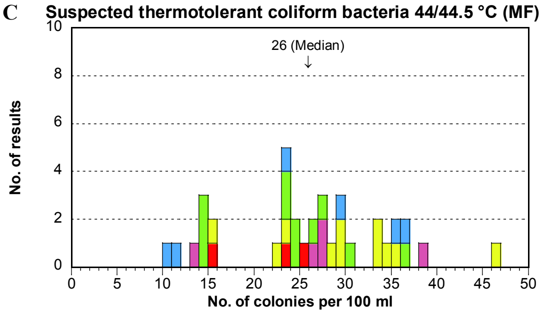
Med = Median; used here instead of mean value

The table shows the *medians* instead of mean values because no outliers have been identified. The reason is that the results are based on suspected (not confirmed) colonies. Such ***results are not included in performance assessment***.









## Mixture A

- There were no coliform bacteria in the mixture.

## Mixture B

- No real thermotolerant coliform bacterium was present. However, there was a strain of *E. cloacae* that sometimes grow as a (suspected) thermotolerant coliform bacterium at 44/44.5 °C. It seems not to grow with typical colonies on LTTC (EN ISO 9308-1:2000) at 44 °C, where all results were zero. However, it grows but in very varying degree on m-FC. Only 9 of the results were there zero. Despite that the table states the median zero with Norwegian standard, in 2 out of 5 laboratories colonies appeared. In one of these the temperature was 44.5 °C.
- Seven laboratories have reported other results than zero cfu per 100 ml.

## Mixture C

- One strain of *E. coli* was included together with a strain of *K. pneumoniae* as coliform bacteria. Both appear with, for coliform bacteria, typical colonies on the MF media, bluish on m-FC and yellow to dark yellow on LTTC at 44/44.5 °C.
- There was no problem with the analysis. No zero results were obtained.

## *Escherichia coli* (MF)

*E. coli* is quantified after confirmation of colonies grown on the primary cultivation media LES and LTTC, incubated either at 36±2 °C or at 44/44.5 °C. Depending on method, either test of indole production or *β*-glucuronidase activity from oxidase negative strains is usually used. A violet to blue colony on CCA indicates positive *β*-glucuronidase activity and is reckoned as a confirmed *E. coli*.

The primary growth media LTTC, LES as well as CCA are used at 36±2 °C and LTTC or m-FC at 44/44.5 °C. The results from the two temperatures are here shown in separate tables. *The 7 results with unclear incubation temperature are not separately shown but are included only in the table "All results".*

Since there are only 12 results from three method groups from incubation at 44/44.5 °C it is not meaningful to discuss differences between them. However, for the results from 36±2 °C discussions are possible.

*All results*

| **Medium** | **N** | **A** | | | | | | **B** | | | | | | **C** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | Mv | CV | F | < | > | n | Mv | CV | F | < | > | n | Mv | CV | F | < | > |
| **Total** | 75 | 75 | **0** | – | 0 | – | – | 73 | **0** | – | 2 | – | – | 72 | **14** | 21 | 3 | 0 | 0 |

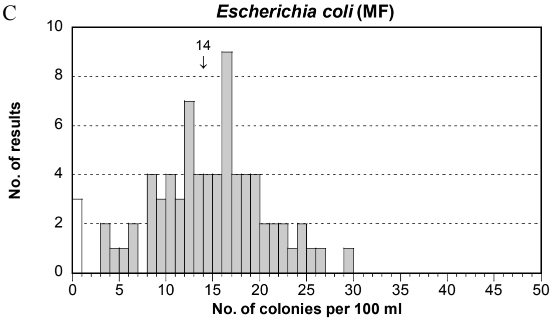
*From 36±2 °C*

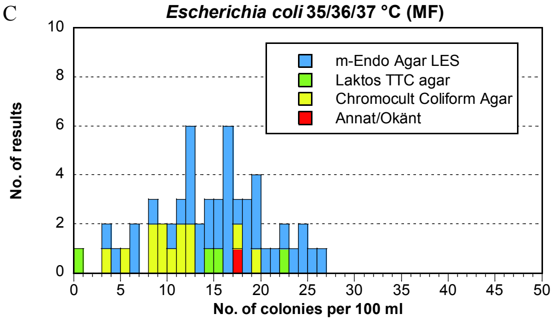
| **Medium** | **N** | **A** | | | | | | **B** | | | | | | **C** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | $^*$**Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | $^*$**Mv** | CV | F | < | > |
| ***Total*** | ***56*** | ***56*** | ***0*** | **–** | ***0*** | – | **–** | ***55*** | ***0*** | **–** | ***1*** | – | **–** | ***55*** | ***14*** | ***22*** | ***1*** | 0 | ***0*** |
| m-Endo Agar LES | 38 | 38 | **0** | – | 0 | – | – | 37 | **0** | – | 1 | – | – | 38 | **15** | 21 | 0 | 0 | 0 |
| Lactose TTC Agar | 4 | 4 | **0** | – | 0 | – | – | 4 | **0** | – | 0 | – | – | 3 | **15**$^*$ | – | 1 | 0 | 0 |
| Chromocult C Agar | 13 | 13 | **0** | – | 0 | – | – | 13 | **0** | – | 0 | – | – | 13 | **10** | 22 | 0 | – | – |
| Other/Unknown | 1 | 1 | **0** | – | 0 | – | – | 1 | **0** | – | 0 | – | – | 1 | **17** | – | 0 | 0 | 0 |

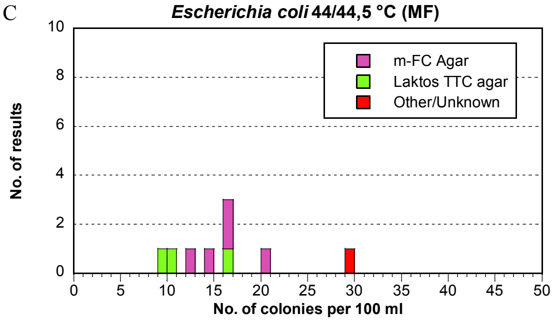
*From 44/44.5 °C*

| **Medium/Standard** | **N** | **A** | | | | | | **B** | | | | | | **C** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| ***Total*** | ***12*** | ***12*** | ***0*** | **–** | ***0*** | **–** | **–** | ***11*** | ***0*** | **–** | ***1*** | **–** | **–** | ***11*** | ***15*** | ***28*** | ***1*** | ***0*** | ***0*** |
| *Medium* | | | | | | | | | | | | | | | | | | | |
| m-FC Agar | 5 | 5 | **0** | – | 0 | – | – | 5 | **0** | – | 0 | – | – | 5 | **15** | 9 | 0 | 0 | 0 |
| Lactose TTC Agar | 3 | 3 | **0** | – | 0 | – | – | 3 | **0** | – | 0 | – | – | 3 | **10**$^*$ | – | 0 | 0 | 0 |
| Other/Unknown | 4 | 4 | **0** | – | 0 | – | – | 3 | **0** | – | 0 | – | – | 3 | **21**$^*$ | – | 1 | 0 | 0 |
| *Standard* | | | | | | | | | | | | | | | | | | | |
| EN ISO 9308-1 | 4 | 4 | **0** | – | 0 | – | – | 4 | **0** | – | 0 | – | – | 4 | **13**$^*$ | – | 0 | 0 | 0 |
| SS 028167 | 0 | 0 | – | – | – | – | – | 0 | – | – | – | – | – | 0 | – | – | – | – | – |
| SFS 4088 | 1 | 1 | **0** | – | 0 | – | – | 1 | **0** | – | 0 | – | – | 1 | **12** | – | 0 | 0 | 0 |
| NS 4792 | 2 | 2 | **0** | – | 0 | – | – | 2 | **0** | – | 0 | – | – | 2 | **18**$^*$ | – | 0 | 0 | 0 |
| Other/Unknown | 5 | 5 | **0** | – | 0 | – | – | 4 | **0** | – | 1 | – | – | 4 | **15**$^*$ | – | 1 | 0 | 0 |

* Median instead of mean value







## Mixture A

- No *E. coli* or other coliform bacterium was included and there were also no false positive results.
- One typical *E. coli* strains was included together with another coliform bacterium. With CCA $\beta$-glucuronidase activity is checked directly on the primary agar plate, no more confirmation is needed.
- Two false negative results were present.

## Mixture B

- No *E. coli* was included but instead two other coliform bacteria. Two false positive results were reported, both with the same colony amount as for coliform bacteria. Thus, it is plausible that colonies of *E. cloacae* have been taken for *E. coli* due to skipped or unsuccessful confirmation.

## Mixture C

- One typical strain of *E. coli* w was present together with another thermotolerant coliform bacterium, *K. pneumoniae*. The distribution of the results was good even though the dispersion was of average size.
- Three false negative results were present.
- When the average results for LES and CCA from incubation at 36±2 °C, it is evident that CCA gives an unexpectedly low result 10 compared to 15 cfu/100 ml. The dispersion is similar in both cases.
- In principle the same average was obtained as with the rapid methods when the zero results are excluded.

## Coliform bacteria & *E. coli* (rapid methods, MPN)

The rapid method used for both these parameters was almost exclusively Colilert® Quanti-Tray® from the manufacturer IDEXX Inc. with incubation at 35, 36 or 37 °C. Out of the about 60 laboratories that reported Colilert some used trays with 51 wells, while others used trays with 97 wells (a few of which, probably incorrectly, have reported 96 wells). Two laboratories reported the use of "Colilert 24 hours". The laboratories often analysed both diluted and undiluted samples.

Neither for coliform bacteria nor for *E. coli*, there seems to be any difference between the use of trays with 51 compared to 97 wells (data not shown).

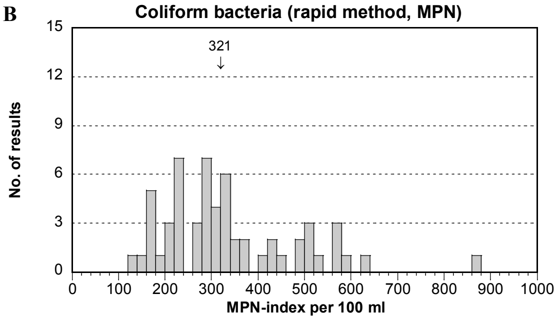
Only one deviating result was present. In no case there seem to have been any problem with interpretation of the results.

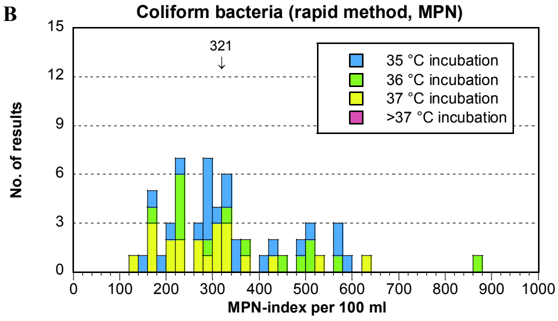
*Coliform bacteria, Rapid method with MPN*

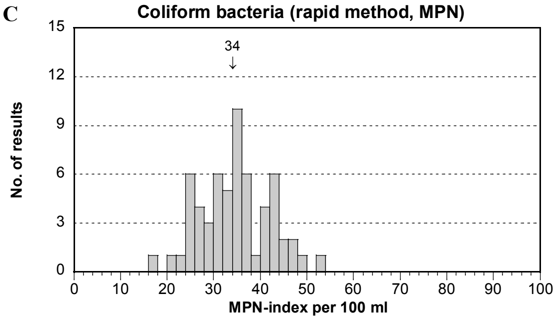
| **Incubation temp.** | **N** | **A** | | | | | | **B** | | | | | | **C** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total, Rapid meth.** | 60 | 60 | **0** | – | 0 | – | – | 58 | **321** | 21 | 0 | 0 | 0 | 60 | **34** | 11 | 0 | 0 | 0 |
| 35 °C incubation | 23 | 23 | **0** | – | 0 | – | – | 23 | **329** | 19 | 0 | 0 | 0 | 23 | **32** | 10 | 0 | 0 | 0 |
| 36 °C incubation | 14 | 14 | **0** | – | 0 | – | – | 14 | **370** | 24 | 0 | 0 | 0 | 14 | **35** | 11 | 0 | 0 | 0 |
| 37 °C incubation | 23 | 23 | **0** | – | 0 | – | – | 21 | **282** | 20 | 0 | 0 | 0 | 23 | **35** | 12 | 0 | 0 | 0 |
| >37 °C incubation | 0 | 0 | **0** | – | 0 | – | – | 0 | **–** | – | 0 | 0 | 0 | 0 | **–** | – | 0 | 0 | 0 |

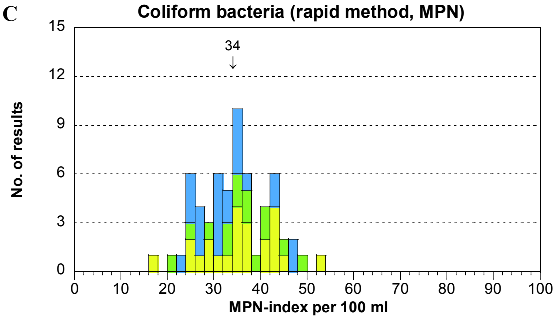
*E. coli, Rapid method with MPN*

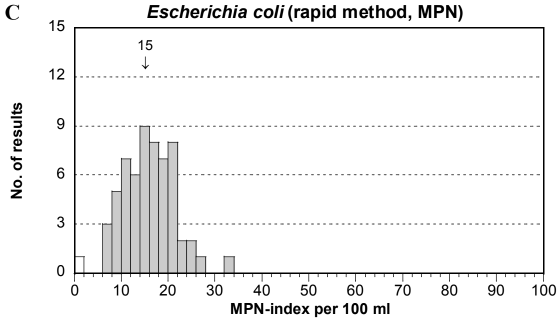
| **Incubation temp.** | **N** | **A** | | | | | | **B** | | | | | | **C** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total, Rapid meth.** | 60 | 60 | **0** | – | 0 | – | – | 59 | **0** | – | 0 | – | – | 59 | **15** | 18 | 1 | 0 | 0 |
| 35 °C incubation | 22 | 22 | **0** | – | 0 | – | – | 22 | **0** | – | 0 | – | – | 22 | **15** | 16 | 0 | 0 | 0 |
| 36 °C incubation | 14 | 14 | **0** | – | 0 | – | – | 14 | **0** | – | 0 | – | – | 13 | **14** | 21 | 1 | 0 | 0 |
| 37 °C incubation | 23 | 23 | **0** | – | 0 | – | – | 22 | **0** | – | 0 | – | – | 23 | **15** | 18 | 0 | 0 | 0 |
| >37 °C incubation | 1 | 1 | **0** | – | 0 | – | – | 1 | **0** | – | 0 | – | – | 1 | **16** | – | 0 | 0 | 0 |

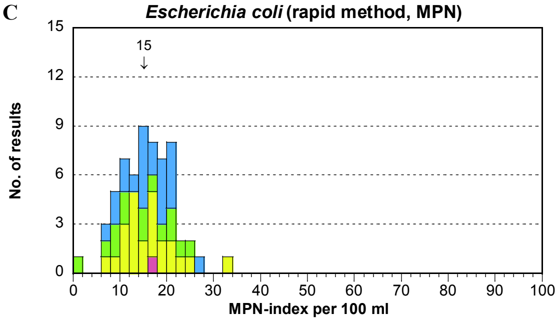












## Mixture A

- No *E. coli* or other coliform bacterium was included and there were also no false positive results.

## Mixture B

- In this mixture were the coliform bacteria *E. cloacae* and *H. alvei* present. Both of them possess *β*-galactosidase but not *β*-glucuronidase and are thus detected as coliform bacteria but not as *E. coli*.
- In the histogram there are so many results present to the right of the main peak that you may state a second lower peak. This is most probably an effect of the weakly positive ONPG reaction of the *H. alvei* strain. After just 18 hours of incubation the reaction is most often negative, while it has usually turned to positive after 22 hours. The main histogram peak, therefore, reflects only activity of *E. cloacae* while the second peak reflects the sum of this strain and *H. alvei*.
- *H. alvei* grows slowly and/or has weaker *β*-galactosidase activity at 37 °C compared to at 35 °C. This is evident from the table for coliform bacteria where the MPN-index per 100 ml was 282 at 37 °C but clearly higher at 35 and 36 °C.
- Poor growth of this strain of *H. alvei* is also seen for the MF method. The total average for coliform bacteria is further also clearly lower by the MF method than for the rapid method because only colonies of *E. cloacae* are detected there.

## Mixture C

- The strains of *E. coli* and *K. pneumoniae* grow in the medium and have the enzyme *β*-galactosidase. Therefore, they are detected as coliform bacteria by methods based on this enzyme (ONPG positive) e.g. Colilert®-18/24 Quanti-Tray® where ONPG is a substrate.

- The strain of *E. coli* has the enzyme *β*-glucuronidase and is also detected as *E. coli*. One false negative result was obtained.
- The average for coliform bacteria is about the same as for the MF methods.

## Presumptive and confirmed *Clostridium perfringens* (MF)

The analysis of *Clostridium perfringens* is performed differently in different countries and laboratories, because no international standard is stated as reference method in the European Drinking Water Directive from 1998 (4). The parameter to be analysed is spores and vegetative cells of *C. perfringens*. In Sweden, the results of presumptive *C. perfringens* have also been accepted and are therefore accounted for separately.

There is one method explicitly described in the Drinking water directive from 1998 (4), the use of m-CP Agar incubated at 44 °C. The method includes a confirmation step with ammonia vapour, where a red coloration of colonies indicates *C. perfringens*. Due to the hesitation in many countries to use this method, the use of a standard still under process (ISO/CD 6461-2:2002-12-20, CD = Committee Draft) was accepted by the responsible group under the EU Commission as an alternative. Adjustments in the draft approved in ISO meetings have been pointed out in the instructions for the proficiency testing rounds.

The ISO version of the standard is available since November 2013. It has got the designation ISO 14189 (2013) and is basically equivalent to the CD version from 2002 after adjustments, but has a much more simplified confirmation step. In the new standard, isolated colonies are only tested for activity of the enzyme acid phosphatase. The new standard has been included in the revised annexes to the directive text and should be taken into usage no later than in October 2017, after being implemented in the national legislations. The CD version will then be invalid to use for official drinking water monitoring. The standard is under the process of being accepted also as an EN standard in June 2016. If approved, the standard will then also become a national standard in most European countries.

Only one participant has used a different method than those mentioned, NMKL 95:5 (2009), modified. For yet another participant the reference is unknown. The results from both these participants are included in the group Other/Unknown.

Using m-CP Agar yielded lower numbers for both presumptive *C. perfringens* and *C. perfringens* in both mixture B and C than using PAB/TSC Agar according to the two method references. The histograms show clearly that the results of m-CP Agar are mainly in the lower end of the results. The dispersion as CV was in all three cases the largest with m-CP agar. These results may not be generally valid but at least for the strains of *C. bifermentans* and *C. perfringens* used in the test items.

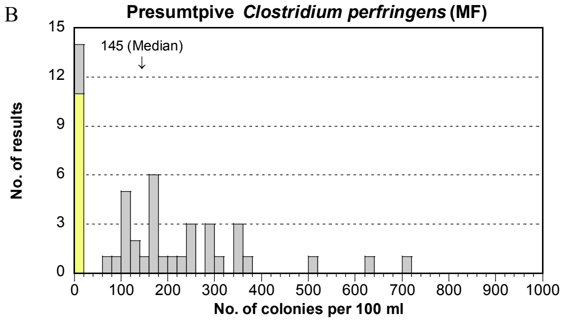
*Presumptive Clostridium perfringens MF*

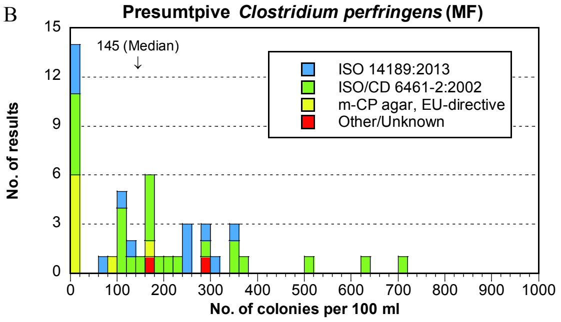
| Standard/Method | N | A |  |  |  |  |  | B |  |  |  |  |  | C |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total** | 47 | 46 | **0** | – | 1 | – | – | 47 | **111** | 73 | 0 | 0 | 0 | 47 | **313** | 27 | 0 | 0 | 0 |
| ISO 14189:2013 | 12 | 11 | **0** | – | 1 | – | – | 12 | **119** | 65 | 0 | 0 | 0 | 12 | **284** | 28 | 0 | 0 | 0 |
| ISO/CD 6461-2:2002 | 25 | 25 | **0** | – | 0 | – | – | 25 | **152** | 61 | 0 | 0 | 0 | 25 | **400** | 14 | 0 | 0 | 0 |
| m-CP agar, EU-direct. | 8 | 8 | **0** | – | 0 | – | – | 8 | **10** | 166 | 0 | 0 | 0 | 8 | **154** | 46 | 0 | 0 | 0 |
| Other/Unknown | 2 | 2 | **0** | – | 0 | – | – | 2 | **220*** | – | 0 | 0 | 0 | 2 | **225*** | – | 0 | 0 | 0 |

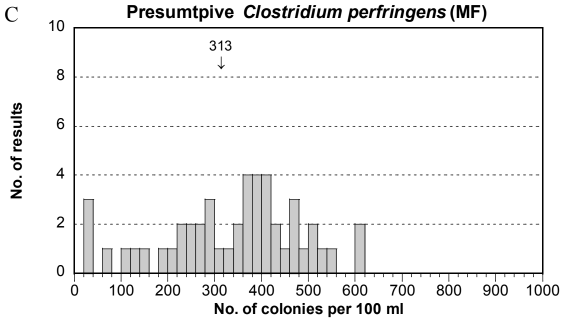
*Clostridium perfringens MF*

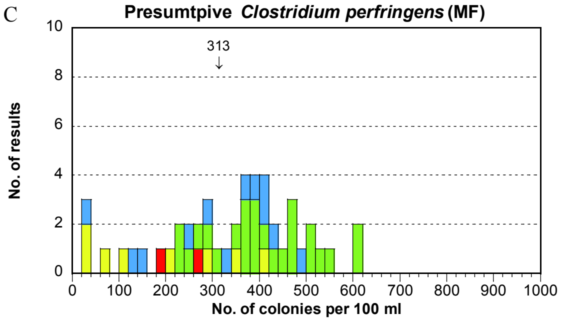
| Standard/Method | N | A |  |  |  |  |  | B |  |  |  |  |  | C |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total** | 40 | 39 | **0** | – | 1 | – | – | 38 | **0** | – | 2 | – | – | 38 | **254** | 33 | 1 | 0 | 0 |
| ISO 14189:2013 | 9 | 8 | **0** | – | 1 | – | – | 8 | **0** | – | 1 | – | – | 9 | **338** | 12 | 0 | 0 | 0 |
| ISO/CD 6461-2:2002 | 13 | 13 | **0** | – | 0 | – | – | 12 | **0** | – | 1 | – | – | 11 | **408** | 18 | 1 | 0 | 0 |
| m-CP agar, EU-direct. | 16 | 16 | **0** | – | 0 | – | – | 16 | **0** | – | 0 | – | – | 16 | **149** | 37 | 0 | 0 | 0 |
| Other/Unknown | 2 | 1 | **0** | – | 0 | – | – | 2 | **0** | – | 0 | – | – | 2 | **157*** | – | 0 | 0 | 0 |

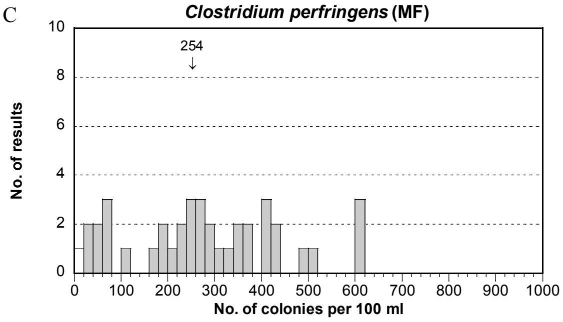
* Median instead of mean value

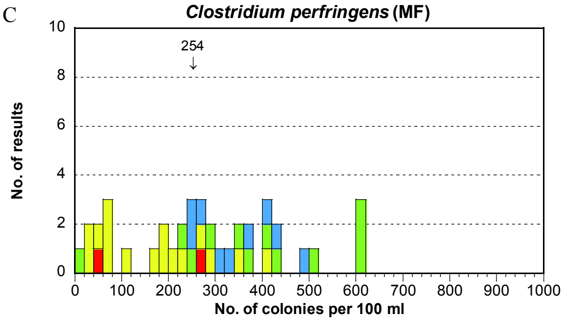












**Mixture A**

- No presumptive *C. perfringens* was included. Yet, one false positive result was present in each of the presumptive analysis and *C. perfringens*.

**Mixtures B**

- No *C. perfringens* was included but a strain of *C. bifermentans*.
- The distribution of the results measured as CV was very large in the presumptive test with the implication that no outliers could be identified. Eleven zero results were obtained.
- In the analyses of *C. perfringens* were 2 false positive results present.

**Mixtures C**

- A strain of *C. perfringens* was included. No deviating results could be identified from the presumptive test while one false positive result was present for *C. perfringens*.
- The colour of the colonies with PAB/TSC/SFP may vary from light grey-brown to completely black, at least partly depending on the condition of the medium and its reduction potential.
- The distribution of the results was quite scattered and low results were over-represented. The large dispersion makes it difficult to identify deviating results. The dispersion as CV was large for the m-CP agar method.

## Moulds and yeasts (MF)

Out of the 42 laboratories that analysed moulds and yeasts, 32 reported that they used the Swedish standard SS 028192. Besides Sweden it is used in Denmark and also in Finland and Norway under their own national designations SFS 5507 and NS 4716, respectively.

Various names, some appropriate and other probably inappropriate, were reported for the media linked to the use of SS 028192. These are "Cooke Rose Bengal" agar, "Rose Bengal agar base", "Rose Bengal Chloramphenicol" (RBC) agar and "Dichloran Rose Bengal Chloramphenicol" (DRBC) agar. According to the standard, dichloran should not be an ingredient (and thus DRBC should not be used) but instead Rose Bengal and the two stronger inhibitory substances chlortetracycline and chloramphenicol are authorized. Both of them are usually used by the Swedish laboratories. Here is shown what the laboratories have really stated and a division is made for those that have used any form of Rose Bengal agar (RBC Agar) and those stating "Dichloran Rose Bengal Chloramphenicol" (DRBC Agar, Water).

Two Finnish laboratories used Glucose Yeast Extract agar with oxytetracycline as inhibiting substance (OGYE) according to the standard ISO 7954 (1987) and two other Finnish laboratories used DRBC connected to NMKL 98, modified. Both these groups are included in the group "Food methods" in the tables and histograms. Four other Finnish laboratories used Malt Extract Agar, out of which two in conjunction with SFS 5507 and the other without mentioning any standard. These are placed in the group (ME Agar). Three other laboratories with unusual or unclear details are placed in the group Other/Unknown. For these groups the numbers of results per group are so few that median is given and thus it is not meaningful to discuss

*Moulds MF*

| **Standard/Method** | N | A | | | | | | B | | | | | | C | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total** | 42 | 41 | **86** | 21 | 0 | 1 | 0 | 42 | **0** | 99 | 0 | 0 | 0 | 40 | **92** | 20 | 1 | 1 | 0 |
| RBC A(gar) | 24 | 24 | **82** | 25 | 0 | 0 | 0 | 24 | **1** | 80 | 0 | 0 | 0 | 23 | **90** | 22 | 1 | 0 | 0 |
| DRBC A "Water" | 7 | 7 | **101** | 16 | 0 | 0 | 0 | 7 | **0** | 133 | 0 | 0 | 0 | 7 | **96** | 17 | 0 | 0 | 0 |
| ME Agar | 4 | 4 | **95*** | – | 0 | 0 | 0 | 4 | **2*** | – | 0 | 0 | 0 | 4 | **93*** | – | 0 | 0 | 0 |
| "Food" methods* | 4 | 4 | **81*** | – | 0 | 0 | 0 | 4 | **0** | – | 0 | 0 | 0 | 4 | **86*** | – | 0 | 0 | 0 |
| Other/Unknown | 3 | 2 | **87*** | – | 0 | 1 | 0 | 3 | **0** | – | 0 | 0 | 0 | 2 | **93*** | – | 0 | 1 | 0 |

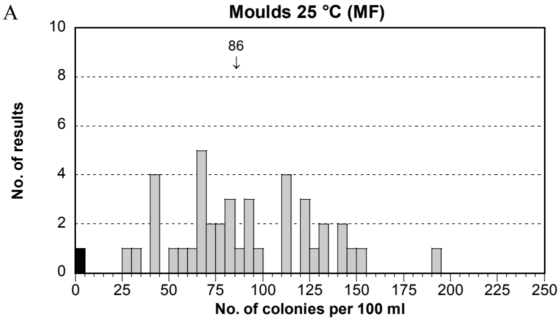
*Yeasts MF*

| **Standard/Method** | N | A | | | | | | B | | | | | | C | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total** | 42 | 41 | **58** | 20 | 0 | 1 | 0 | 36 | **8** | 17 | 2 | 1 | 3 | 41 | **0** | – | 1 | – | – |
| RBC A(gar) | 24 | 24 | **50** | 20 | 0 | 0 | 0 | 22 | **7** | 19 | 1 | 0 | 1 | 23 | **0** | – | 1 | – | – |
| DRBC A "Water" | 7 | 7 | **72** | 24 | 0 | 0 | 0 | 6 | **7** | 7 | 0 | 0 | 1 | 7 | **0** | – | 0 | – | – |
| ME Agar | 4 | 4 | **67*** | – | 0 | 0 | 0 | 3 | **10*** | – | 0 | 0 | 1 | 4 | **0** | – | 0 | – | – |
| "Food" methods# | 4 | 4 | **59*** | – | 0 | 0 | 0 | 4 | **7*** | – | 0 | 0 | 0 | 4 | **0** | – | 0 | – | – |
| Other/Unknown | 3 | 2 | **66*** | – | 0 | 1 | 0 | 1 | **9** | – | 1 | 1 | 0 | 3 | **0*** | – | 0 | – | – |

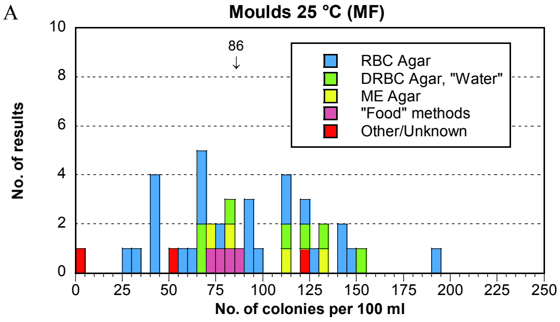
* Median instead of mean value

# 2 laboratories each with DRBC A based on NMKL 98 (2005) and OGYE A based on ISO 7954 (1987)

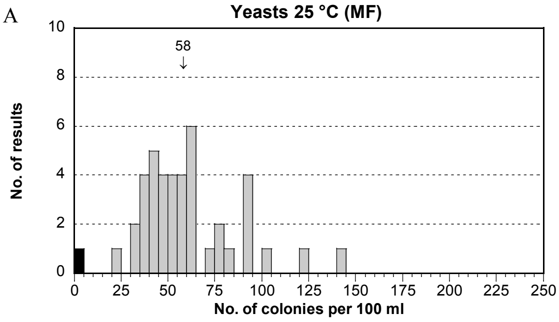
A


Moulds 25 °C (MF)
86
↓
No. of results
0
2
4
6
8
10
0
25
50
75
100
125
150
175
200
225
250
No. of colonies per 100 ml

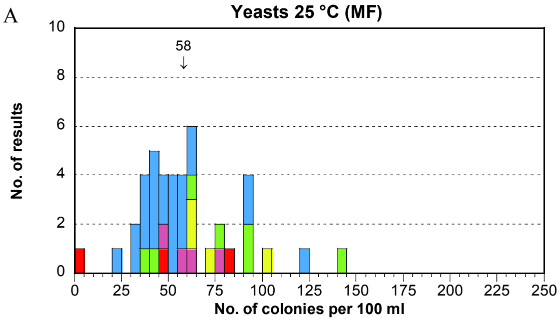
A


Moulds 25 °C (MF)
86
↓
🟦 RBC Agar
🟩 DRBC Agar, "Water"
🟨 ME Agar
🟪 "Food" methods
🟥 Other/Unknown
No. of results
0
2
4
6
8
10
0
25
50
75
100
125
150
175
200
225
250
No. of colonies per 100 ml

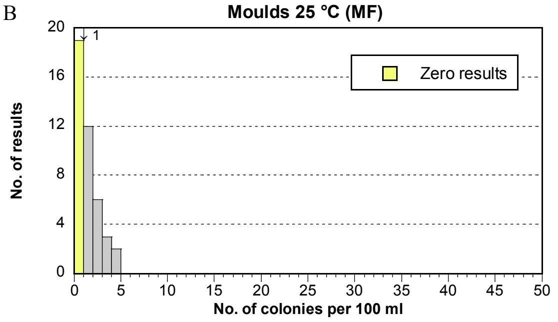
A


Yeasts 25 °C (MF)
58
↓
No. of results
0
2
4
6
8
10
0
25
50
75
100
125
150
175
200
225
250
No. of colonies per 100 ml

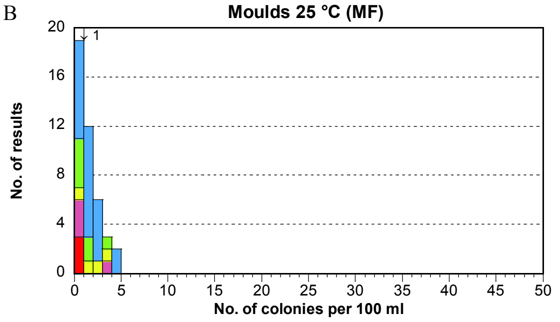
A


Yeasts 25 °C (MF)
58
↓
No. of results
0
2
4
6
8
10
0
25
50
75
100
125
150
175
200
225
250
No. of colonies per 100 ml

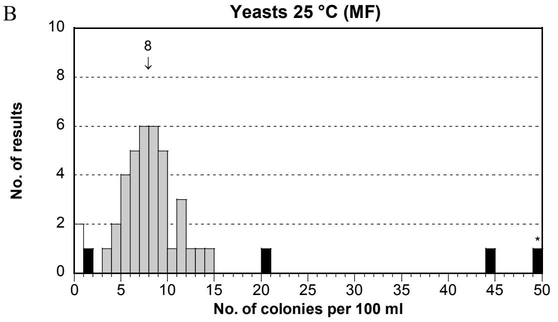
B


Moulds 25 °C (MF)
↓ 1
🟨 Zero results
No. of results
0
4
8
12
16
20
0
5
10
15
20
25
30
35
40
45
50
No. of colonies per 100 ml

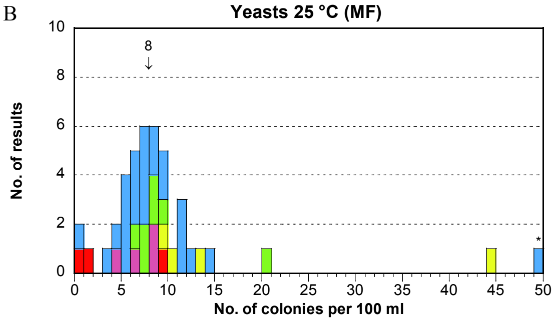
B


Moulds 25 °C (MF)
↓ 1
No. of results
0
4
8
12
16
20
0
5
10
15
20
25
30
35
40
45
50
No. of colonies per 100 ml

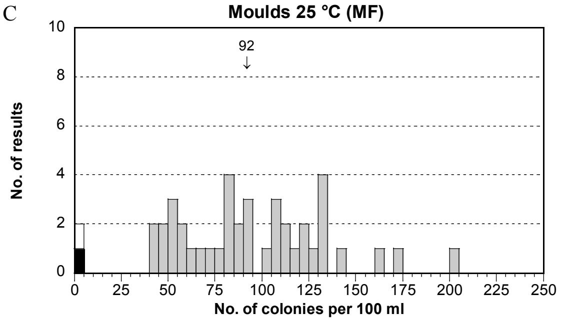
B


Yeasts 25 °C (MF)
8
↓
*
No. of results
0
2
4
6
8
10
0
5
10
15
20
25
30
35
40
45
50
No. of colonies per 100 ml

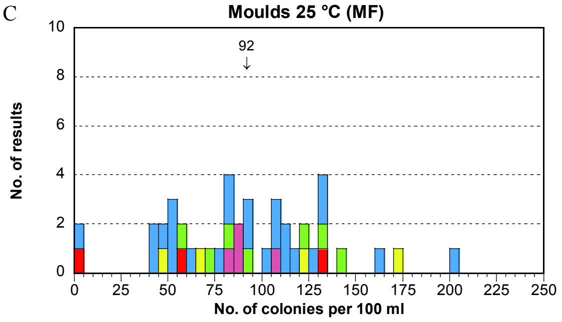
B


Yeasts 25 °C (MF)
8
↓
*
No. of results
0
2
4
6
8
10
0
5
10
15
20
25
30
35
40
45
50
No. of colonies per 100 ml

C



C



seemingly numerical differences. However, in the group Other/Unknown 3 low outliers are present.

There is a tendency that the results are somewhat higher for both moulds and yeasts with DRBC agar "Water" compared to RBC agar for yeasts in mixture A. This is even not contradicted by the results from the other mixtures.

### Mixture A

- The mould *Cladosporium cladosporoides* and the yeast *Saccharomyces cerevisiae* were included. The distributions of the results were quite good to be fungi. The dispersion as CV was small to medium.
- One low outlier was present in each group of target organisms.

### Mixture B

- The yeast *Rhodotorula minuta* and the mould *Pleurophoma sp.* were included, the latter in very low concentration. This implies that zero results also are accepted for moulds. No outliers were found for that analysis.
- Also yeasts were present in fairly low numbers with a good distribution of results and small dispersion. Two false negative results and 3 high outliers were present.

### Mixture C

- No yeasts were included but the same mould strain as in mixture A. The distribution and dispersion of moulds were also about the same as for mixture A.
- One false positive result was present for yeasts, while one false negative result and another low outlier were present for moulds.

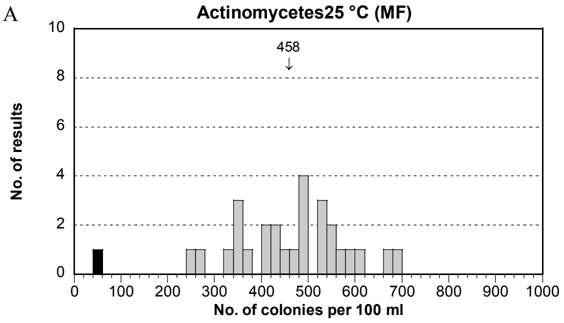
## Actinomycetes (MF)

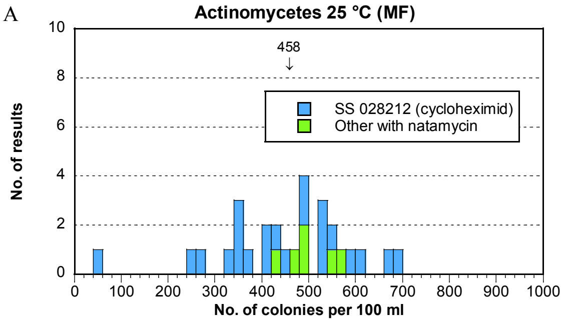
The analysis of actinomycetes is included because it is among the methods that should regularly be used according to the Swedish regulations. Therefore, it is mainly Swedish laboratories that performed the analysis according to the Swedish standard for actinomycetes in water, SS 028212 (1994). Six laboratories, that probably not have performed the analysis based on the Swedish regulation, have performed the analyses with other methods. In those cases have natamycin been used as selective substance instead of cycloheximide. The agar medium used is sometimes also different from that in the Swedish standard.

It is clear from the table that mixture A that somewhat higher results were obtained with the methods Other/Unknown containing natamycin compared to the Swedish standard. This pertains to the strain and sample included here but cannot from the data here be considered to be generally valid.

*All results*

| **Standard/Method** | N | **A** | | | | | | **B** | | | | | | **C** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total** | 28 | 27 | **458** | 12 | 0 | 1 | 0 | 27 | **0** | – | 0 | – | – | 21 | **0** | – | 6 | – | – |
| SS 028212 | 22 | 21 | **448** | 14 | 0 | 1 | 0 | 22 | **0** | – | 0 | – | – | 16 | **0** | – | 6 | – | – |
| Other/Unknown | 6 | 6 | **492** | 5 | 0 | 0 | 0 | 5 | **0** | – | 0 | – | – | 5 | **0** | – | 0 | – | – |





### Mixtures A

- One actinomycete within the group *Streptomyces sp*. was included. One low and outlier was present, but generally the laboratories quantified the bacterium correctly. The dispersion was small.
- The average difference between methods according to the table seems, based on the histogram, be due to the fact that there were more low results present for the four times more abundant number of results reported for the Swedish standard compared to the other method.

### Mixture B and C

- These mixtures contained no actinomycetes. Despite this, six false positive results were present in mixture C.

## Culturable microorganisms 22 °C, 3 days

Eighty five of the 89 laboratories performing the analysis reported EN ISO 6222:1999 as method, which prescribes the use of Yeast extract Agar. Six laboratories used Plate Count Agar, of which 5 together with EN ISO 6222:1999. The sixth laboratory used "Standard methods" (5). One laboratory used Nutrient Agar together with membrane filtration and "Nutrient pads" but in this case not based on EN ISO 6222:1999. Five laboratories reported spread plating, four of these referring to EN ISO 6222:1999. The last one reported a method for pharmaceuticals.

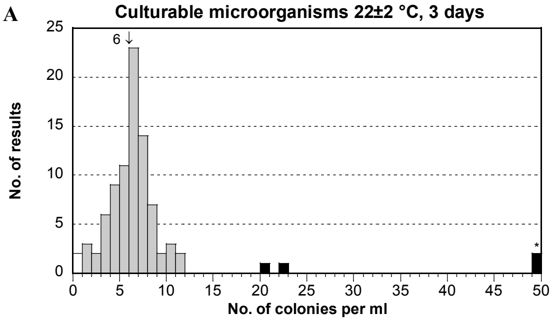
Only comparisons of method variants in connection to EN ISO 6222:1999 are relevant to discuss. Results are shown for culture media and magnification of reading.

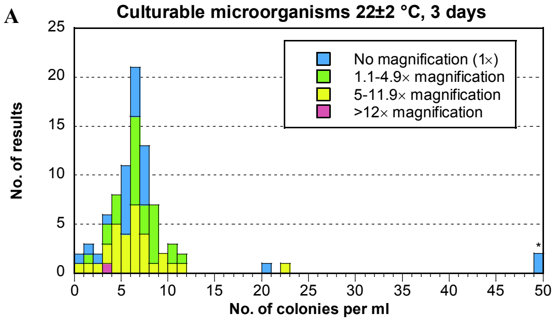
There is no method difference to report for any sample mixture. In the mixtures A and C the group means are too low to be able to detect any differences.

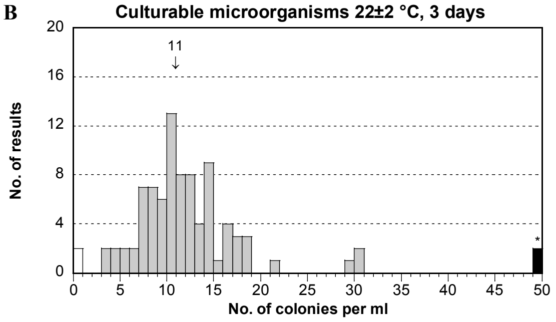
Although the distributions were good, the dispersion as CV was of medium size both in mixture A and B due to the fairly low concentrations of organisms. In mixture C the CV turned, as normally, out to be very large because of very low organism content, about 1 cfu/ml.

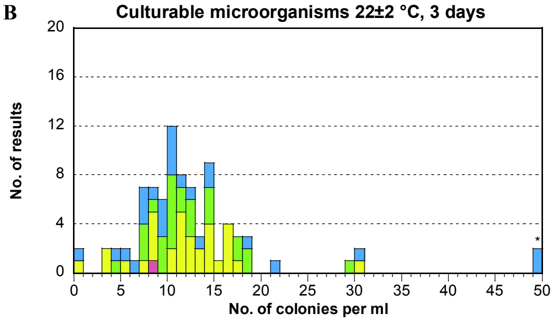
| Group of results | N | A | | | | | | B | | | | | | C | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > | n | **Mv** | CV | F | < | > |
| **Total, all results** | 89 | 82 | **6** | 20 | 2 | 0 | 4 | 85 | **11** | 21 | 2 | 0 | 2 | 85 | **1** | 74 | 0 | 0 | 4 |
| ***EN ISO 6222*** | *85* | *78* | ***6*** | *21* | *2* | *0* | *4* | *81* | ***11*** | *22* | *2* | *0* | *2* | *81* | ***1*** | *77* | *0* | *0* | *4* |
| *Medium* | | | | | | | | | | | | | | | | | | | |
| Yeast extract Agar | 79 | 74 | **6** | 21 | 1 | 0 | 3 | 77 | **11** | 21 | 1 | 0 | 1 | 77 | **1** | 76 | 0 | 0 | 2 |
| Plate Count Agar | 5 | 3 | **6***  | – | 1 | 0 | 1 | 3 | **10*** | – | 1 | 0 | 1 | 3 | **0*** | – | 0 | 0 | 2 |
| Other/Unknown | 1 | 1 | **6** | – | 0 | 0 | 0 | 1 | **12** | – | 0 | 0 | 0 | 1 | **3** | – | 0 | 0 | 0 |
| *Magnification* | | | | | | | | | | | | | | | | | | | |
| None | 25 | 21 | **5** | 19 | 1 | 0 | 3 | 22 | **10** | 24 | 1 | 0 | 2 | 23 | **1** | 74 | 0 | 0 | 2 |
| 1,1–4,9× | 27 | 27 | **6** | 20 | 0 | 0 | 0 | 27 | **11** | 20 | 0 | 0 | 0 | 26 | **1** | 78 | 0 | 0 | 1 |
| 5–11,9× | 32 | 29 | **5** | 22 | 1 | 0 | 1 | 31 | **11** | 22 | 1 | 0 | 0 | 31 | **1** | 78 | 0 | 0 | 1 |
| > 12× | 1 | 1 | **3** | – | 0 | 0 | 0 | 1 | **1** | – | 0 | 0 | 0 | 1 | **0** | – | 0 | 0 | 0 |
| ***Other method*** | 4 | 4 | **6*** | – | 0 | 0 | 0 | 4 | **11*** | – | 0 | 0 | 0 | 4 | **2*** | – | 0 | 0 | 0 |

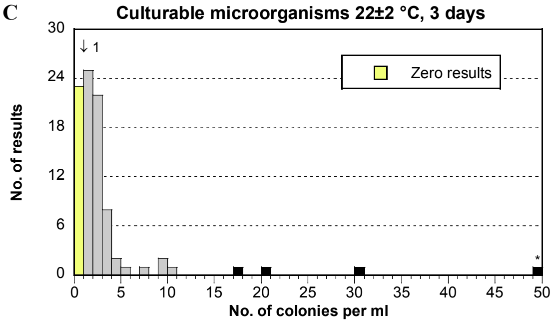
* Median instead of mean value

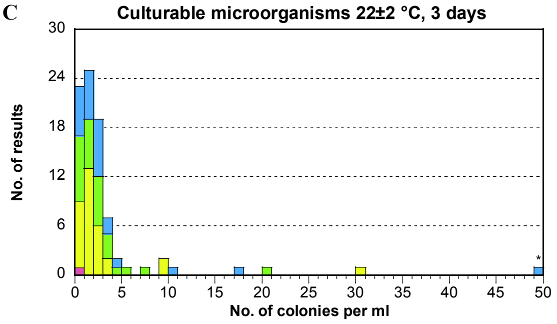












## Mixture A

- It is mainly colonies of the actinomycete that appears as culturable microorganisms. Even the yeast strain are able to grow but has to low concentration to have any effect.
- The distribution of the results was good. Two false negative and 4 high outliers were present.

## Mixture B

- The colonies are mainly made up of the strain of *Stenotrophomonas maltophilia* but also the coliform bacteria may appear with individual colonies.
- The distribution was good with only 2 low and 2 high outliers.

## Mixture C

- The number of colonies appearing was very low, about 1 cfu/ml. What mainly grow are colonies of *Staphylococcus saprophyticus*. Also individual colonies of coliform bacteria and perhaps a colony of moulds may sometimes appear.
- Due to the very low average, also a zero result is appropriate and acceptable. The distribution was, however, good in general but with 4 results with >10 cfu/ml as high outliers.

# Outcome of the results and laboratory assessment

## General information about reported results

The distributions of results for the respective analysis are shown in histograms. A box plot (see below) gives a summarizing image of all the results of a laboratory, except false results. The number of false results and outliers are given below the plot for each laboratory. These values are highlighted with bold text on yellow background in annex A. The limit values for lowest and highest accepted results are given for each analyse in the summarizing lines at the end of annex A, together with the measurement uncertainty of the mean.

## Base for assessment of the performance

The laboratories are not grouped or ranked in relation to their performances. The performance can broadly be assessed by the numbers of false results and outliers given beneath the box plots.

Generally, the laboratories that did not report their results in due time, have to compare their results themselves with all other laboratory's by looking in tables, figures and annex A.

## Mixed up results and other practical errors

A number of laboratories have several deviating results. When whole samples seem to have been mixed up, the corresponding sample numbers are hatched in annex A. No laboratory seems to have mixed up the vials for any sample this time and even not sample/results for individual analyses. One laboratory (7191) seems to have performed incorrect calculations from the results of presumptive coliform bacteria.

## Z-scores, box plots and deviating results for each laboratory

The square root transformed results of the laboratories are calculated to standard scores, z-scores, to be comparable between analyses. They are reported in annex B but not further evaluated here. They are given explicitly to facilitate the follow-up process for laboratories using z-scores in control charts etc. For interpretation and calculation of z-scores, see the scheme protocol (1) and the explanation to annex A.

The z-scores are the base for the box plots. The range of the z-scores for each laboratory is shown by a rectangle (box) and lines and/or circles above and beneath the box. The smaller the range from lowest to highest value is in the plot and the more centred around zero the values are, the better is the agreement between the laboratory's results and the means from all laboratories.

### *Box plots and numbers of deviating results for each participating laboratory*

- *Z-scores are calculated from the formula z = (x – mv) / s (see annex A).*
- *False results do not generate z-scores and are not included in 'No. of results'.*
- *The outliers are included in the plots after recalculation to standardised values with the same standard deviation (s) as the rest of the results.*
- *Z-scores > +4 and < –4 have in the plots been set to +4 and –4, respectively.*
- *The numbers of false positives and false negatives are given in the table under the plots together with the numbers of outliers.*
- *The horizontal red line in each box indicates the median for the laboratory.*
- *The box includes 25% of the results above and below the median. The lines protruding from the box and/or the circles embrace the remaining 50% of the results, false results excluded.*
- *A circle is shown when a result is to a certain degree deviating* from the rest.*
- *The background is divided into coloured fields in order to simplify localization of the laboratory results.*

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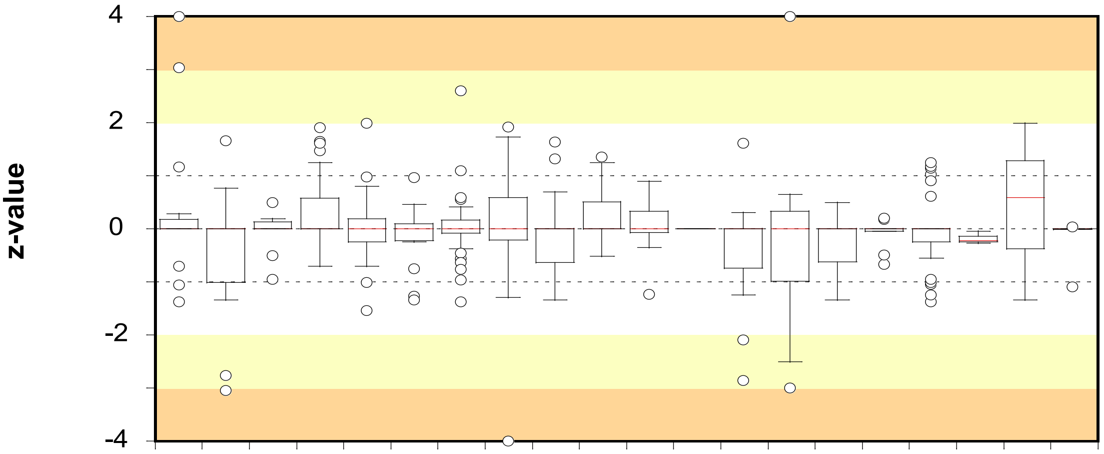
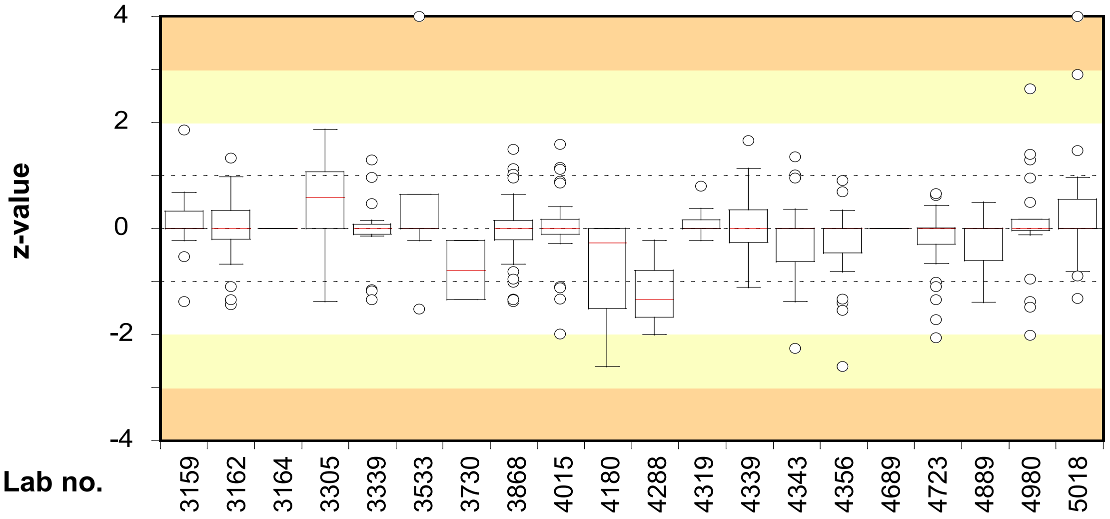
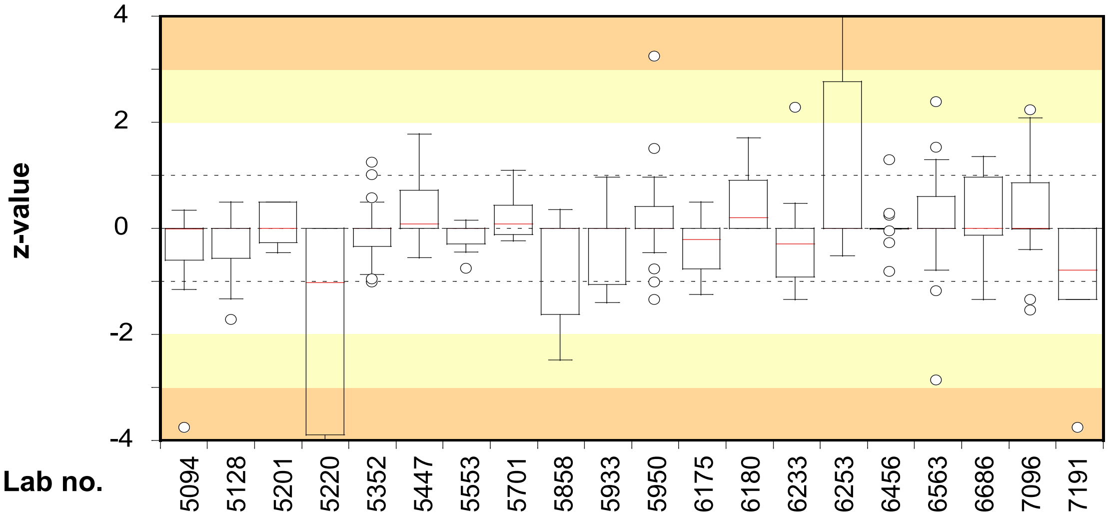
* < [smallest value of the box - 1.5 × (largest value of the box - smallest value of the box)] *or* > [largest value of the box + 1.5 × (largest value of the box - smallest value of the box)]



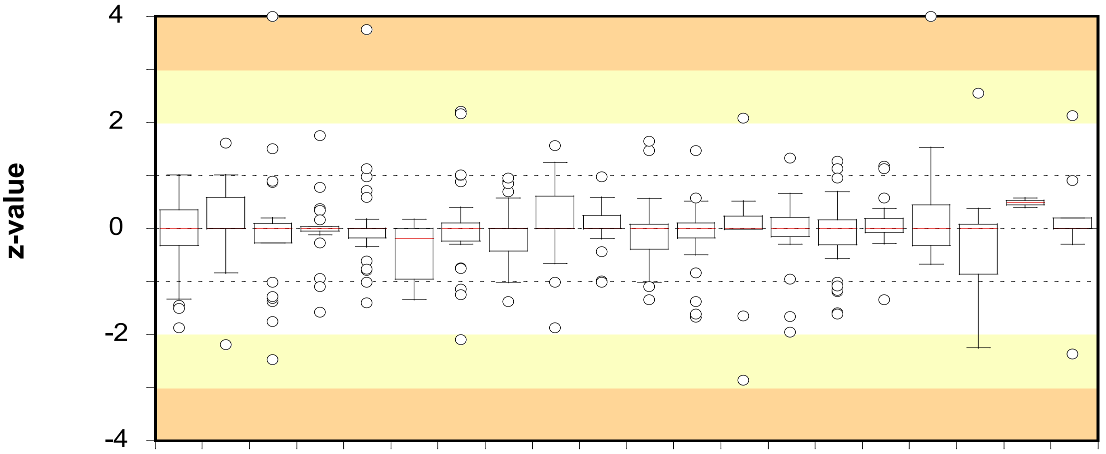
| Lab no. | 1131 | 1237 | 1290 | 1545 | 1594 | 1611 | 1753 | 1868 | 1970 | 2050 | 2386 | 2534 | 2637 | 2670 | 2704 | 2745 | 2797 | 3055 | 3076 | 3145 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| No. of results | 18 | 20 | 11 | 29 | 21 | 15 | 29 | 26 | 21 | 26 | 12 | - | 12 | 15 | 18 | 9 | 27 | 3 | 3 | 6 |
| False positive | - | - | 1 | 1 | - | - | - | 1 | - | 1 | - | - | - | - | - | - | - | - | - | - |
| False negative | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| Low outliers | - | - | - | - | - | - | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - |
| High outliers | 1 | - | - | - | - | - | - | - | - | - | - | - | - | 3 | - | - | - | - | - | - |



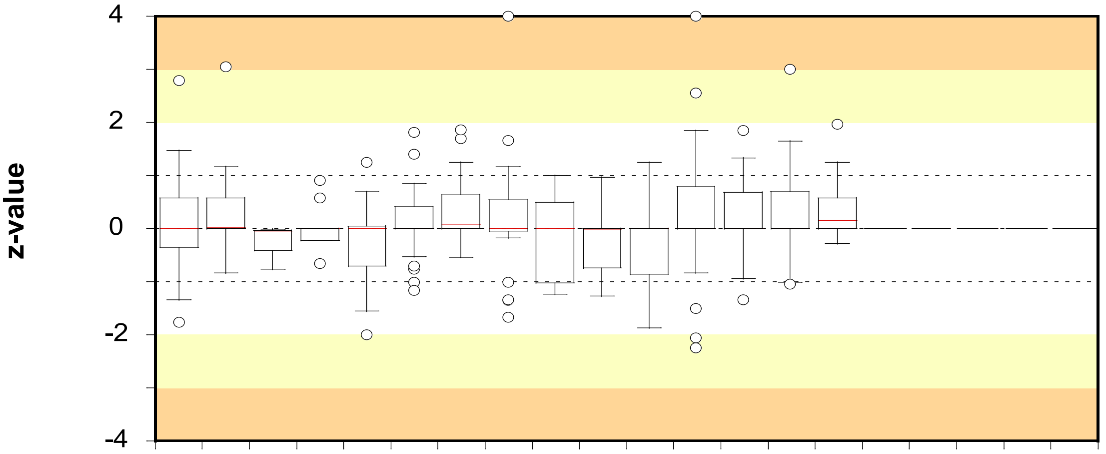
| Lab no. | 3159 | 3162 | 3164 | 3305 | 3339 | 3533 | 3730 | 3868 | 4015 | 4180 | 4288 | 4319 | 4339 | 4343 | 4356 | 4689 | 4723 | 4889 | 4980 | 5018 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| No. of results | 18 | 26 | - | 30 | 15 | 9 | 2 | 30 | 27 | 9 | 3 | 15 | 28 | 27 | 21 | - | 27 | 18 | 21 | 30 |
| False positive | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| False negative | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| Low outliers | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| High outliers | - | - | - | - | - | 2 | - | - | - | - | - | - | - | - | - | - | - | - | - | 1 |



| Lab no. | 5094 | 5128 | 5201 | 5220 | 5352 | 5447 | 5553 | 5701 | 5858 | 5933 | 5950 | 6175 | 6180 | 6233 | 6253 | 6456 | 6563 | 6686 | 7096 | 7191 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| No. of results | 8 | 15 | 6 | 12 | 21 | 18 | 9 | 8 | 15 | 12 | 28 | 9 | 21 | 15 | 9 | 13 | 27 | 12 | 20 | 6 |
| False positive | - | - | - | - | - | - | - | 1 | - | - | 1 | - | - | - | - | - | - | - | - | 1 |
| False negative | 1 | - | - | - | - | - | - | - | - | - | 1 | - | - | - | - | 2 | - | - | - | 2 |
| Low outliers | 1 | - | - | 4 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 1 |
| High outliers | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 1 | - | - | - | - | - |



| Lab no. | 7248 | 7302 | 7442 | 7596 | 7688 | 7728 | 7876 | 7896 | 7930 | 7962 | 7968 | 8068 | 8252 | 8260 | 8329 | 8380 | 8435 | 8569 | 8598 | 8626 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| No. of results | 27 | 26 | 25 | 21 | 26 | 9 | 27 | 23 | 26 | 21 | 27 | 27 | 12 | 15 | 27 | 15 | 12 | 12 | 3 | 9 |
| False positive | - | 1 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| False negative | - | - | - | - | 1 | - | - | 2 | 1 | - | - | - | - | - | - | - | - | - | - | - |
| Low outliers | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| High outliers | - | - | 1 | - | 1 | - | - | - | - | - | - | - | - | - | - | - | 1 | - | - | - |



| Lab no. | 8628 | 8663 | 8742 | 8751 | 8766 | 8862 | 8898 | 8955 | 8971 | 8998 | 9051 | 9436 | 9736 | 9899 | 9903 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| No. of results | 18 | 19 | 3 | 9 | 27 | 27 | 26 | 23 | 9 | 12 | 12 | 27 | 27 | 27 | 18 |
| False positive | - | 2 | - | - | - | - | 1 | - | - | - | - | - | - | - | - |
| False negative | - | - | - | - | - | - | - | 1 | - | - | - | - | - | - | - |
| Low outliers | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| High outliers | - | - | - | - | - | - | - | 1 | - | - | - | 1 | - | - | - |

# Test material, quality controls and processing of data

## Description of the test material

This round comprised three test items with different microorganism mixtures. The test material was manufactured and freeze-dried in portions of 0.5 ml in small vials, according to the description by Peterz and Steneryd (2). The simulated water samples were prepared by dissolving the content of the vials in 800 ml of sterile diluent. The composition and approximate concentrations in each mixture is listed in table 2. The participating laboratories were assigned to perform the analyses according to the methods routinely used by them.

The test material is primarily adapted to the EN ISO methods for analyses of drinking water referred to in the European Drinking water directive (4) and its updates (6). Alternative methods and other standards may usually also be used without any problem.

**Table 2** *Microorganisms present in the mixtures*

| **Mixture** [1] | **Microorganisms** | **Strain collection no.** | | **cfu/100 ml** [2] |
|---|---|---|---|---|
| | | SLV (own) | Reference [3] | |
| A | *Saccharomyces cerevisiae* | 375 | Typed at CBS | 38 |
| | *Cladosporium cladosporoides* | 488 | CBS 812.96 | 120 |
| | *Streptomyces sp.* | 548 | From "water" | 500 |
| B | *Enterobacter cloacae* | 187 | CCUG 43599 | 290 |
| | *Hafnia alvei* | 015 | CCUG 45642 | 140 |
| | *Clostridium bifermentans* | 009 | CCUG 43592 | 120 |
| | *Stenotrophomonas maltophilia* | 041 | CCUG 46537 | 10 * |
| | *Rhodotorula minuta* | 506 | Typed at CBS | 7 |
| | *Pleurophoma sp.* | 543 | CBS 119226 | 1 |
| C | *Escherichia coli* | 084 | From water | 18 |
| | *Klebsiella pneumoniae* | 186 | CCUG 45102 | 20 |
| | *Clostridium perfringens* | 442 | CCUG 43593 | 380 |
| | *Cladosporium cladosporoides* | 488 | CBS 812.96 | 140 |
| | *Staphylococcus saprophyticus* | 013 | CCUG 45100 | 1 * |

1 The links between the mixtures and the randomised sample numbers are shown in annex A; the analyses were performed at the times given in note 1 of table 3

2 cfu = colony forming units

3 Origin or typing collection no.; CCUG: Culture Collection University of Gothenburg, Sweden; CBS: Centraalbureau vor Schimmelcultures, Utrecht, Holland

* Indicates cfu per ml

## Quality control of the test material

It is essential to have a homogeneous mixture and a uniform volume in all vials in order to allow comparison of all freeze-dried samples derived from one mixture. The volume was checked by weighing 15 and 20 dispensed aliquots in vials, for mixture A and C, respectively. The largest differences between vials were 7 and 10 mg, respectively, in the mixtures. The largest accepted difference is 15 mg (3%). Result for mixture B is missing due to a data file error. However, there is no reason to suspect a difference of more than 10 mg even there, based on general knowledge of our freeze-drying process.

**Table 3** *Contents (cfu) and measures of homogeneity ($I_2$ and T, see reference 1) in relevant sample volumes for the various parameters in the mixtures*

| **Analysis parameter**<br>***Method standard for analysis*** | **Mixture** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | **A**[1] | | | **B**[2] | | | **C**[2] | | |
| | **cfu** | **$I_2$** | **T** | **cfu** | **$I_2$** | **T** | **cfu** | **$I_2$** | **T** |
| Coliform bacteria (MF)<br>*m-Endo Agar LES according to SS 028167* | – | – | – | 29[b] | 0.9 | 1.4 | 39 | 0.4 | 1.2 |
| Suspected thermotolerant colif. bact. (MF)<br>*m-FC Agar, 44 °C according to SS 028167* | – | – | – | – | – | – | 30 | 1.0 | 1.4 |
| *Escherichia coli* (MF)<br>*m-Endo Agar LES according to SS 028167* | – | – | – | – | – | – | 18 | 0.8 | 1.6 |
| Presumptive *Clostridium perfringens* (MF)<br>*TSC Agar according to ISO/CD 6461-2:2002* | – | – | – | 121 | 12 | 1.8 | 38[b] | 1.0 | 1.4 |
| Moulds (MF)<br>*Rose Bengal Agar with both chloramphenicol and chlortetracycline according to SS 028192* | 33[b] | 1.3 | 1.5 | 1 | 0.7 | 5.7 | 14[b] | 1.9 | 2.0 |
| Yeasts (MF)<br>*Rose Bengal Agar with both chloramphenicol and chlortetracycline according to SS 028192* | 10[b] | 0.7 | 1.7 | 7 | 1.8 | 2.2 | – | – | – |
| Actinomycetes (MF)<br>*Actinomycete Isolation Agar with cycloheximide according to SS 028212* | 67[a] | 2.2 | 1.4 | – | – | – | – | – | – |
| Culturable microorg., 3d 22 °C (pour plate)<br>*Yeast extract Agar according to SS-EN ISO 6222:1999* | 18 | 0.4 | 1.4 | 14 | 1.7 | 2.5 | 2 | 0.7 | 4.5 |

1 5 vials analysed in duplicate (stability check; 6 weeks ahead of the testing round) with the test material dissolved in 300 ml diluent

2 10 vials analysed in duplicate, normally100 ml for MF and 1 ml for pour plate, with the test material dissolved in 800 ml diluent, analysed 13 and 15 weeks ahead of the testing round for the mixtures B and C, respectively

a Determined for the volume 5 ml

b Determined for the volume 10 ml

– No target organism and thus no analysis

Table 3 presents the results from the organizer in the form of concentration means (cfu) and the measures ($I_2$ and T; see reference 1) used to assess homogeneity from duplicate analyses of 10 vials from each mixture. The results relate to the volume that was used for counting the colonies. The criterion used for a mixture to be considered homogenous is that $I_2$ and T are *not simultaneously* higher than 2. According to that criterion, all mixtures were homogeneous regarding the parameters that were about to be analysed.

## Processing of numerical results

Most histograms have "tails" in either or both directions, due to values that do not belong to a normal distribution. Calculations are performed after square root transformations of the results that give better normal distributions by decreasing the significance of the high end "tails". Very deviating values are still present in most analyses and are identified as outliers (black bars). False negative results are presented with white bars in the histograms.

Outliers are identified by use of Grubbs' test according to a modification by Kelly (3). A level of 1% is set as the risk to incorrectly assess a result as being an outlier. Although the method is objective, there is a prerequisite that the results are normally distributed in order to obtain correct outliers at the 1% level. A zero result that is a low outlier is considered a false negative result. In special situations, e.g. when many zero results are reported and in some borderline cases, a few subjective adjustments are made in order to set the right limits based on the knowledge of the mixture's contents. False results and outliers are not included in the calculations of mean values and measures of distribution.

The coefficient of variation (CV) for square root transformed results is given as a measure of dispersion. When the dispersion is <10% it is regarded as very small, 10–20% as small, 20–30 % as medium, 30–40% as large and >40% as very large.

The calculation of uncertainty of measurement of the assigned value is described in the scheme protocol (1). The assigned value for an analysis is calculated from the square root transformed results and is the square root of "Mean" in Annex A. It is there denoted as mv. Hence, also the measurement uncertainty will be expressed as a square root value. The standard uncertainty of measurement ($u$) correspond to the standard deviation of the assigned value ($s$) divided by the number of results squared-root transformed, i.e.: $u = s/\sqrt{n_{mv}}$ where $n_{mv}$ is the number of results in annex A, except the deviating ones. Here is the relative uncertainty ($u_{rel}$) used and expressed as per cent after division by the mean value *mv* and multiplication by 100.

More about result processing and recommendations on follow-up work are given in the scheme protocol (1). A PDF of that document is available on the website www2.slv.se/absint.

# References

1. Anonymous 2015. Scheme protocol, Microbiology, Drinking water & Food, 4th ed. National Food Agency, Sweden.
2. Peterz, M., Steneryd, A.-C. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. J. Appl. Bacteriol. 74:143-148.
3. Kelly, K. 1990. Outlier detection in collaborative studies. J. Assoc. Off. Chem. 73:58-64.
4. Anonymous 1998. Council Directive 98/83/EC of 3 November 1998 on the quality of water intended for human consumption. Official Journal of the European Communities. 5.12.98, L 330/32-54 *(national translations available)*.
5. Standard Methods for the Examination of Water and Wastewater, http://www.standardmethods.org/
6. Anonymous 2015. Commission Directive (EU) 2015/1787 of 6 October 2015 amending Annexes II and III to Council Directive 98/83/EC on the quality of water intended for human consumption. Official Journal of the European Union. 7.10.2015, L 260/6-17 *(national translations available)*.

**Annex A** *Results of the participants. Susp. = suspected on membrane filter before confirmation. Results given as <1, <2, <10 and <100 are treated as zero. The fields with other results given as < 'value' and results given as > 'value' are* ***yellow****, and those results are not included in calculations or evaluations, as are also not results in* ***shaded columns****.* ***Empty hatched fields*** *indicate that the result has been deleted due to misunderstanding of instructions or use of improper method. A* ***hyphen*** *indicate that no result has been reported.* ***Figures written in bold in yellow fields*** *indicate outliers, false positive and false negative results.* ***Underlined zero values*** *indicate results characterized as 'False negative ?'.* ***Crossed out sample numbers*** *in a row indicate that the samples probably are mixed up. False positive and false negative values are excluded, as well as other outliers, in the summarizing*

| Lab no. | Sample | | | Suspected coliform bacteria (MF) | | | Coliform bacteria (MF) | | | Susp. thermotolerant coliform bact. (MF) | | | *E. coli* (MF) | | | Coliform bacteria ("rapid" MPN) | | | *E. coli* ("rapid" MPN) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C |
| **1131** | 2 | 3 | 1 | 0 | 260 | 25 | 0 | 260 | 25 | - | - | - | 0 | 0 | 15 | 0 | 326 | 36 | 0 | 0 | 10 |
| **1237** | 3 | 1 | 2 | - | - | - | <1 | 170 | 8 | - | - | - | <1 | <1 | **<1** | <1 | 276 | 16 | <1 | <1 | 9 |
| **1290** | 2 | 1 | 3 | - | - | - | <1 | 195 | 34 | - | - | - | <1 | <1 | 14 | - | - | - | - | - | - |
| **1545** | 2 | 1 | 3 | 0 | 330 | 36 | 0 | 330 | 36 | 0 | 0 | 36 | 0 | 0 | 13 | 0 | 313 | 34 | 0 | 0 | 16 |
| **1594** | 1 | 3 | 2 | 0 | 215 | 43 | 0 | 215 | 43 | 0 | 0 | 23 | 0 | 0 | 19 | 0 | 235 | 36 | 0 | 0 | 8 |
| **1611** | 3 | 2 | 1 | 0 | 172 | 37 | 0 | 172 | 37 | 0 | 160 | 33 | 0 | 0 | 16 | 0 | 172 | 32 | 0 | 0 | 14 |
| **1753** | 2 | 1 | 3 | 0 | 590 | 38 | 0 | 590 | 38 | - | - | - | 0 | 0 | 21 | 0 | 488 | 31 | 0 | 0 | 16 |
| **1868** | 3 | 1 | 2 | 0 | 457 | 28 | 0 | 457 | 28 | - | - | - | 0 | 0 | 12 | 0 | 576 | 47 | 0 | 0 | 27 |
| **1970** | 3 | 1 | 2 | 0 | 400 | 31 | 0 | 400 | 31 | 0 | 330 | 25 | 0 | 0 | 25 | - | - | - | - | - | - |
| **2050** | 1 | 2 | 3 | - | - | - | 0 | 300 | 37 | - | - | - | 0 | 0 | 13 | 0 | 346 | 30 | 0 | 0 | 18 |
| **2386** | 1 | 2 | 3 | 0 | 320 | 42 | 0 | 320 | 42 | 0 | 230 | 26 | 0 | 0 | 12 | - | - | - | - | - | - |
| **2534** | 2 | 1 | 3 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **2637** | 2 | 3 | 1 | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 364 | 25 | 0 | 0 | 6 |
| **2670** | 1 | 2 | 3 | 0 | 32 | 26 | 0 | 32 | 26 | 0 | 0 | 23 | 0 | 0 | 18 | - | - | - | - | - | - |
| **2704** | 3 | 1 | 2 | - | - | - | 0 | 160 | 25 | - | - | - | 0 | 0 | 11 | <1 | 165 | 34 | <1 | <1 | 10 |
| **2745** | 3 | 2 | 1 | 0 | 180 | 27 | 0 | 180 | 27 | 0 | 180 | 27 | 0 | 0 | 14 | - | - | - | - | - | - |
| **2797** | 3 | 1 | 2 | 0 | 230 | 22 | 0 | 230 | 22 | 0 | 0 | 11 | 0 | 0 | 11 | 0 | 161 | 42 | 0 | 0 | 15 |
| **3055** | 2 | 1 | 3 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **3076** | 3 | 2 | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **3145** | 1 | 3 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 326 | 26 | 0 | 0 | 15 |
| **3159** | 2 | 3 | 1 | - | - | - | 0 | 320 | 35 | - | - | - | 0 | 0 | 17 | <1 | 624 | 36.4 | <1 | <1 | 12.4 |
| **3162** | 2 | 3 | 1 | 0 | 180 | 33 | 0 | 180 | 33 | - | - | - | 0 | 0 | 16 | 0 | 326 | 35 | 0 | 0 | 18 |
| **3164** | 3 | 2 | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **3305** | 1 | 2 | 3 | - | - | - | <1 | 340 | 47 | - | - | - | <1 | <1 | 19 | <1 | 490 | 45 | <1 | <1 | 21 |
| **3339** | 2 | 3 | 1 | 0 | 230 | 21 | 0 | 230 | 21 | - | - | - | 0 | 0 | 8 | - | - | - | - | - | - |
| **3533** | 3 | 2 | 1 | - | - | - | 0 | 290 | 18 | - | - | - | 0 | 0 | 18 | - | - | - | - | - | - |
| **3730** | 1 | 2 | 3 | - | 280 | 41 | - | - | - | - | 280 | 14 | - | - | - | - | - | - | - | - | - |
| **3868** | 2 | 1 | 3 | 0 | 180 | 38 | 0 | 180 | 38 | 0 | 90 | 28 | 0 | 0 | 18 | 0 | 220 | 43 | 0 | 0 | 21 |
| **4015** | 1 | 2 | 3 | 0 | 264 | 42 | 0 | 264 | 42 | - | - | - | 0 | 0 | 15 | 0 | 290 | 47 | 0 | 0 | 20 |
| **4180** | 3 | 2 | 1 | - | - | - | 0 | 113 | 20 | - | - | - | 0 | 0 | 3 | - | - | - | - | - | - |
| **4288** | 3 | 1 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **4319** | 2 | 1 | 3 | 0 | 305 | 33 | 0 | 285 | 33 | 0 | 305 | 33 | 0 | 0 | 16 | 0 | 440 | 35 | 0 | 0 | 16 |
| **4339** | 3 | 2 | 1 | 0 | 320 | 24 | 0 | 320 | 24 | 0 | 210 | 29 | 0 | 0 | 16 | 0 | 236 | 38 | 0 | 0 | 11 |
| **4343** | 2 | 3 | 1 | 0 | 405 | 23 | 0 | 405 | 23 | - | - | - | 0 | 0 | 4 | 0 | 261 | 34 | 0 | 0 | 9 |
| **4356** | 1 | 3 | 2 | 0 | 280 | 24 | 0 | 280 | 24 | 0 | 70 | 22 | 0 | 0 | 3 | 0 | 370 | 24 | 0 | 0 | 8 |
| **4689** | 1 | 3 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **4723** | 1 | 3 | 2 | 0 | 291 | 32 | 0 | 291 | 32 | - | - | - | 0 | 0 | 12 | 0 | 411 | 32 | 0 | 0 | 15 |
| **4889** | 1 | 2 | 3 | - | - | - | 0 | 200 | 26 | - | - | - | 0 | 0 | 15 | 0 | 200 | 25 | 0 | 0 | 12 |
| **4980** | 1 | 3 | 2 | 0 | 370 | 47 | 0 | 240 | 47 | 0 | 0 | 38 | 0 | 0 | 20 | <1 | 306 | 45.3 | <1 | <1 | 32.4 |
| **5018** | 3 | 1 | 2 | 0 | 400 | 24 | 0 | 160 | 24 | - | - | - | 0 | 0 | 10 | 0 | 167 | 33 | 0 | 0 | 20 |
| **5094** | 1 | 3 | 2 | 0 | 10 | 49 | 0 | **10** | 21 | - | 0 | 36 | 0 | 0 | 16 | - | - | - | - | - | - |
| **5128** | 3 | 2 | 1 | - | - | - | - | - | - | 0 | 0 | 15 | 0 | 0 | 8 | 0 | 130 | 29 | 0 | 0 | 15 |
| **5201** | 3 | 2 | 1 | 0 | 150 | 32 | - | - | - | - | - | - | 0 | 0 | 17 | - | - | - | - | - | - |
| **5220** | 3 | 2 | 1 | - | - | - | 0 | 95 | 22 | - | - | - | 0 | 0 | 9 | - | - | - | - | - | - |
| **5352** | 3 | 2 | 1 | <1 | 480 | 24 | <1 | 250 | 24 | <1 | <1 | 24 | <1 | <1 | 14 | - | - | - | - | - | - |
| **5447** | 2 | 3 | 1 | - | - | - | 0 | 330 | 27 | - | - | - | 0 | 0 | 11 | - | - | - | - | - | - |
| **5553** | 1 | 3 | 2 | - | - | - | **<1,0** | 200 | 29 | - | - | - | **<1,0** | **<1,0** | 10 | - | - | - | - | - | - |
| **5701** | 2 | 1 | 3 | 0 | 220 | 36 | 0 | 220 | 36 | - | - | - | 0 | **194** | 21 | - | - | - | - | - | - |
| **5858** | 2 | 1 | 3 | - | - | - | - | - | - | - | - | - | - | - | - | <1 | 220 | 20 | <1 | <1 | 6 |
| **5933** | 3 | 1 | 2 | - | - | - | <1 | 120 | 23 | <1 | <1 | 23 | <1 | <1 | 8 | - | - | - | - | - | - |
| **5950** | 3 | 1 | 2 | <1 | 270 | 58 | <1 | 270 | 75 | <1 | 13 | 23 | <1 | <1 | 24 | <1 | 261.3 | 41.6 | <1 | <1 | 13.5 |
| **6175** | 2 | 3 | 1 | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 200 | 25 | 0 | 0 | 14 |
| **6180** | 2 | 3 | 1 | 0 | 370 | 39 | 0 | 370 | 39 | 0 | 230 | 35 | 0 | 0 | 23 | 0 | 500 | 48 | 0 | 0 | 24 |
| **6233** | 1 | 3 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 282 | 29 | 0 | 0 | 10 |
| **6253** | 1 | 3 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | 0 | 280 | 30 | 0 | 0 | 20 |
| **6456** | 1 | 2 | 3 | - | - | - | 0 | 270 | 24 | - | - | - | 0 | 0 | **0** | 0 | 320 | 36 | 0 | 0 | **0** |
| **6563** | 3 | 2 | 1 | 0 | 300 | 39 | 0 | 300 | 39 | - | - | - | 0 | 0 | 8 | 0 | 563 | 35 | 0 | 0 | 20 |
| **6686** | 2 | 3 | 1 | - | - | - | - | - | - | - | - | - | - | - | - | <1 | 531 | 42.9 | <1 | <1 | 13.7 |
| **7096** | 1 | 3 | 2 | - | - | - | 0 | 380 | 38 | - | - | - | 0 | 0 | 22 | 0 | - | 53 | 0 | 0 | 25 |
| **7191** | 2 | 3 | 1 | 980 | 100 | 240 | **98** | **10** | 24 | 0 | 0 | 10 | 0 | 0 | 10 | - | - | - | - | - | - |
| **7248** | 1 | 2 | 3 | <1 | 147 | 40 | <1 | 147 | 40 | <1 | <1 | 23 | <1 | <1 | 16 | <1 | 154 | 35 | <1 | <1 | 16 |
| **7302** | 1 | 3 | 2 | <1 | 245 | 34 | <1 | 245 | 34 | <1 | <1 | 30 | <1 | **245** | 20 | <1 | 579 | 40 | <1 | <1 | 19 |
| **7442** | 2 | 1 | 3 | 0 | 343 | 42 | 0 | 343 | 42 | - | - | - | 0 | 0 | 24 | 0 | 342 | 33 | 0 | 0 | 15 |
| **7596** | 3 | 1 | 2 | 0 | 460 | 36 | 0 | 460 | 36 | 0 | 0 | 27 | 0 | 0 | 16 | 0 | 326 | 27 | 0 | 0 | 16 |
| **7688** | 1 | 3 | 2 | - | - | - | 0 | 120 | 43 | - | - | - | 0 | 0 | 15 | 0 | 310 | 43 | 0 | 0 | 12 |
| **7728** | 2 | 1 | 3 | - | - | - | 0 | 155 | 30 | - | - | - | 0 | 0 | 9 | - | - | - | - | - | - |
| **7876** | ~~2~~ | ~~1~~ | 3 | <1 | 173 | 29 | <1 | 173 | 29 | <1 | 127 | 14 | <1 | <1 | 10 | <1 | 185 | 25 | <1 | <1 | 6 |
| **7896** | 2 | 3 | 1 | <1 | 160 | 24 | <1 | 160 | 24 | <1 | 140 | 27 | <1 | <1 | **<1** | <1 | - | 41 | <1 | - | 19 |
| **Mean** | | | | | | | **0** | **244** | **32** | | | | **0** | **0** | **14** | **0** | **321** | **34** | **0** | **0** | **15** |
| **CV (%)** | | | | | | | - | 21 | 16 | | | | - | - | 21 | - | 21 | 11 | - | - | 18 |

*calculated results at the end of the table. The mean value (Mean) is the square of the mean value for the square root transformed results (mv). The coefficient of variation (CV) is the standard deviation (s) in percentage of the mean value for the square root transformed results. As means to calculate the z-values of your own, the appropriate values of mv and s are given at the end of the table. The x-values of a laboratory are obtained as the square roots of each reported result, respectively.*
*z = (x - mv) / s. $u_{rel,mv}$ is the relative standard uncertainty of mv in per cent. For calculation see the scheme protocol (1); also briefly described in the text.*

| **Presumptive *C. perfringens* (MF)** | | | ***Clostridium perfringens* (MF)** | | | **Moulds (MF)** | | | **Yeasts (MF)** | | | **Actinomycetes (MF)** | | | **Total plate count 36±2 °C, 2 days** | | | **Lab no.** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | | | | |
| 0 | 0 | 540 | - | - | - | - | - | - | - | - | - | - | - | - | 6 | 30 | **30** | **1131** |
| <1 | 6 | 400 | <1 | <1 | 400 | - | - | - | - | - | - | - | - | - | 10 | 7 | <1 | **1237** |
| - | - | - | <1 | **369** | 269 | - | - | - | - | - | - | - | - | - | 6 | 7 | 2 | **1290** |
| 0 | 630 | 610 | 0 | **630** | 610 | 120 | 1 | 90 | 90 | 9 | 0 | 660 | 0 | 0 | 7 | 8 | 2 | **1545** |
| - | - | - | - | - | - | 89 | 0 | 83 | 76 | 8 | 0 | - | - | - | 11 | 8 | 1 | **1594** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 8 | 12 | 0 | **1611** |
| 0 | 0 | 370 | 0 | 0 | - | 67 | 1 | 76 | 56 | 6 | 0 | 355 | 0 | 0 | 4 | 14 | 1 | **1753** |
| 0 | 295 | 133 | - | - | - | 124 | 1 | 52 | 38 | 7 | 0 | **55** | 0 | **35** | 6 | 14 | 2 | **1868** |
| 0 | 160 | 270 | 0 | 0 | 270 | 68 | 0 | 70 | 75 | 6 | 0 | - | - | - | 3 | 8 | 0 | **1970** |
| 0 | 350 | 445 | - | - | - | 90 | 1 | 80 | 93 | 11 | 0 | 454 | 0 | **29** | 8 | 10 | 1 | **2050** |
| - | - | - | 0 | 0 | 230 | - | - | - | - | - | - | - | - | - | 6 | 6 | 2 | **2386** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **2534** |
| - | - | - | <1 | <1 | 600 | - | - | - | - | - | - | - | - | - | 1 | 10 | 1 | **2637** |
| 0 | 0 | 33 | 0 | 0 | 33 | - | - | - | - | - | - | - | - | - | **248** | **720** | **17** | **2670** |
| - | - | - | 0 | 0 | 160 | - | - | - | - | - | - | - | - | - | 5 | 11 | 2 | **2704** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 6 | 12 | 1 | **2745** |
| 0 | 1 | 485 | 0 | 0 | 485 | 110 | 0 | 140 | 90 | 7 | 0 | - | - | - | 5 | 7 | 1 | **2797** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 5 | 10 | 1 | **3055** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 11 | 14 | 0 | **3076** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **3145** |
| - | - | - | 0 | 0 | 74 | - | - | - | - | - | - | - | - | - | 6 | 10 | 2 | **3159** |
| 0 | 200 | 500 | - | - | - | 44 | 1 | 47 | 45 | 5 | 0 | 436 | 0 | **17** | 9 | 16 | 0 | **3162** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **3164** |
| <1 | <1 | 420 | <1 | <1 | 420 | 130 | 2 | 170 | 100 | 13 | <1 | 560 | <1 | <1 | 7 | 10 | 5 | **3305** |
| 0 | 100 | 340 | 0 | 0 | 340 | - | - | - | - | - | - | - | - | - | 8 | 18 | 0 | **3339** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **370** | 10 | **100** | **3533** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 10 | 0 | **3730** |
| 0 | 0 | 280 | 0 | 0 | 280 | 150 | 0 | 130 | 60 | 7 | 0 | 480 | 0 | 0 | 3 | 7 | 0 | **3868** |
| 0 | 373 | 532 | - | - | - | 29 | 1 | 82 | 54 | 5 | 0 | 340 | 0 | 0 | 3 | 11 | 1 | **4015** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 5 | 5 | 1 | **4180** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 2 | 10 | <1 | **4288** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 6 | 10 | 1 | **4319** |
| 0 | 180 | 220 | 0 | 0 | 220 | 67 | 1 | 81 | 35 | 8 | 0 | 550 | - | - | 10 | 17 | 1 | **4339** |
| 0 | 0 | 378 | - | - | - | 44 | 2 | 54 | 54 | 7 | 0 | 405 | 0 | 0 | 4 | 16 | 1 | **4343** |
| 0 | 250 | 240 | 0 | 0 | 240 | - | - | - | - | - | - | - | - | - | 3 | 10 | 3 | **4356** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **4689** |
| 0 | 164 | 318 | - | - | - | 64 | 0 | 40 | 20 | 5 | 0 | 536 | 0 | 0 | 6 | 12 | 0 | **4723** |
| - | - | - | 0 | 0 | 73 | - | - | - | - | - | - | - | - | - | 6 | 9 | 2 | **4889** |
| 0 | 0 | 65 | 0 | 0 | 65 | - | - | - | - | - | - | - | - | - | 6 | 7 | 2 | **4980** |
| 0 | 120 | 360 | 0 | 0 | 360 | 110 | 3 | 65 | 70 | 9 | 0 | 460 | 0 | 0 | 8 | 29 | **20** | **5018** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **0** | 11 | 1 | **5094** |
| - | - | - | 0 | 0 | 180 | - | - | - | - | - | - | - | - | - | 3 | 11 | 2 | **5128** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 5 | 9 | 2 | **5201** |
| - | - | - | - | - | - | **2** | 0 | **2** | **1** | **1** | 0 | - | - | - | - | - | - | **5220** |
| - | - | - | <1 | <1 | 510 | 65 | <1 | 63 | 50 | 7 | <1 | 580 | <1 | <1 | 7 | 7 | 2 | **5352** |
| - | - | - | - | - | - | 70 | 1 | 120 | 64 | 10 | 0 | 490 | 0 | 0 | 6 | 21 | 3 | **5447** |
| - | - | - | **<1,0** | **<1,0** | 280 | - | - | - | - | - | - | - | - | - | - | - | - | **5553** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 6 | 10 | 2 | **5701** |
| <1 | 175 | 34 | <1 | <1 | 34 | - | - | - | - | - | - | - | - | - | 6 | 9 | <1 | **5858** |
| - | - | - | <1 | <1 | 270 | - | - | - | - | - | - | - | - | - | 8 | 11 | <1 | **5933** |
| <1 | 145 | 420 | <1 | <1 | 420 | 75 | <1 | 130 | 58 | **<1** | <1 | 480 | <1 | **47** | 4 | 16 | <1 | **5950** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 4 | 10 | 2 | **6175** |
| 0 | 170 | 400 | 0 | 0 | 400 | - | - | - | - | - | - | - | - | - | 6 | 12 | 3 | **6180** |
| - | - | - | - | - | - | 190 | 1 | 110 | 35 | 5 | 0 | - | - | - | 4 | 9 | 0 | **6233** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **20** | 30 | 10 | **6253** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 5 | 18 | 1 | **6456** |
| 0 | 177 | 510 | - | - | - | 140 | 1 | 200 | 41 | 9 | 0 | 540 | 0 | 0 | 1 | 11 | 1 | **6563** |
| <10 | 280 | 180 | - | - | - | - | - | - | - | - | - | - | - | - | 7 | 18 | <1 | **6686** |
| 0 | 700 | 250 | 0 | 0 | 250 | - | - | - | - | - | - | - | - | - | 5 | 5 | 0 | **7096** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | **0** | **0** | 0 | **7191** |
| <1 | 295 | 380 | - | - | - | 40 | 2 | 110 | 43 | 6 | <1 | 270 | <1 | <1 | 3 | 14 | 2 | **7248** |
| <1 | 166 | 291 | - | - | - | 91 | 2 | 127 | 40 | 3 | <10 | 527 | <10 | <1 | 6 | 13 | 1 | **7302** |
| 0 | 0 | 35 | - | - | - | 34 | 0 | 50 | 60 | **591** | **16** | 324 | 0 | **21** | 5 | 12 | 1 | **7442** |
| 0 | 93 | 103 | 0 | 0 | 103 | - | - | - | - | - | - | - | - | - | 5 | 15 | 1 | **7596** |
| - | - | - | 0 | 0 | **0** | 80 | 0 | 120 | 41 | **20** | 0 | 420 | 0 | 0 | 4 | 14 | 1 | **7688** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 6 | 8 | 0 | **7728** |
| <1 | 300 | 282 | - | - | - | 127 | 2 | 91 | 120 | 14 | <1 | 482 | <1 | <1 | 5 | 13 | 1 | **7876** |
| <1 | <1 | 200 | <1 | <1 | 200 | 120 | <1 | 130 | 49 | **<1** | <1 | - | - | - | 7 | 9 | 1 | **7896** |
| **0** | **111** | **313** | **0** | **0** | **254** | **86** | **0** | **92** | **58** | **8** | **0** | **458** | **0** | **0** | **6** | **11** | **1** | **Mean** |
| - | 73 | 27 | - | - | 33 | 21 | 99 | 20 | 20 | 17 | - | 12 | - | - | 20 | 21 | 74 | **CV (%)** |

| Lab no. | Sample | | | Suspected coliform bacteria (MF) | | | Coliform bacteria (MF) | | | Susp. thermotolerant coliform bact. (MF) | | | *E. coli* (MF) | | | Coliform bacteria ("rapid" MPN) | | | *E. coli* ("rapid" MPN) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C |
| **7930** | 3 | 1 | 2 | 0 | 340 | 26 | 0 | 340 | 26 | - | - | - | 0 | 0 | 13 | 0 | 238 | 34 | 0 | 0 | 22 |
| **7962** | 3 | 1 | 2 | 0 | 270 | 43 | 0 | 270 | 43 | 0 | 60 | 15 | 0 | 0 | 17 | 0 | 201 | 35 | 0 | 0 | 16 |
| **7968** | 2 | 1 | 3 | 0 | 200 | 36 | 0 | 200 | 36 | 0 | 175 | 46 | 0 | 0 | 12 | 0 | 284 | 26 | 0 | 0 | 13 |
| **8068** | 2 | 1 | 3 | 0 | 270 | 32 | 0 | 270 | 32 | 0 | 240 | 29 | 0 | 0 | 6 | 0 | 291 | 31 | 0 | 0 | 11 |
| **8252** | 2 | 3 | 1 | - | - | - | - | - | - | - | - | - | - | - | - | <1 | 320 | 36 | <1 | <1 | 18 |
| **8260** | 1 | 2 | 3 | <1 | 214 | 17 | <1 | 214 | 17 | - | - | - | <1 | <1 | 5 | - | - | - | - | - | - |
| **8329** | 1 | 3 | 2 | 0 | 261 | 33 | 0 | 261 | 33 | - | - | - | 0 | 0 | 16 | 0 | 517 | 43 | 0 | 0 | 19 |
| **8380** | 2 | 1 | 3 | 0 | 240 | 36 | 0 | 240 | 36 | - | - | - | 0 | 0 | 13 | 0 | 284 | 33 | 0 | 0 | 22 |
| **8435** | 2 | 3 | 1 | - | - | - | 0 | 180 | 50 | - | - | - | 0 | 0 | 12 | - | - | - | - | - | - |
| **8569** | 2 | 1 | 3 | 0 | 200 | 20 | 0 | 200 | 20 | 0 | 0 | 14 | 0 | 0 | 14 | - | - | - | - | - | - |
| **8598** | 3 | 2 | 1 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **8626** | 2 | 3 | 1 | 0 | 100 | 29 | 0 | 60 | 29 | 0 | 0 | 29 | 0 | 0 | 29 | - | - | - | - | - | - |
| **8628** | 1 | 3 | 2 | - | - | - | <1 | 190 | 31 | <1 | 0 | 13 | <1 | 0 | 12 | - | - | - | - | - | - |
| **8663** | 2 | 3 | 1 | 0 | 380 | 37 | 0 | 380 | 37 | 0 | 320 | 34 | 0 | 0 | 18 | 0 | 870 | 34 | 0 | 0 | 11 |
| **8742** | 2 | 1 | 3 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **8751** | 1 | 2 | 3 | - | - | - | - | - | - | - | - | - | - | - | - | <1 | 238 | 29 | <1 | <1 | 15 |
| **8766** | 2 | 3 | 1 | <1 | 140 | 25 | <1 | 140 | 25 | <1 | 120 | 24 | <1 | <1 | 12 | <1 | 160 | 23 | <1 | <1 | 11 |
| **8862** | 1 | 2 | 3 | 0 | 469 | 36 | 0 | 469 | 36 | - | - | - | 0 | 0 | 17 | 0 | 427 | 31 | 0 | 0 | 17 |
| **8898** | 1 | 3 | 2 | 0 | 270 | 39 | 0 | 270 | 39 | - | - | - | 0 | 0 | 22 | 0 | 316 | 31 | 0 | 0 | 16 |
| **8955** | 3 | 2 | 1 | - | - | - | 0 | 330 | 31 | - | - | - | 0 | 0 | 6 | 0 | 500 | 41 | 0 | 0 | 20 |
| **8971** | 1 | 3 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| **8998** | 1 | 3 | 2 | - | - | - | - | - | - | - | - | - | - | - | - | <1 | 289.9 | 24.9 | <1 | <1 | 9.1 |
| **9051** | 2 | 1 | 3 | - | - | - | 0 | 160 | 24 | - | - | - | 0 | 0 | 9 | - | - | - | - | - | - |
| **9436** | 2 | 3 | 1 | 0 | 227 | 53 | 0 | 227 | 53 | 0 | 218 | 26 | 0 | 0 | 26 | 0 | 225 | 36 | 0 | 0 | 20 |
| **9736** | 3 | 2 | 1 | 0 | 222 | 42 | 0 | 222 | 42 | - | - | - | 0 | 0 | 19 | 0 | 428 | 27 | 0 | 0 | 15 |
| **9899** | 3 | 2 | 1 | 0 | 273 | 71 | 0 | 273 | 71 | - | - | - | 0 | 0 | 19 | 0 | 584 | 43 | 0 | 0 | 18 |
| **9903** | 2 | 1 | 3 | 0 | 492 | 38 | 0 | 492 | 38 | 0 | 0 | 35 | 0 | 0 | 16 | - | - | - | - | - | - |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **n** | 53 | 54 | 54 | 73 | 73 | 73 | 34 | 36 | 36 | 75 | 75 | 75 | 60 | 58 | 60 | 60 | 59 | 60 |
| **Min** | 0 | 10 | 17 | 0 | 10 | 8 | 0 | 0 | 10 | 0 | 0 | 0 | 0 | 130 | 16 | 0 | 0 | 0 |
| **Max** | 980 | 590 | 240 | 98 | 590 | 75 | 0 | 330 | 46 | 0 | 245 | 29 | 0 | 870 | 53 | 0 | 0 | 32.4 |
| **Median** | 0 | 267 | 36 | 0 | 245 | 32 | 0 | 36.5 | 26 | 0 | 0 | 15 | 0 | 308 | 34 | 0 | 0 | 15 |
| **Mean** | | | | **0** | **244** | **32** | | | | **0** | **0** | **14** | **0** | **321** | **34** | **0** | **0** | **15** |
| **CV (%)** | | | | - | 21 | 16 | | | | - | - | 21 | - | 21 | 11 | - | - | 18 |
| **False positive** | | | | 1 | 0 | 0 | | | | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **False negative** | | | | 0 | 0 | 0 | | | | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 | 1 |
| **Outliers, low** | | | | 0 | 2 | 0 | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Outliers, high** | | | | 0 | 0 | 0 | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Low limit OK** | 0 | 10 | 17 | 0 | 32 | 8 | 0 | 0 | 10 | 0 | 0 | 3 | 0 | 130 | 16 | 0 | 0 | 6 |
| **High limit OK** | 980 | 590 | 240 | 0 | 590 | 75 | 0 | 330 | 46 | 0 | 0 | 29 | 0 | 870 | 53 | 0 | 0 | 33 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **mv** *( √Mean)* | | | | 0.000 | 15.623 | 5.652 | | | | 0.000 | 0.000 | 3.738 | 0.000 | 17.919 | 5.813 | 0.000 | 0.000 | 3.884 |
| **s** *(CV*mv/100)* | | | | 0.000 | 3.326 | 0.926 | | | | 0.000 | 0.000 | 0.771 | 0.000 | 3.796 | 0.655 | 0.000 | 0.000 | 0.685 |
| ***u*** $_{rel,mv}$ **(%)** *(100*s/ √n* $_{mv}$*)* | | | | | 2.5 | 1.9 | | | | | | 2.4 | | 2.8 | 1.5 | | | 2.3 |
| **x** *( √Result)* | | | | | | | | | | | | | | | | | | |
| **z** *([x-mv]/s)* | | | | | | | | | | | | | | | | | | |

| Presumptive *C. perfringens* (MF) | | | *Clostridium perfringens* (MF) | | | Moulds (MF) | | | Yeasts (MF) | | | Actinomycetes (MF) | | | Total plate count 36±2 °C, 2 days | | | Lab no. |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| A | B | C | A | B | C | A | B | C | A | B | C | A | B | C | | | | |
| 0 | 350 | 410 | 0 | 0 | 410 | 110 | 0 | **0** | 50 | 12 | 0 | - | - | - | 6 | 4 | 4 | **7930** |
| - | - | - | - | - | - | 71 | 0 | 85 | 55 | 8 | 0 | - | - | - | 7 | 14 | 2 | **7962** |
| 0 | 220 | 610 | 0 | 0 | 610 | 79 | 0 | 106 | 63 | 6 | 0 | - | - | - | 6 | 9 | 0 | **7968** |
| 0 | 0 | 350 | 0 | 0 | 350 | 83 | 3 | 87 | 47 | 4 | 0 | - | - | - | 7 | 13 | 2 | **8068** |
| - | - | - | <1 | <1 | 52 | - | - | - | - | - | - | - | - | - | 1 | 12 | 7 | **8252** |
| <1 | 120 | 378 | <1 | <1 | 378 | - | - | - | - | - | - | - | - | - | 9 | 7 | 2 | **8260** |
| 0 | 2 | 395 | - | - | - | 67 | 0 | 43 | 34 | 4 | 0 | 343 | 0 | 0 | 6 | 16 | 1 | **8329** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 7 | 17 | 0 | **8380** |
| - | - | - | 0 | 0 | 190 | - | - | - | - | - | - | - | - | - | 5 | **300** | 3 | **8435** |
| 0 | 0 | 380 | - | - | - | - | - | - | - | - | - | - | - | - | 6 | 3 | 9 | **8569** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 7 | 13 | 2 | **8598** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 6 | 12 | 3 | **8626** |
| - | - | - | <1 | 0 | 43 | 130 | 3 | 57 | 140 | 8 | <1 | - | - | - | 7 | 14 | <1 | **8628** |
| **1** | 110 | 330 | **1** | 0 | 330 | - | - | - | - | - | - | - | - | - | 8 | 17 | 2 | **8663** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 4 | 11 | 1 | **8742** |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 7 | 10 | 3 | **8751** |
| <1 | 252 | 396 | - | - | - | 90 | 1 | 100 | 60 | 11 | <1 | 360 | <1 | <1 | 2 | 8 | 1 | **8766** |
| 0 | 118 | 473 | - | - | - | 145 | 0 | 109 | 34 | 8 | 0 | 400 | 0 | 0 | 4 | 8 | 2 | **8862** |
| 0 | 105 | 473 | - | - | - | 113 | 1 | 164 | 46 | 11 | 0 | 694 | 0 | **60** | 6 | 12 | 2 | **8898** |
| - | - | - | 0 | 0 | 310 | 80 | 0 | 49 | 64 | **44** | 0 | - | - | - | 10 | **0** | 0 | **8955** |
| - | - | - | - | - | - | 53 | <1 | 56 | 83 | 9 | <1 | - | - | - | 6 | 6 | 2 | **8971** |
| <1 | 61 | 151 | - | - | - | - | - | - | - | - | - | - | - | - | 8 | 14 | 1 | **8998** |
| - | - | - | 0 | 0 | 255 | - | - | - | - | - | - | - | - | - | 7 | 4 | 4 | **9051** |
| 0 | 254 | 409 | - | - | - | 40 | 4 | 130 | 40 | 8 | 0 | 254 | 0 | 0 | **22** | 3 | 9 | **9436** |
| 0 | 354 | 236 | - | - | - | 142 | 4 | 117 | 59 | 6 | 0 | 617 | 0 | 0 | 7 | 14 | 0 | **9736** |
| 0 | 500 | 477 | - | - | - | 55 | 0 | 92 | 36 | 9 | 0 | 527 | 0 | 0 | 4 | 8 | 3 | **9899** |
| 0 | 116 | 267 | - | - | - | 97 | 2 | 108 | 90 | 7 | 0 | - | - | - | 7 | 11 | 3 | **9903** |
| 47 | 47 | 47 | 40 | 40 | 39 | 42 | 42 | 42 | 42 | 42 | 42 | 28 | 27 | 27 | 88 | 89 | 89 | **n** |
| 0 | 0 | 33 | 0 | 0 | 0 | 2 | 0 | 0 | 1 | 0 | 0 | 55 | 0 | 0 | 0 | 0 | 0 | **Min** |
| 1 | 700 | 610 | 1 | 630 | 610 | 190 | 4 | 200 | 140 | 591 | 16 | 694 | 0 | 60 | 370 | 720 | 100 | **Max** |
| 0 | 145 | 370 | 0 | 0 | 270 | 83 | 1 | 90.5 | 55 | 7.5 | 0 | 480 | 0 | 0 | 6 | 11 | 1 | **Median** |
| **0** | **111** | **313** | **0** | **0** | **254** | **86** | **0** | **92** | **58** | **8** | **0** | **458** | **0** | **0** | **6** | **11** | **1** | **Mean** |
| - | 73 | 27 | - | - | 33 | 21 | 99 | 20 | 20 | 17 | - | 12 | - | - | 20 | 21 | 74 | **CV (%)** |
| 1 | 0 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 6 | 0 | 0 | 0 | **False pos.** |
| 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 2 | 0 | 0 | 0 | 0 | 2 | 2 | 0 | **False neg.** |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | **Outliers <** |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 4 | 2 | 4 | **Outliers >** |
| 0 | 0 | 33 | 0 | 0 | 33 | 29 | 0 | 40 | 20 | 3 | 0 | 254 | 0 | 0 | 1 | 3 | 0 | **Low limit** |
| 0 | 700 | 610 | 0 | 0 | 610 | 190 | 4 | 200 | 140 | 14 | 0 | 694 | 0 | 0 | 11 | 30 | 10 | **High limit** |
| 0.000 | 10.520 | 17.691 | 0.000 | 0.000 | 15.941 | 9.289 | 0.707 | 9.582 | 7.596 | 2.741 | 0.000 | 21.396 | 0.000 | 0.000 | 2.367 | 3.324 | 1.035 | **mv** |
| 0.000 | 7.648 | 4.775 | 0.000 | 0.000 | 5.321 | 1.969 | 0.699 | 1.903 | 1.518 | 0.461 | 0.000 | 2.661 | 0.000 | 0.000 | 0.478 | 0.708 | 0.770 | **s** |
| | 10.6 | 3.9 | | | 5.4 | 3.3 | 15.3 | 3.1 | 3.1 | 2.8 | | 2.4 | | | 2.2 | 2.3 | 8.1 | **$u_{rel,mv}$ *(%)*** |
| | | | | | | | | | | | | | | | | | | **x** |
| | | | | | | | | | | | | | | | | | | **z** |

**Annex B** *Z-scores calculated from the laboratory results. Susp. = Suspected on the membrane filters before confirmation. z = (x - mv) / s. Z-scores are calculated also for outliers (excluding false negative results) in the same way as ordinary z-scores. From false*

| Lab no. | Sample | | | Suspected coliform bacteria (MF) | | | Coliform bacteria (MF) | | | Susp. thermotolerant coliform bact. (MF) | | | *E. coli* (MF) | | | Coliform bacteria ("rapid" MPN) | | | *E. coli* ("rapid" MPN) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C | A | B | C |
| **1131** | 2 | 3 | 1 | | | | 0.000 | 0.151 | -0.705 | | | | 0.000 | 0.000 | 0.176 | 0.000 | 0.036 | 0.285 | 0.000 | 0.000 | -1.053 |
| **1237** | 3 | 1 | 2 | | | | 0.000 | -0.777 | **-3.050** | | | | 0.000 | 0.000* | | 0.000 | -0.344 | **-2.768** | 0.000 | 0.000 | -1.290 |
| **1290** | 2 | 1 | 3 | | | | 0.000 | -0.499 | 0.193 | | | | 0.000 | 0.000 | 0.005 | | | | | | |
| **1545** | 2 | 1 | 3 | | | | 0.000 | 0.764 | 0.376 | | | | 0.000 | 0.000 | -0.171 | 0.000 | -0.060 | 0.027 | 0.000 | 0.000 | 0.170 |
| **1594** | 1 | 3 | 2 | | | | 0.000 | -0.289 | 0.977 | | | | 0.000 | 0.000 | 0.806 | 0.000 | -0.682 | 0.285 | 0.000 | 0.000 | -1.541 |
| **1611** | 3 | 2 | 1 | | | | 0.000 | -0.754 | 0.465 | | | | 0.000 | 0.000 | 0.340 | 0.000 | -1.266 | -0.239 | 0.000 | 0.000 | -0.207 |
| **1753** | 2 | 1 | 3 | | | | 0.000 | **2.606** | 0.553 | | | | 0.000 | 0.000 | 1.096 | 0.000 | 1.099 | -0.375 | 0.000 | 0.000 | 0.170 |
| **1868** | 3 | 1 | 2 | | | | 0.000 | 1.730 | -0.390 | | | | 0.000 | 0.000 | -0.355 | 0.000 | 1.602 | 1.591 | 0.000 | 0.000 | 1.916 |
| **1970** | 3 | 1 | 2 | | | | 0.000 | 1.316 | -0.091 | | | | 0.000 | 0.000 | 1.638 | | | | | | |
| **2050** | 1 | 2 | 3 | | | | 0.000 | 0.510 | 0.465 | | | | 0.000 | 0.000 | -0.171 | 0.000 | 0.180 | -0.513 | 0.000 | 0.000 | 0.524 |
| **2386** | 1 | 2 | 3 | | | | 0.000 | 0.681 | 0.895 | | | | 0.000 | 0.000 | -0.355 | | | | | | |
| **2534** | 2 | 1 | 3 | | | | | | | | | | | | | | | | | | |
| **2637** | 2 | 3 | 1 | | | | | | | | | | | | | 0.000 | 0.306 | -1.242 | 0.000 | 0.000 | **-2.094** |
| **2670** | 1 | 2 | 3 | | | | 0.000 | **-2.996** | -0.598 | | | | 0.000 | 0.000 | 0.655 | | | | | | |
| **2704** | 3 | 1 | 2 | | | | 0.000 | -0.894 | -0.705 | | | | 0.000 | 0.000 | -0.546 | 0.000 | -1.337 | 0.027 | 0.000 | 0.000 | -1.053 |
| **2745** | 3 | 2 | 1 | | | | 0.000 | -0.664 | -0.493 | | | | 0.000 | 0.000 | 0.005 | | | | | | |
| **2797** | 3 | 1 | 2 | | | | 0.000 | -0.138 | -1.039 | | | | 0.000 | 0.000 | -0.546 | 0.000 | -1.378 | 1.019 | 0.000 | 0.000 | -0.016 |
| **3055** | 2 | 1 | 3 | | | | | | | | | | | | | | | | | | |
| **3076** | 3 | 2 | 1 | | | | | | | | | | | | | | | | | | |
| **3145** | 1 | 3 | 2 | | | | | | | | | | | | | 0.000 | 0.036 | -1.091 | 0.000 | 0.000 | -0.016 |
| **3159** | 2 | 3 | 1 | | | | 0.000 | 0.681 | 0.285 | | | | 0.000 | 0.000 | 0.500 | 0.000 | 1.860 | 0.336 | 0.000 | 0.000 | -0.529 |
| **3162** | 2 | 3 | 1 | | | | 0.000 | -0.664 | 0.100 | | | | 0.000 | 0.000 | 0.340 | 0.000 | 0.036 | 0.157 | 0.000 | 0.000 | 0.524 |
| **3164** | 3 | 2 | 1 | | | | | | | | | | | | | | | | | | |
| **3305** | 1 | 2 | 3 | | | | 0.000 | 0.847 | 1.300 | | | | 0.000 | 0.000 | 0.806 | 0.000 | 1.111 | 1.366 | 0.000 | 0.000 | 1.020 |
| **3339** | 2 | 3 | 1 | | | | 0.000 | -0.138 | -1.155 | | | | 0.000 | 0.000 | -1.180 | | | | | | |
| **3533** | 3 | 2 | 1 | | | | 0.000 | 0.423 | -1.522 | | | | 0.000 | 0.000 | 0.655 | | | | | | |
| **3730** | 1 | 2 | 3 | | | | | | | | | | | | | | | | | | |
| **3868** | 2 | 1 | 3 | | | | 0.000 | -0.664 | 0.553 | | | | 0.000 | 0.000 | 0.655 | 0.000 | -0.813 | 1.136 | 0.000 | 0.000 | 1.020 |
| **4015** | 1 | 2 | 3 | | | | 0.000 | 0.188 | 0.895 | | | | 0.000 | 0.000 | 0.176 | 0.000 | -0.235 | 1.591 | 0.000 | 0.000 | 0.859 |
| **4180** | 3 | 2 | 1 | | | | 0.000 | -1.501 | -1.275 | | | | 0.000 | 0.000 | **-2.602** | | | | | | |
| **4288** | 3 | 1 | 2 | | | | | | | | | | | | | | | | | | |
| **4319** | 2 | 1 | 3 | | | | 0.000 | 0.378 | 0.100 | | | | 0.000 | 0.000 | 0.340 | 0.000 | 0.805 | 0.157 | 0.000 | 0.000 | 0.170 |
| **4339** | 3 | 2 | 1 | | | | 0.000 | 0.681 | -0.814 | | | | 0.000 | 0.000 | 0.340 | 0.000 | -0.674 | 0.536 | 0.000 | 0.000 | -0.828 |
| **4343** | 2 | 3 | 1 | | | | 0.000 | 1.353 | -0.925 | | | | 0.000 | 0.000 | **-2.254** | 0.000 | -0.465 | 0.027 | 0.000 | 0.000 | -1.290 |
| **4356** | 1 | 3 | 2 | | | | 0.000 | 0.334 | -0.814 | | | | 0.000 | 0.000 | **-2.602** | 0.000 | 0.347 | -1.396 | 0.000 | 0.000 | -1.541 |
| **4689** | 1 | 3 | 2 | | | | | | | | | | | | | | | | | | |
| **4723** | 1 | 3 | 2 | | | | 0.000 | 0.432 | 0.005 | | | | 0.000 | 0.000 | -0.355 | 0.000 | 0.620 | -0.239 | 0.000 | 0.000 | -0.016 |
| **4889** | 1 | 2 | 3 | | | | 0.000 | -0.445 | -0.598 | | | | 0.000 | 0.000 | 0.176 | 0.000 | -0.995 | -1.242 | 0.000 | 0.000 | -0.613 |
| **4980** | 1 | 3 | 2 | | | | 0.000 | -0.040 | 1.300 | | | | 0.000 | 0.000 | 0.953 | 0.000 | -0.112 | 1.400 | 0.000 | 0.000 | **2.640** |
| **5018** | 3 | 1 | 2 | | | | 0.000 | -0.894 | -0.814 | | | | 0.000 | 0.000 | -0.747 | 0.000 | -1.316 | -0.105 | 0.000 | 0.000 | 0.859 |
| **5094** | 1 | 3 | 2 | | | | 0.000 | **-3.746** | -1.155 | | | | 0.000 | 0.000 | 0.340 | | | | | | |
| **5128** | 3 | 2 | 1 | | | | | | | | | | 0.000 | 0.000 | -1.180 | 0.000 | -1.717 | -0.654 | 0.000 | 0.000 | -0.016 |
| **5201** | 3 | 2 | 1 | | | | | | | | | | 0.000 | 0.000 | 0.500 | | | | | | |
| **5220** | 3 | 2 | 1 | | | | 0.000 | -1.767 | -1.039 | | | | 0.000 | 0.000 | -0.957 | | | | | | |
| **5352** | 3 | 2 | 1 | | | | 0.000 | 0.057 | -0.814 | | | | 0.000 | 0.000 | 0.005 | | | | | | |
| **5447** | 2 | 3 | 1 | | | | 0.000 | 0.764 | -0.493 | | | | 0.000 | 0.000 | -0.546 | | | | | | |
| **5553** | 1 | 3 | 2 | | | | 0.000 | -0.445 | -0.289 | | | | 0.000 | 0.000 | -0.747 | | | | | | |
| **5701** | 2 | 1 | 3 | | | | 0.000 | -0.238 | 0.376 | | | | 0.000 | | 1.096 | | | | | | |
| **5858** | 2 | 1 | 3 | | | | | | | | | | | | | 0.000 | -0.813 | **-2.048** | 0.000 | 0.000 | **-2.094** |
| **5933** | 3 | 1 | 2 | | | | 0.000 | -1.404 | -0.925 | | | | 0.000 | 0.000 | -1.180 | | | | | | |
| **5950** | 3 | 1 | 2 | | | | 0.000 | 0.243 | **3.248** | | | | 0.000 | 0.000 | 1.507 | 0.000 | -0.462 | 0.971 | 0.000 | 0.000 | -0.306 |
| **6175** | 2 | 3 | 1 | | | | | | | | | | | | | 0.000 | -0.995 | -1.242 | 0.000 | 0.000 | -0.207 |
| **6180** | 2 | 3 | 1 | | | | 0.000 | 1.086 | 0.640 | | | | 0.000 | 0.000 | 1.373 | 0.000 | 1.170 | 1.702 | 0.000 | 0.000 | 1.482 |
| **6233** | 1 | 3 | 2 | | | | | | | | | | | | | 0.000 | -0.297 | -0.654 | 0.000 | 0.000 | -1.053 |
| **6253** | 1 | 3 | 2 | | | | | | | | | | | | | 0.000 | -0.313 | -0.513 | 0.000 | 0.000 | 0.859 |
| **6456** | 1 | 2 | 3 | | | | 0.000 | 0.243 | -0.814 | | | | 0.000 | 0.000 | | 0.000 | -0.008 | 0.285 | 0.000 | 0.000 | |
| **6563** | 3 | 2 | 1 | | | | 0.000 | 0.510 | 0.640 | | | | 0.000 | 0.000 | -1.180 | 0.000 | 1.530 | 0.157 | 0.000 | 0.000 | 0.859 |
| **6686** | 2 | 3 | 1 | | | | | | | | | | | | | 0.000 | 1.350 | 1.124 | 0.000 | 0.000 | -0.266 |
| **7096** | 1 | 3 | 2 | | | | 0.000 | 1.164 | 0.553 | | | | 0.000 | 0.000 | 1.236 | 0.000 | | **2.239** | 0.000 | 0.000 | 1.630 |
| **7191** | 2 | 3 | 1 | | | | | **-3.746** | -0.814 | | | | 0.000 | 0.000 | -0.747 | | | | | | |
| **7248** | 1 | 2 | 3 | | | | 0.000 | -1.052 | 0.726 | | | | 0.000 | 0.000 | 0.340 | 0.000 | -1.452 | 0.157 | 0.000 | 0.000 | 0.170 |
| **7302** | 1 | 3 | 2 | | | | 0.000 | 0.009 | 0.193 | | | | 0.000 | | 0.953 | 0.000 | 1.618 | 0.780 | 0.000 | 0.000 | 0.694 |
| **7442** | 2 | 1 | 3 | | | | 0.000 | 0.871 | 0.895 | | | | 0.000 | 0.000 | 1.507 | 0.000 | 0.151 | -0.105 | 0.000 | 0.000 | -0.016 |
| **7596** | 3 | 1 | 2 | | | | 0.000 | 1.751 | 0.376 | | | | 0.000 | 0.000 | 0.340 | 0.000 | 0.036 | -0.942 | 0.000 | 0.000 | 0.170 |
| **7688** | 1 | 3 | 2 | | | | 0.000 | -1.404 | 0.977 | | | | 0.000 | 0.000 | 0.176 | 0.000 | -0.082 | 1.136 | 0.000 | 0.000 | -0.613 |
| **7728** | 2 | 1 | 3 | | | | 0.000 | -0.954 | -0.189 | | | | 0.000 | 0.000 | -0.957 | | | | | | |
| **7876** | 2 | 1 | 3 | | | | 0.000 | -0.743 | -0.289 | | | | 0.000 | 0.000 | -0.747 | 0.000 | -1.138 | -1.242 | 0.000 | 0.000 | **-2.094** |
| **7896** | 2 | 3 | 1 | | | | 0.000 | -0.894 | -0.814 | | | | 0.000 | 0.000 | | 0.000 | | 0.900 | 0.000 | | 0.694 |
| **7930** | 3 | 1 | 2 | | | | 0.000 | 0.847 | -0.598 | | | | 0.000 | 0.000 | -0.171 | 0.000 | -0.657 | 0.027 | 0.000 | 0.000 | 1.178 |
| **7962** | 3 | 1 | 2 | | | | 0.000 | 0.243 | 0.977 | | | | 0.000 | 0.000 | 0.500 | 0.000 | -0.986 | 0.157 | 0.000 | 0.000 | 0.170 |
| **7968** | 2 | 1 | 3 | | | | 0.000 | -0.445 | 0.376 | | | | 0.000 | 0.000 | -0.355 | 0.000 | -0.281 | -1.091 | 0.000 | 0.000 | -0.406 |
| **8068** | 2 | 1 | 3 | | | | 0.000 | 0.243 | 0.005 | | | | 0.000 | 0.000 | -1.671 | 0.000 | -0.227 | -0.375 | 0.000 | 0.000 | -0.828 |
| **8252** | 2 | 3 | 1 | | | | | | | | | | | | | 0.000 | -0.008 | 0.285 | 0.000 | 0.000 | 0.524 |
| **8260** | 1 | 2 | 3 | | | | 0.000 | -0.299 | -1.651 | | | | 0.000 | 0.000 | -1.948 | | | | | | |
| **8329** | 1 | 3 | 2 | | | | 0.000 | 0.160 | 0.100 | | | | 0.000 | 0.000 | 0.340 | 0.000 | 1.269 | 1.136 | 0.000 | 0.000 | 0.694 |
| **8380** | 2 | 1 | 3 | | | | 0.000 | -0.040 | 0.376 | | | | 0.000 | 0.000 | -0.171 | 0.000 | -0.281 | -0.105 | 0.000 | 0.000 | 1.178 |
| **8435** | 2 | 3 | 1 | | | | 0.000 | -0.664 | 1.532 | | | | 0.000 | 0.000 | -0.355 | | | | | | |
| **8569** | 2 | 1 | 3 | | | | 0.000 | -0.445 | -1.275 | | | | 0.000 | 0.000 | 0.005 | | | | | | |
| **8598** | 3 | 2 | 1 | | | | | | | | | | | | | | | | | | |
| **8626** | 2 | 3 | 1 | | | | 0.000 | **-2.368** | -0.289 | | | | 0.000 | 0.000 | **2.138** | | | | | | |
| **8628** | 1 | 3 | 2 | | | | 0.000 | -0.553 | -0.091 | | | | 0.000 | 0.000 | -0.355 | | | | | | |
| **8663** | 2 | 3 | 1 | | | | 0.000 | 1.164 | 0.465 | | | | 0.000 | 0.000 | 0.655 | 0.000 | **3.050** | 0.027 | 0.000 | 0.000 | -0.828 |
| **8742** | 2 | 1 | 3 | | | | | | | | | | | | | | | | | | |
| **8751** | 1 | 2 | 3 | | | | | | | | | | | | | 0.000 | -0.657 | -0.654 | 0.000 | 0.000 | -0.016 |
| **8766** | 2 | 3 | 1 | | | | 0.000 | -1.140 | -0.705 | | | | 0.000 | 0.000 | -0.355 | 0.000 | -1.389 | -1.553 | 0.000 | 0.000 | -0.828 |

*positive results no z-scores can be calculated. Z-scores form outliers are not real z-scores but a practical means to express also the results from the outliers. Very low and high values are here limited to –4 and +4, respectively.*

| **Presumptive *C. perfringens* (MF)** | | | ***Clostridium perfringens* (MF)** | | | **Moulds (MF)** | | | **Yeasts (MF)** | | | **Actinomycetes (MF)** | | | **Total plate count 22 °C, 3 days** | | | **Lab no.** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | |
| 0.000 | -1.376 | 1.162 | | | | | | | | | | | | | 0.172 | **3.042** | **4.000** | **1131** |
| 0.000 | -1.055 | 0.484 | 0.000 | 0.000 | 0.763 | | | | | | | | | | 1.665 | -0.957 | -1.344 | **1237** |
| | | | 0.000 | | 0.087 | | | | | | | | | | 0.172 | -0.957 | 0.492 | **1290** |
| 0.000 | 1.906 | 1.468 | 0.000 | | 1.646 | 0.846 | 0.420 | -0.050 | 1.245 | 0.561 | 0.000 | 1.614 | 0.000 | 0.000 | 0.583 | -0.699 | 0.492 | **1545** |
| | | | | | | 0.074 | -1.011 | -0.248 | 0.739 | 0.189 | 0.000 | | | | 1.988 | -0.699 | -0.046 | **1594** |
| | | | | | | | | | | | | | | | 0.966 | 0.199 | -1.344 | **1611** |
| 0.000 | -1.376 | 0.323 | 0.000 | 0.000 | | -0.561 | 0.420 | -0.454 | -0.074 | -0.633 | 0.000 | -0.960 | 0.000 | 0.000 | -0.769 | 0.591 | -0.046 | **1753** |
| 0.000 | 0.870 | -1.290 | | | | 0.938 | 0.420 | -1.246 | -0.943 | -0.208 | 0.000 | **-4.000** | 0.000 | | 0.172 | 0.591 | 0.492 | **1868** |
| 0.000 | 0.278 | -0.264 | 0.000 | 0.000 | 0.092 | -0.530 | -1.011 | -0.639 | 0.701 | -0.633 | 0.000 | | | | -1.330 | -0.699 | -1.344 | **1970** |
| 0.000 | 1.071 | 0.713 | | | | 0.100 | 0.420 | -0.335 | 1.349 | 1.248 | 0.000 | -0.033 | 0.000 | | 0.966 | -0.228 | -0.046 | **2050** |
| | | | 0.000 | 0.000 | -0.146 | | | | | | | | | | 0.172 | -1.235 | 0.492 | **2386** |
| | | | | | | | | | | | | | | | | | | **2534** |
| | | | 0.000 | 0.000 | 1.608 | | | | | | | | | | **-2.863** | -0.228 | -0.046 | **2637** |
| 0.000 | -1.376 | **-2.502** | 0.000 | 0.000 | -1.916 | | | | | | | | | | **4.000** | **4.000** | **4.000** | **2670** |
| | | | 0.000 | 0.000 | -0.619 | | | | | | | | | | -0.275 | -0.010 | 0.492 | **2704** |
| | | | | | | | | | | | | | | | 0.172 | 0.199 | -0.046 | **2745** |
| 0.000 | -1.245 | 0.907 | 0.000 | 0.000 | 1.143 | 0.609 | -1.011 | 1.182 | 1.245 | -0.208 | 0.000 | | | | -0.275 | -0.957 | -0.046 | **2797** |
| | | | | | | | | | | | | | | | -0.275 | -0.228 | -0.046 | **3055** |
| | | | | | | | | | | | | | | | 1.988 | 0.591 | -1.344 | **3076** |
| | | | | | | | | | | | | | | | | | | **3145** |
| | | | 0.000 | 0.000 | -1.379 | | | | | | | | | | 0.172 | -0.228 | 0.492 | **3159** |
| 0.000 | 0.474 | 0.978 | | | | -1.349 | 0.420 | -1.432 | -0.585 | -1.096 | 0.000 | -0.194 | 0.000 | | 1.325 | 0.956 | -1.344 | **3162** |
| | | | | | | | | | | | | | | | | | | **3164** |
| 0.000 | -1.376 | 0.587 | 0.000 | 0.000 | 0.856 | 1.073 | 1.012 | 1.816 | 1.584 | 1.874 | 0.000 | 0.853 | 0.000 | 0.000 | 0.583 | -0.228 | 1.558 | **3305** |
| 0.000 | -0.068 | 0.157 | 0.000 | 0.000 | 0.470 | | | | | | | | | | 0.966 | 1.298 | -1.344 | **3339** |
| | | | | | | | | | | | | | | | **4.000** | -0.228 | **4.000** | **3533** |
| | | | | | | | | | | | | | | | | -0.228 | -1.344 | **3730** |
| 0.000 | -1.376 | -0.201 | 0.000 | 0.000 | 0.149 | 1.503 | -1.011 | 0.956 | 0.099 | -0.208 | 0.000 | 0.193 | 0.000 | 0.000 | -1.330 | -0.957 | -1.344 | **3868** |
| 0.000 | 1.150 | 1.126 | | | | -1.983 | 0.420 | -0.277 | -0.163 | -1.096 | 0.000 | -1.111 | 0.000 | 0.000 | -1.330 | -0.010 | -0.046 | **4015** |
| | | | | | | | | | | | | | | | -0.275 | -1.536 | -0.046 | **4180** |
| | | | | | | | | | | | | | | | -1.995 | -0.228 | -1.344 | **4288** |
| | | | | | | | | | | | | | | | 0.172 | -0.228 | -0.046 | **4319** |
| 0.000 | 0.379 | -0.599 | 0.000 | 0.000 | -0.208 | -0.561 | 0.420 | -0.306 | -1.107 | 0.189 | 0.000 | 0.773 | | | 1.665 | 1.129 | -0.046 | **4339** |
| 0.000 | -1.376 | 0.367 | | | | -1.349 | 1.012 | -1.174 | -0.163 | -0.208 | 0.000 | -0.478 | 0.000 | 0.000 | -0.769 | 0.956 | -0.046 | **4343** |
| 0.000 | 0.692 | -0.461 | 0.000 | 0.000 | -0.084 | | | | | | | | | | -1.330 | -0.228 | 0.904 | **4356** |
| | | | | | | | | | | | | | | | | | | **4689** |
| 0.000 | 0.299 | 0.030 | | | | -0.655 | -1.011 | -1.711 | **-2.058** | -1.096 | 0.000 | 0.660 | 0.000 | 0.000 | 0.172 | 0.199 | -1.344 | **4723** |
| | | | 0.000 | 0.000 | -1.390 | | | | | | | | | | 0.172 | -0.457 | 0.492 | **4889** |
| 0.000 | -1.376 | **-2.017** | 0.000 | 0.000 | -1.481 | | | | | | | | | | 0.172 | -0.957 | 0.492 | **4980** |
| 0.000 | 0.057 | 0.269 | 0.000 | 0.000 | 0.570 | 0.609 | 1.467 | -0.799 | 0.508 | 0.561 | 0.000 | 0.020 | 0.000 | 0.000 | 0.966 | **2.912** | **4.000** | **5018** |
| | | | | | | | | | | | | | | | | -0.010 | -0.046 | **5094** |
| | | | 0.000 | 0.000 | -0.475 | | | | | | | | | | -1.330 | -0.010 | 0.492 | **5128** |
| | | | | | | | | | | | | | | | -0.275 | -0.457 | 0.492 | **5201** |
| | | | | | | **-4.000** | -1.011 | **-4.000** | **-4.000** | **-3.777** | 0.000 | | | | | | | **5220** |
| | | | 0.000 | 0.000 | 1.248 | -0.623 | -1.011 | -0.864 | -0.346 | -0.208 | 0.000 | 1.010 | 0.000 | 0.000 | 0.583 | -0.957 | 0.492 | **5352** |
| | | | | | | -0.469 | 0.420 | 0.721 | 0.266 | 0.913 | 0.000 | 0.278 | 0.000 | 0.000 | 0.172 | 1.778 | 0.904 | **5447** |
| | | | 0.000 | 0.000 | 0.149 | | | | | | | | | | | | | **5553** |
| | | | | | | | | | | | | | | | 0.172 | -0.228 | 0.492 | **5701** |
| 0.000 | 0.354 | **-2.484** | 0.000 | 0.000 | -1.900 | | | | | | | | | | 0.172 | -0.457 | -1.344 | **5858** |
| | | | 0.000 | 0.000 | 0.092 | | | | | | | | | | 0.966 | -0.010 | -1.344 | **5933** |
| 0.000 | 0.199 | 0.587 | 0.000 | 0.000 | 0.856 | -0.320 | -1.011 | 0.956 | 0.013 | | 0.000 | 0.193 | 0.000 | | -0.769 | 0.956 | -1.344 | **5950** |
| | | | | | | | | | | | | | | | -0.769 | -0.228 | 0.492 | **6175** |
| 0.000 | 0.329 | 0.484 | 0.000 | 0.000 | 0.763 | | | | | | | | | | 0.172 | 0.199 | 0.904 | **6180** |
| | | | | | | **2.283** | 0.420 | 0.476 | -1.107 | -1.096 | 0.000 | | | | -0.769 | -0.457 | -1.344 | **6233** |
| | | | | | | | | | | | | | | | **4.000** | **3.042** | **2.760** | **6253** |
| | | | | | | | | | | | | | | | -0.275 | 1.298 | -0.046 | **6456** |
| 0.000 | 0.364 | 1.025 | | | | 1.292 | 0.420 | **2.396** | -0.786 | 0.561 | 0.000 | 0.692 | 0.000 | 0.000 | **-2.863** | -0.010 | -0.046 | **6563** |
| 0.000 | 0.812 | -0.895 | | | | | | | | | | | | | 0.583 | 1.298 | -1.344 | **6686** |
| 0.000 | **2.084** | -0.394 | 0.000 | 0.000 | -0.024 | | | | | | | | | | -0.275 | -1.536 | -1.344 | **7096** |
| | | | | | | | | | | | | | | | | | -1.344 | **7191** |
| 0.000 | 0.870 | 0.377 | | | | -1.506 | 1.012 | 0.476 | -0.684 | -0.633 | 0.000 | -1.865 | 0.000 | 0.000 | -1.330 | 0.591 | 0.492 | **7248** |
| 0.000 | 0.309 | -0.133 | | | | 0.127 | 1.012 | 0.886 | -0.838 | **-2.189** | 0.000 | 0.587 | 0.000 | 0.000 | 0.172 | 0.398 | -0.046 | **7302** |
| 0.000 | -1.376 | **-2.466** | | | | -1.757 | -1.011 | -1.319 | 0.099 | **4.000** | | -1.276 | 0.000 | | -0.275 | 0.199 | -0.046 | **7442** |
| 0.000 | -0.115 | -1.580 | 0.000 | 0.000 | -1.089 | | | | | | | | | | -0.275 | 0.776 | -0.046 | **7596** |
| | | | 0.000 | 0.000 | | -0.175 | -1.011 | 0.721 | -0.786 | **3.754** | 0.000 | -0.339 | 0.000 | 0.000 | -0.769 | 0.591 | -0.046 | **7688** |
| | | | | | | | | | | | | | | | 0.172 | -0.699 | -1.344 | **7728** |
| 0.000 | 0.889 | -0.188 | | | | 1.006 | 1.012 | -0.023 | **2.212** | **2.169** | 0.000 | 0.210 | 0.000 | 0.000 | -0.275 | 0.398 | -0.046 | **7876** |
| 0.000 | -1.376 | -0.743 | 0.000 | 0.000 | -0.338 | 0.846 | -1.011 | 0.956 | -0.393 | | 0.000 | | | | 0.583 | -0.457 | -0.046 | **7896** |
| 0.000 | 1.071 | 0.536 | 0.000 | 0.000 | 0.810 | 0.609 | -1.011 | | -0.346 | 1.567 | 0.000 | | | | 0.172 | -1.869 | 1.252 | **7930** |
| | | | | | | -0.438 | -1.011 | -0.191 | -0.119 | 0.189 | 0.000 | | | | 0.583 | 0.591 | 0.492 | **7962** |
| 0.000 | 0.564 | 1.468 | 0.000 | 0.000 | 1.646 | -0.204 | -1.011 | 0.375 | 0.225 | -0.633 | 0.000 | | | | 0.172 | -0.457 | -1.344 | **7968** |
| 0.000 | -1.376 | 0.213 | 0.000 | 0.000 | 0.520 | -0.091 | 1.467 | -0.134 | -0.488 | -1.608 | 0.000 | | | | 0.583 | 0.398 | 0.492 | **8068** |
| | | | 0.000 | 0.000 | -1.641 | | | | | | | | | | **-2.863** | 0.199 | **2.090** | **8252** |
| 0.000 | 0.057 | 0.367 | 0.000 | 0.000 | 0.658 | | | | | | | | | | 1.325 | -0.957 | 0.492 | **8260** |
| 0.000 | -1.191 | 0.457 | | | | -0.561 | -1.011 | -1.589 | -1.163 | -1.608 | 0.000 | -1.080 | 0.000 | 0.000 | 0.172 | 0.956 | -0.046 | **8329** |
| | | | | | | | | | | | | | | | 0.583 | 1.129 | -1.344 | **8380** |
| | | | 0.000 | 0.000 | -0.405 | | | | | | | | | | -0.275 | **4.000** | 0.904 | **8435** |
| 0.000 | -1.376 | 0.377 | | | | | | | | | | | | | 0.172 | **-2.248** | **2.550** | **8569** |
| | | | | | | | | | | | | | | | 0.583 | 0.398 | 0.492 | **8598** |
| | | | | | | | | | | | | | | | 0.172 | 0.199 | 0.904 | **8626** |
| | | | 0.000 | 0.000 | -1.764 | 1.073 | 1.467 | -1.068 | **2.790** | 0.189 | 0.000 | | | | 0.583 | 0.591 | -1.344 | **8628** |
| | -0.004 | 0.099 | | 0.000 | 0.418 | | | | | | | | | | 0.966 | 1.129 | 0.492 | **8663** |
| | | | | | | | | | | | | | | | -0.769 | -0.010 | -0.046 | **8742** |
| | | | | | | | | | | | | | | | 0.583 | -0.228 | 0.904 | **8751** |
| 0.000 | 0.700 | 0.463 | | | | 0.100 | 0.420 | 0.220 | 0.099 | 1.248 | 0.000 | -0.910 | 0.000 | 0.000 | -1.995 | -0.699 | -0.046 | **8766** |

| **Lab no.** | **Sample** | | | **Suspected coliform bacteria (MF)** | | | **Coliform bacteria (MF)** | | | **Susp. thermotolerant coliform bact. (MF)** | | | ***E. coli* (MF)** | | | **Coliform bacteria ("rapid" MPN)** | | | ***E. coli* ("rapid" MPN)** | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** |
| **8862** | 1 | 2 | 3 | | | | 0.000 | 1.814 | 0.376 | | | | 0.000 | 0.000 | 0.500 | 0.000 | 0.723 | -0.375 | 0.000 | 0.000 | 0.350 |
| **8898** | 1 | 3 | 2 | | | | 0.000 | 0.243 | 0.640 | | | | 0.000 | 0.000 | 1.236 | 0.000 | -0.038 | -0.375 | 0.000 | 0.000 | 0.170 |
| **8955** | 3 | 2 | 1 | | | | 0.000 | 0.764 | -0.091 | | | | 0.000 | 0.000 | -1.671 | 0.000 | 1.170 | 0.900 | 0.000 | 0.000 | 0.859 |
| **8971** | 1 | 3 | 2 | | | | | | | | | | | | | | | | | | |
| **8998** | 1 | 3 | 2 | | | | | | | | | | | | | 0.000 | -0.235 | -1.257 | 0.000 | 0.000 | -1.266 |
| **9051** | 2 | 1 | 3 | | | | 0.000 | -0.894 | -0.814 | | | | 0.000 | 0.000 | -0.957 | | | | | | |
| **9436** | 2 | 3 | 1 | | | | 0.000 | -0.167 | 1.758 | | | | 0.000 | 0.000 | 1.766 | 0.000 | -0.769 | 0.285 | 0.000 | 0.000 | 0.859 |
| **9736** | 3 | 2 | 1 | | | | 0.000 | -0.218 | 0.895 | | | | 0.000 | 0.000 | 0.806 | 0.000 | 0.730 | -0.942 | 0.000 | 0.000 | -0.016 |
| **9899** | 3 | 2 | 1 | | | | 0.000 | 0.270 | **2.996** | | | | 0.000 | 0.000 | 0.806 | 0.000 | 1.646 | 1.136 | 0.000 | 0.000 | 0.524 |
| **9903** | 2 | 1 | 3 | | | | 0.000 | 1.972 | 0.553 | | | | 0.000 | 0.000 | 0.340 | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| **n** | | | | 0 | 0 | 0 | 72 | 73 | 73 | 0 | 0 | 0 | 75 | 73 | 72 | 60 | 58 | 60 | 60 | 59 | 59 |
| **Min** | | | | | | | 0.000 | -3.746 | -3.050 | | | | 0.000 | 0.000 | -2.602 | 0.000 | -1.717 | -2.768 | 0.000 | 0.000 | -2.094 |
| **Max** | | | | | | | 0.000 | 2.606 | 3.248 | | | | 0.000 | 0.000 | 2.138 | 0.000 | 3.050 | 2.239 | 0.000 | 0.000 | 2.640 |
| | | | | | | | | | | | | | | | | | | | | | |
| **Median** | | | | | | | 0.000 | -0.040 | 0.005 | | | | 0.000 | 0.000 | 0.176 | 0.000 | -0.097 | 0.027 | 0.000 | 0.000 | -0.016 |
| **Medel** | | | | | | | 0.000 | -0.103 | 0.000 | | | | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| **SD** | | | | | | | 0.000 | 1.162 | 1.000 | | | | 0.000 | 0.000 | 1.000 | 0.000 | 1.000 | 1.000 | 0.000 | 0.000 | 1.000 |
| | | | | | | | | | | | | | | | | | | | | | |
| **z<-3** | | | | | | | 0 | 2 | 1 | | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **-3<z<-2** | | | | | | | 0 | 2 | 0 | | | | 0 | 0 | 3 | 0 | 0 | 2 | 0 | 0 | 3 |
| **2<z<3** | | | | | | | 0 | 1 | 1 | | | | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 1 |
| **z>3** | | | | | | | 0 | 0 | 1 | | | | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |

| **Presumptive *C. perfringens* (MF)** | | | ***Clostridium perfringens* (MF)** | | | **Moulds (MF)** | | | **Yeasts (MF)** | | | **Actinomycetes (MF)** | | | **Total plate count 22 °C, 3 days** | | | **Lab no.** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | **A** | **B** | **C** | |
| 0.000 | 0.045 | 0.850 | | | | 1.398 | -1.011 | 0.451 | -1.163 | 0.189 | 0.000 | -0.524 | 0.000 | 0.000 | -0.769 | -0.699 | 0.492 | **8862** |
| 0.000 | -0.036 | 0.850 | | | | 0.681 | 0.420 | 1.694 | -0.536 | 1.248 | 0.000 | 1.859 | 0.000 | | 0.172 | 0.199 | 0.492 | **8898** |
| | | | 0.000 | 0.000 | 0.313 | -0.175 | -1.011 | -1.357 | 0.266 | **4.000** | 0.000 | | | | 1.665 | | -1.344 | **8955** |
| | | | | | | -1.021 | -1.011 | -1.103 | 0.998 | 0.561 | 0.000 | | | | 0.172 | -1.235 | 0.492 | **8971** |
| 0.000 | -0.354 | -1.132 | | | | | | | | | | | | | 0.966 | 0.591 | -0.046 | **8998** |
| | | | 0.000 | 0.000 | 0.005 | | | | | | | | | | 0.583 | -1.869 | 1.252 | **9051** |
| 0.000 | 0.708 | 0.530 | | | | -1.506 | 1.851 | 0.956 | -0.838 | 0.189 | 0.000 | **-2.051** | 0.000 | 0.000 | **4.000** | **-2.248** | **2.550** | **9436** |
| 0.000 | 1.085 | -0.488 | | | | 1.334 | 1.851 | 0.649 | 0.056 | -0.633 | 0.000 | 1.294 | 0.000 | 0.000 | 0.583 | 0.591 | -1.344 | **9736** |
| 0.000 | 1.548 | 0.869 | | | | -0.951 | -1.011 | 0.005 | -1.052 | 0.561 | 0.000 | 0.587 | 0.000 | 0.000 | -0.769 | -0.699 | 0.904 | **9899** |
| 0.000 | 0.033 | -0.283 | | | | 0.284 | 1.012 | 0.426 | 1.245 | -0.208 | 0.000 | | | | 0.583 | -0.010 | 0.904 | **9903** |

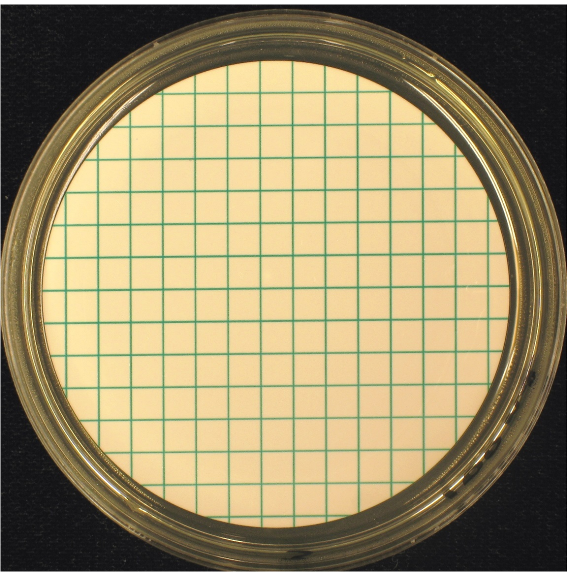
| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 46 | 47 | 47 | 39 | 38 | 38 | 42 | 42 | 41 | 42 | 40 | 41 | 28 | 27 | 21 | 86 | 87 | 89 | **n** |
| 0.000 | -1.376 | -2.502 | 0.000 | 0.000 | -1.916 | -4.000 | -1.011 | -4.000 | -4.000 | -3.777 | 0.000 | -4.000 | 0.000 | 0.000 | -2.863 | -2.248 | -1.344 | **Min** |
| 0.000 | 2.084 | 1.468 | 0.000 | 0.000 | 1.646 | 2.283 | 1.851 | 2.396 | 2.790 | 4.000 | 0.000 | 1.859 | 0.000 | 0.000 | 4.000 | 4.000 | 4.000 | **Max** |
| 0.000 | 0.199 | 0.323 | 0.000 | 0.000 | 0.092 | -0.133 | 0.420 | -0.050 | -0.141 | 0.189 | 0.000 | 0.106 | 0.000 | 0.000 | 0.172 | -0.010 | -0.046 | **Median** |
| 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | -0.095 | 0.000 | -0.098 | -0.095 | 0.199 | 0.000 | -0.143 | 0.000 | 0.000 | 0.186 | 0.092 | 0.180 | **Mean** |
| 0.000 | 1.000 | 1.000 | 0.000 | 0.000 | 1.000 | 1.165 | 1.000 | 1.168 | 1.165 | 1.551 | 0.000 | 1.239 | 0.000 | 0.000 | 1.293 | 1.158 | 1.284 | **SD** |
| | | | | | | | | | | | | | | | | | | **Sum** |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 8 |
| 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 3 | 2 | 0 | 22 |
| 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 4 | 16 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 4 | 4 | 4 | 17 |

## Mixture A

**m-Endo Agar LES, 37 °C**

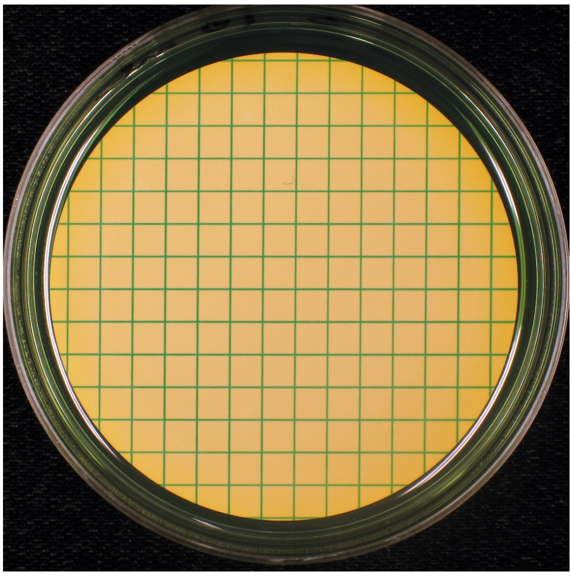
100 ml

**Chromocult Coliform Agar, 37 °C**



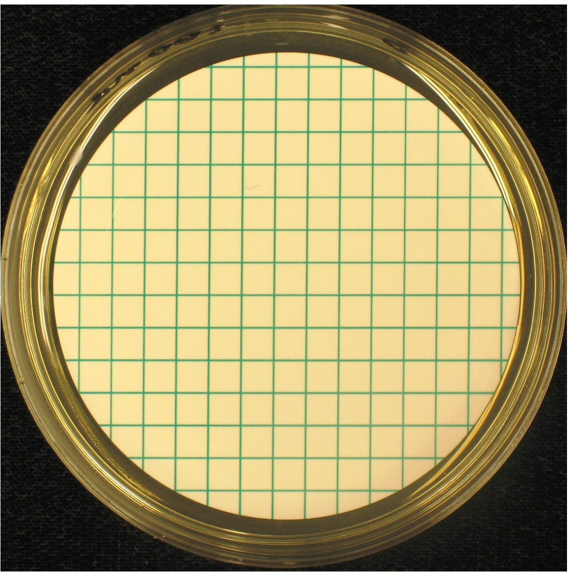
100 ml

**m-Lactose TTC Agar, 37 °C**



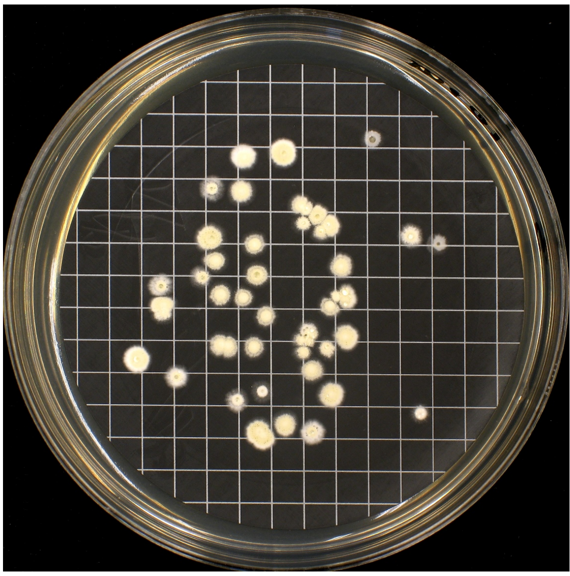
100 ml

**m-TSC Agar, 44 °C**



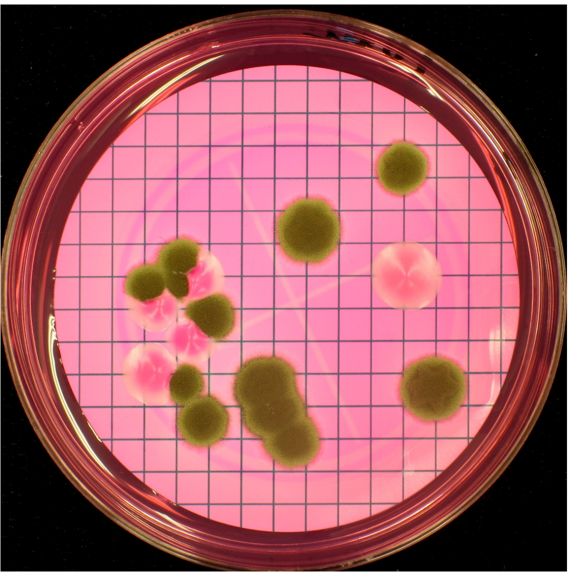
100 ml

**Actinomycete Isolation Agar, 25 °C**



10 ml, 7 days

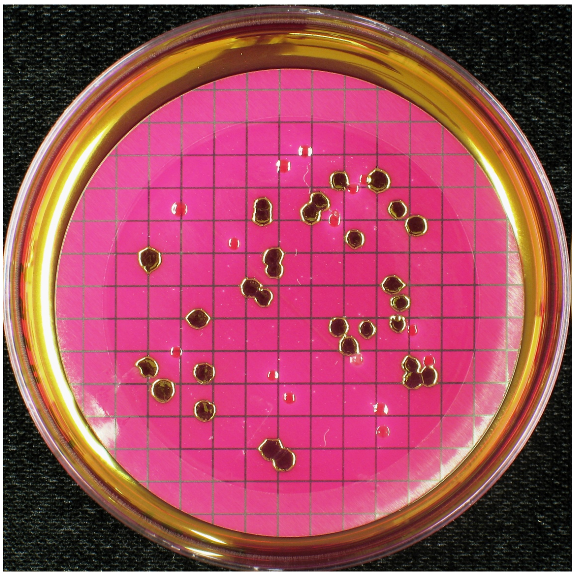
**m-RBCC Agar, 25 °C**



10 ml, 7 days

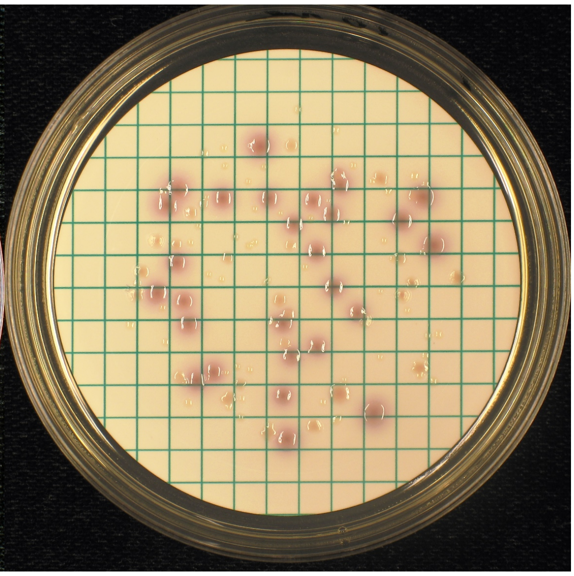
# Mixture B

m-Endo Agar LES, 37 °C



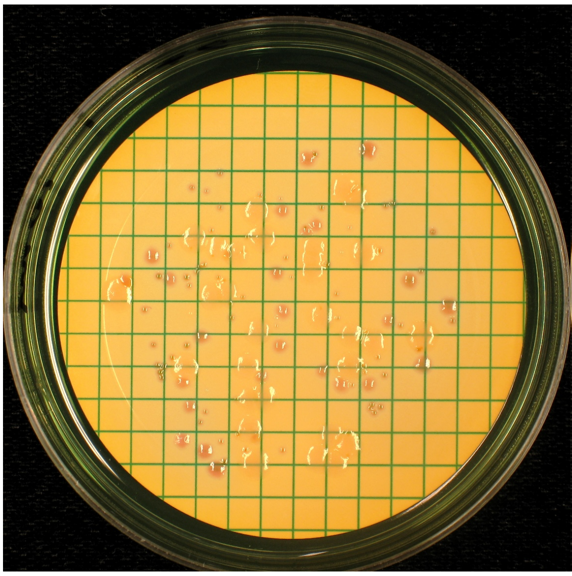
10 ml

Chromocult Coliform Agar, 37 °C



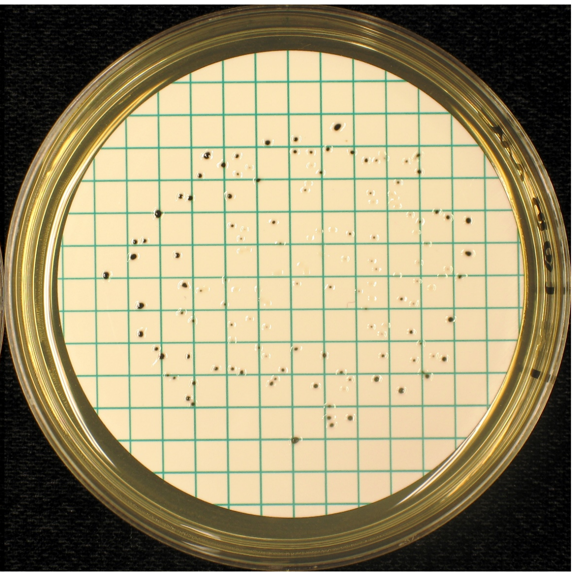
10 ml

m-Lactose TTC Agar, 37 °C



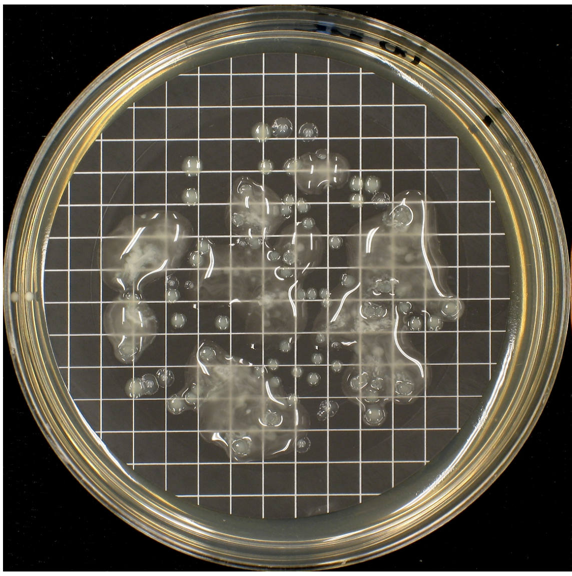
10 ml

m-TSC Agar, 44 °C



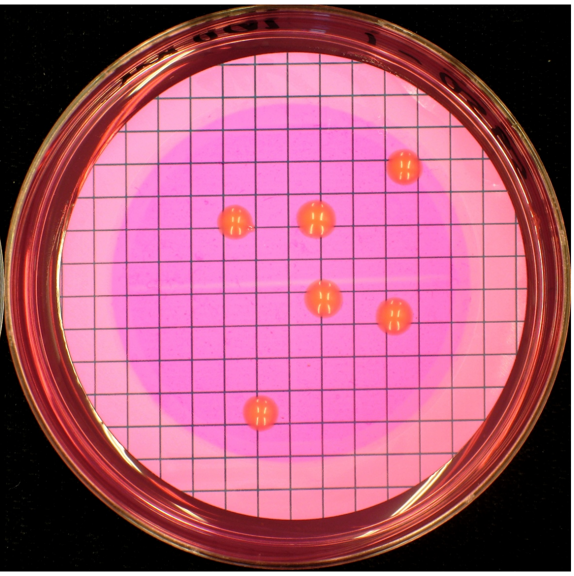
100 ml

Actinomycete Isolation Agar, 25 °C



10 ml, 7 days

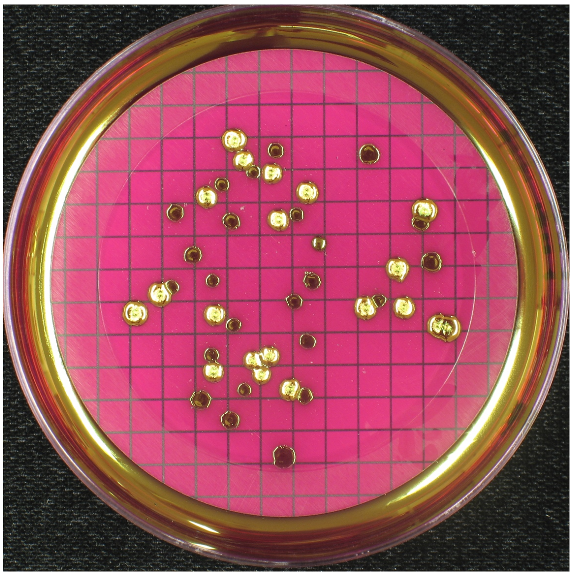
m-RBCC Agar, 25 °C



100 ml, 7 days

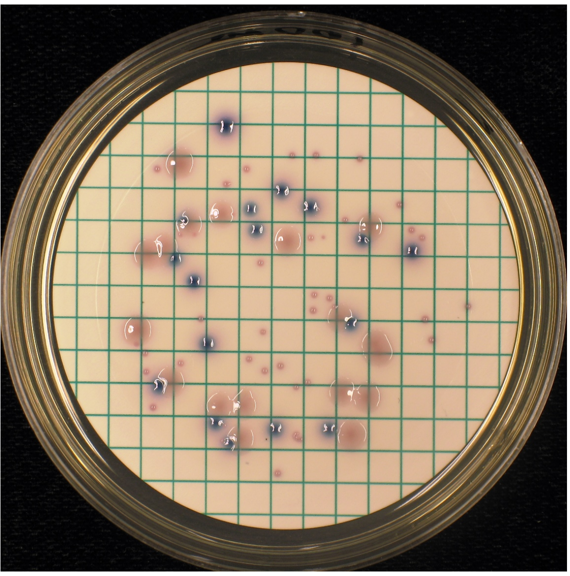
# Mixture C

m-Endo Agar LES, 37 °C



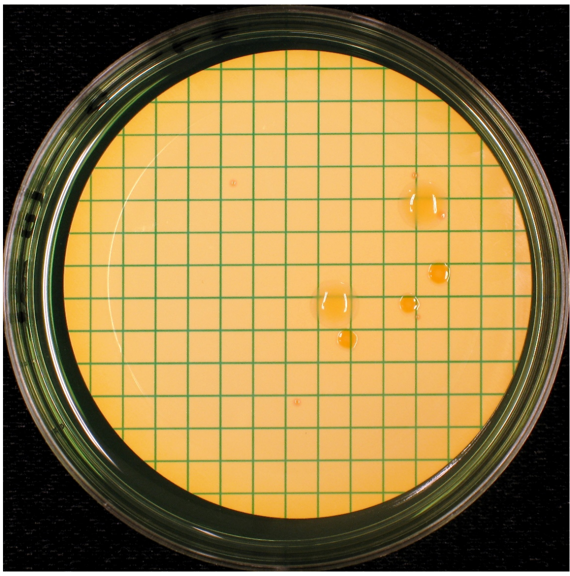
100 ml

Chromocult Coliform Agar, 37 °C



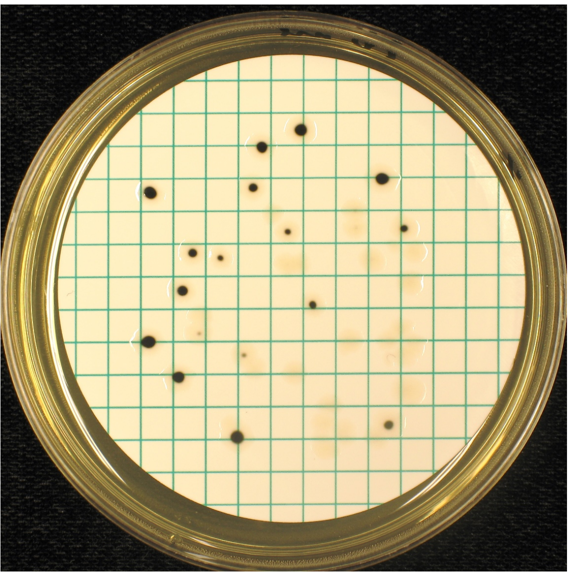
100 ml

m-Lactose TTC Agar, 37 °C



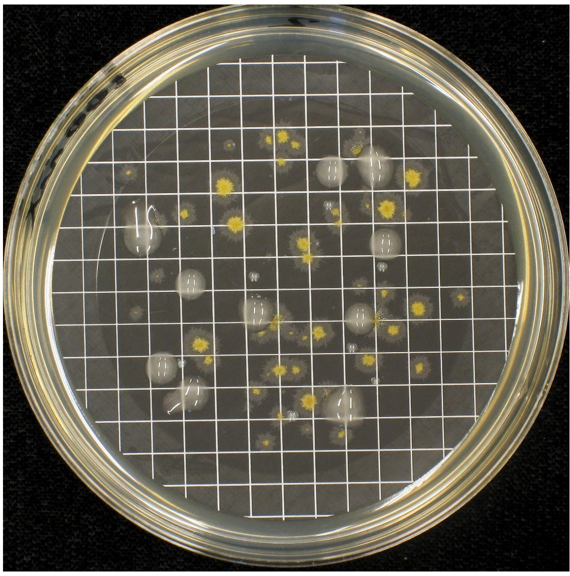
10 ml

m-TSC Agar, 44 °C



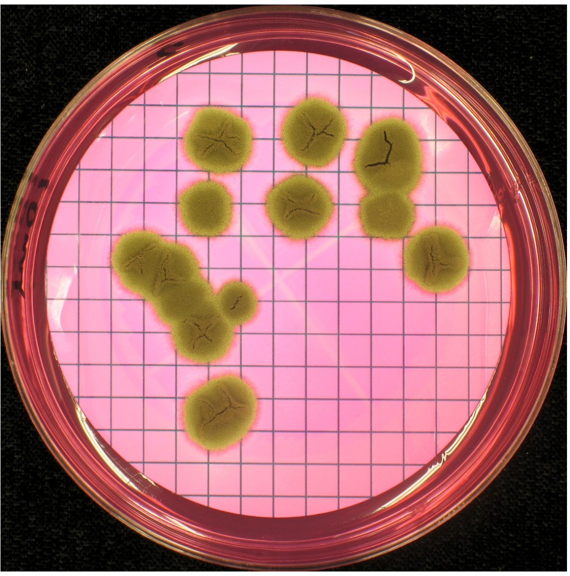
10 ml

Actinomycete Isolation Agar, 25 °C



100 ml, 7 days

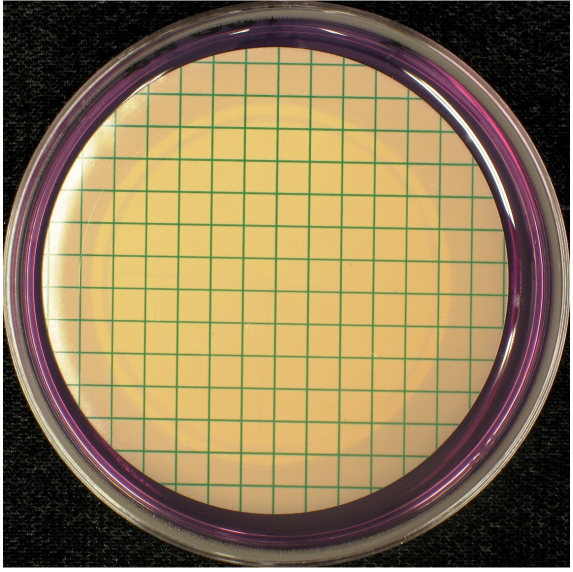
m-RBCC Agar, 25 °C



10 ml, 7 days

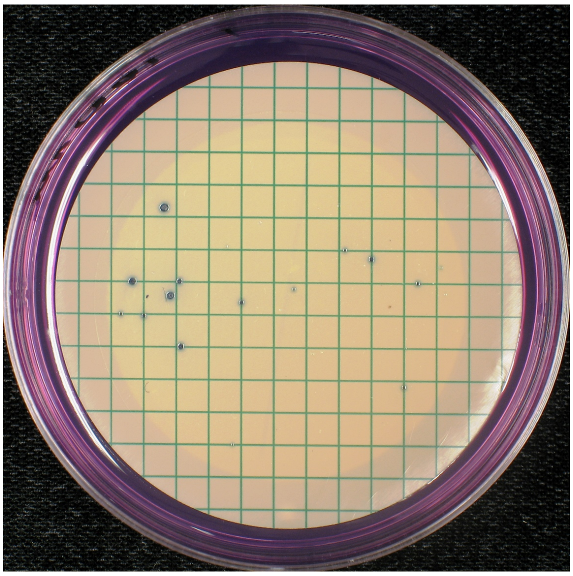
# m-FC Agar, 44 °C in mixture A, B and C, respectively

**(A) m-FC Agar, 44 °C**



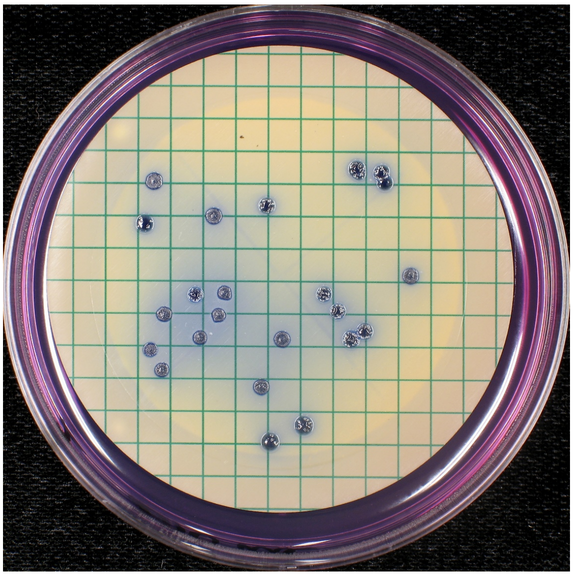
100 ml

**(B) m-FC Agar, 44 °C**



100 ml

**(C) m-FC Agar, 44 °C**



100 ml

## PT reports published 2015

Proficiency Testing – Food Microbiology, January 2015

Proficiency Testing – Drinking Water Microbiology, March 2015, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2015

Proficiency Testing – Drinking Water Microbiology, September 2015, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, October 2015

## PT reports published 2016

Proficiency Testing – Food Microbiology, January 2016, by Kirsi Mykkänen

## Internal and external control for microbiological analyses of food and drinking water

All analytical activities require work of a high standard that is accurately documented. For this purpose, most laboratories carry out some form of internal quality assurance, but their analytical work also has to be evaluated by an independent party. Such external quality control of laboratory competence is commonly required by accreditation bodies and can be done by taking part in proficiency testing (PT).

In a proficiency test, identical test material is analysed by a number of laboratories using their routine methods. The laboratories report their results to the organiser that evaluates them and compiles them in a report.

## The National Food Agency's PT program offers

- External and independent evaluation of laboratories analytical competence.
- Improved knowledge of analytical methods with respect to various types of organisms.
- Expert support.
- Tool for inspections regarding accreditation.
- Free extra material for follow-up analyses

For more information visit our website: www2.slv.se/absint

## The National Food Agency's reference material

As a complement to the proficiency testing, National Food Agency also produces reference material (RM) for internal quality control: a total of 8 RM for food and drinking water microbiological analyses, including pathogens, are available.

Information available on our website: www.livsmedelsverket.se/en/RM-micro