

## Drinking Water Microbiology

September 2015

by Tommy Šlapokas



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*Proficiency testing*

# **Drinking water Microbiology**

September 2015



## **Parameters included**

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

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

**Intestinal enterococci** with MF

*Pseudomonas aeruginosa* with MF

**Culturable microorganisms** (total count) 3 days incubation at **22±2 °C**

**Culturable microorganisms** (total count) 2 days incubation at **36±2 °C**

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## Abbreviations and explanations




### *Microbiological media*

CCA	Chromocult Coliform Agar <sup>®</sup> (Merck; EN ISO 9308-1:2014)
Colilert	Colilert <sup>®</sup> Quanti-Tray <sup>®</sup> (IDEXX Inc.; 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-Ent	m-Enterococcus Agar (Slanetz & Bartley; according to EN ISO 8799-2:2000)
m-FC	m-FC Agar (acc. to SS 028167)
PACN	Pseudomonas Agar base/CN agar (with ceftrimide and nalidixic acid; according to EN ISO 16266:2008)
YeA	Yeast extract Agar (acc. 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*

Tot 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 <i>excluded</i> )
Med	median value (with outliers and false results <i>included</i> )
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
	remarkably low result
	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

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<b>Abbreviations and explanations</b> .....	2
<b>Contents</b> .....	3
<b>General information on results evaluation</b> .....	4
<b>Results of the PT round</b> .....	4
- General outcome .....	4
- Coliform bacteria (MF) .....	6
- Suspected thermotolerant coliform bacteria (MF) .....	8
- <i>Escherichia coli</i> (MF) .....	9
- Coliform bacteria and <i>E. coli</i> (rapid method, MPN) .....	12
- Intestinal enterococci (MF) .....	14
- <i>Pseudomonas aeruginosa</i> (MF) .....	16
- Culturable microorganisms 22 °C, 3 days .....	18
- Culturable microorganisms 36 °C, 2 days .....	20
<b>Outcome of the results and laboratory assessment</b> .....	22
- General information about reported results .....	22
- Base for assessment of the performance .....	22
- Mixed up results and other practical errors .....	22
- Z-scores, box plots and deviating results for each laboratory .....	22
<b>Test material, quality control and processing of data</b> .....	27
- Description of the test material .....	27
- Quality control of the test material .....	27
- Processing of numerical results .....	29
<b>References</b> .....	30
<b>Annex A – All reported results</b> .....	32
<b>Annex B – Z-scores of the results</b> .....	36
<b>Annex C – Photo example of colony appearance on some media</b> .....	40

## 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.

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.

## Results of the PT round

### General outcome

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Test items were sent to 109 laboratories, 41 in Sweden, 52 in other Nordic countries (Faeroe Islands, Greenland and Åland included), 3 more from EU, 5 from the rest of Europe and 8 from countries outside Europe. Results were reported from 102 laboratories.

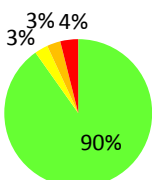
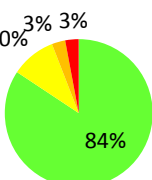
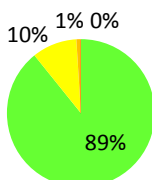
The percentages of false results and outliers are compiled in **table 1**. These deviating results are excluded in most calculations.

Microorganisms and parameters of analyses are also compiled in **table 1**. For the MF analyses the parameters *suspected* coliform bacteria and thermotolerant coliform bacteria, as well as *suspected* intestinal enterococci and *Pseudomonas aeruginosa* on primary media 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](http://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									
No. of evaluable results	588			591			589		
No. of deviating results *	27 (5 %)			26 (4 %)			12 (2 %)		
Microorganisms	<i>Escherichia coli</i> <i>Citrobacter freundii</i> <i>Enterococcus faecalis</i> <i>Pseudomonas aeruginosa</i>			<i>Enterobacter cloacae</i> <i>Klebsiella oxytoca</i> <i>Enterococcus durans</i> <i>Staphylococcus capitis</i>			<i>Escherichia coli</i> (weak $\beta$ -glu) <i>Aeromonas hydrophila</i> <i>Pseudomonas aeruginosa</i> <i>Pseudomonas fluorescens</i>		
Analysis	Målorganism	F%	X%	Målorganism	F%	X%	Målorganism	F%	X%
Coliform bacteria (MF)	<i>E. coli</i> <i>C. freundii</i>	0	5	<i>E. cloacae</i> <i>K. oxytoca</i>	0	4	<i>E. coli</i> [ <i>A. hydrophila</i> ]	2	1
Susp. thermotolerant coliform bact. (MF)	<i>E. coli</i>	–	–	<i>E. cloacae</i>	–	–	<i>E. coli</i>	–	–
<i>E. coli</i> (MF)	<i>E. coli</i>	2	1	[ <i>E. cloacae</i> ]	5	–	{ <i>E. coli</i> }	0	1
Coliform bacteria (rapid method)	<i>E. coli</i> <i>C. freundii</i>	0	2	<i>E. cloacae</i> <i>K. oxytoca</i>	0	3	<i>E. coli</i>	0	2
<i>E. coli</i> (rapid meth.)	<i>E. coli</i>	0	5	–	0	–	–	2	–
Intestinal enterococci (MF)	<i>E. faecalis</i>	0	4	<i>E. durans</i>	1	7	–	1	–
<i>Pseudomonas aeruginosa</i> (MF)	<i>P. aeruginosa</i>	2	0	–	2	–	<i>P. aeruginosa</i>	2	0
Culturable microorganisms (total count), 3 days 22 °C	<i>E. faecalis</i> <i>E. coli</i> <i>C. freundii</i> ( <i>P. aeruginosa</i> )	1	5	( <i>E. durans</i> ) ( <i>E. cloacae</i> ) ( <i>K. oxytoca</i> )	0	3	<i>P. fluorescens</i> ( <i>P. aeruginosa</i> ) ( <i>A. hydrophila</i> ) ( <i>E. coli</i> )	0	2
Culturable microorganisms (total count), 2 days 36 °C	<i>E. faecalis</i> <i>E. coli</i> <i>C. freundii</i> ( <i>P. aeruginosa</i> )	1	7	<i>S. capitis</i> ( <i>E. durans</i> ) ( <i>E. cloacae</i> ) ( <i>K. oxytoca</i> )	0	9	( <i>P. aeruginosa</i> ) ( <i>A. hydrophila</i> ) ( <i>E. coli</i> )	0	1

\* In total 26 of 102 laboratories (25%) reported at least one deviating result

– Organism missing or numerical result irrelevant

() The organism contributes with only very few colonies

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

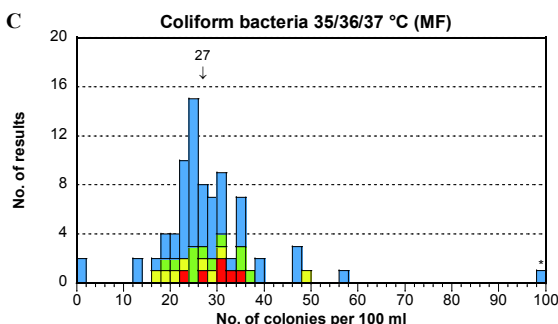
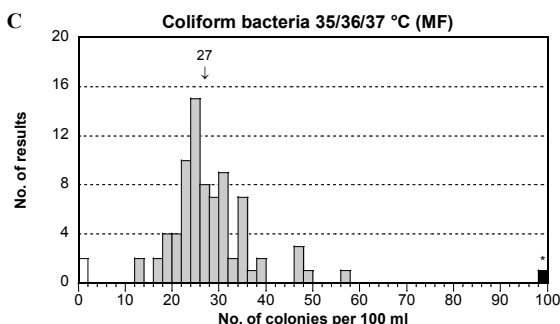
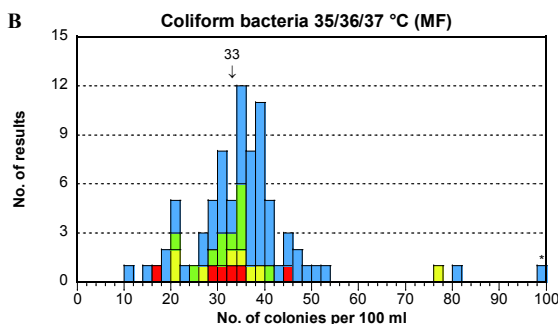
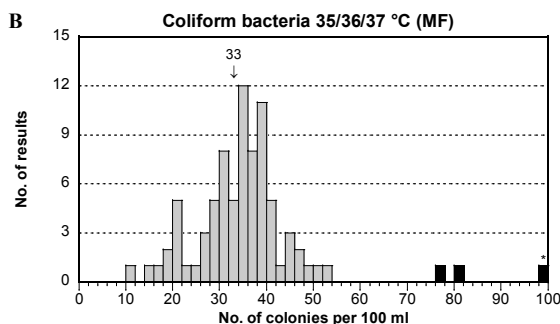
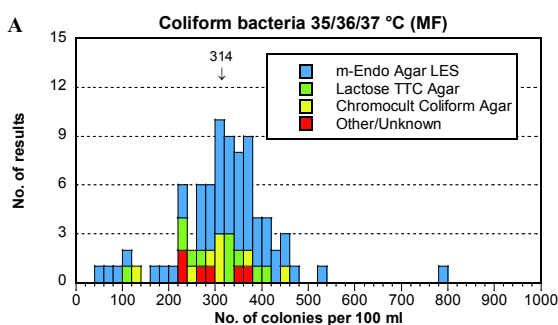
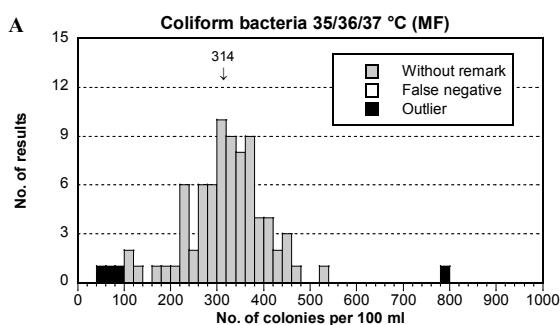
{ } The organism may give different results depending on method or definition used

## Coliform bacteria (MF)

In two cases the primary medium reported was not the one prescribed in the standard referred to. There 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 5 times more frequently used than LTTC, while CCA was also used by some laboratories. There is an indication that LES gave

Medium	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total</b>	<b>81</b>	<b>77</b>	<b>314</b>	<b>13</b>	<b>0</b>	<b>3</b>	<b>1</b>	<b>78</b>	<b>33</b>	<b>13</b>	<b>0</b>	<b>0</b>	<b>3</b>	<b>78</b>	<b>27</b>	<b>14</b>	<b>2</b>	<b>0</b>	<b>1</b>
m-Endo Agar LES	56	52	327	12	0	3	1	54	34	14	0	0	2	53	27	14	2	0	1
Lactose TTC Agar	11	11	284	16	0	0	0	11	31	9	0	0	0	11	27	11	0	0	0
Chromocult C Agar	8	8	295	16	0	0	0	7	29	13	0	0	1	8	26	18	0	0	0
Other/Unknown	6	6	286	10	0	0	0	6	31	16	0	0	0	6	29	8	0	0	0



a somewhat higher mean result compared to both LTTC and CCA in the mixtures A and B. The relative dispersion for a medium varies between the mixtures, in particular for LTTC and CCA with fewer results. The category Other/Unknown medium does not show deviating results for any mixture.

#### **Mixture A**

- Two strains of coliform bacteria were included in the mixture. Both *E. coli* and *C. freundii* grow with typical colonies, with a metallic sheen on LES and light to dark yellow on LTTC and bluish and pink, respectively, on CCA at 37 °C (see annex C). There was no general problem with this analysis.
- The average recovery is somewhat lower than for coliform bacteria with the rapid methods (see page 12). The whole histogram is for MF dislocated towards lower results. There is also a tail with low results, out of which some are outliers.

#### **Mixture B**

- Two strains of coliform bacteria were included in the mixture. Both *E. cloacae* and *K. oxytoca* grow with typical colonies, with a metallic sheen on LES and light yellow to yellow on LTTC and pink on CCA at 37 °C. The analysis was without problem.
- The average recovery is somewhat lower for the MF method compared with the rapid methods (see page 13) because there were a larger proportion of low results.

#### **Mixture C**

- One strain of *E. coli* was the only coliform bacterium. It grows with for coliform bacteria typical colonies on the MF media, a metallic sheen on LES and yellow on LTTC and pink to violet on CCA at 37 °C. There was no problem with this analysis.
- Two false negative results were present.
- A strain of *A. hydrophila* was also included in the mixture. It grows usually with for coliform bacteria more or less typical colonies on these media. *A. hydrophila* is oxidase positive and the colonies can be excluded as coliform bacteria after confirmation by the oxidase test (see below).
- The used *A. hydrophila* strain seems – at least occasionally – to have weaker metallic sheen than coliform bacteria on LES and consequently more reddish colonies. This was not as evident at this occasion as it was in September 2014.
- The average number of coliform bacteria in this analysis was identical to that for the rapid methods (page 14). This might indicate that *A. hydrophila* is not included among the coliform bacteria with the MF method. However, as you usually obtain a bit lower average result for coliform bacteria with the MF method, it is plausible that the average for the MF method is compensated upwards because some laboratories include colonies of *A. hydrophila*.
- For 36 out of 56 cases with results for both suspected coliform bacteria and coliform bacteria the results are equal. For the remaining 26 cases, the results for suspected coliform bacteria are higher, indicating that *A. hydrophila* has then been excluded there after confirmation

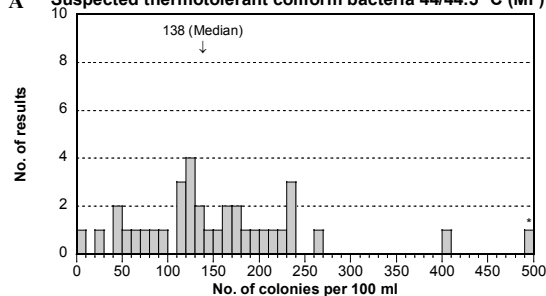
## Suspected thermotolerant coliform bacteria (MF)

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.

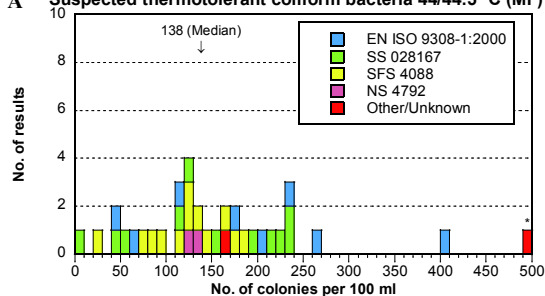
The table shows the *medians* instead of mean values because no outliers have been identified. The reason is that *the analysis is not included in performance assessment*.

Standard, Method	Tot n	A						B						C					
		n	Med	CV	F	<	>	n	Med	CV	F	<	>	n	Med	CV	F	<	>
Total	35	35	138	—	—	—	—	35	0	—	—	—	—	35	25	—	—	—	—
EN ISO 9308-1	8	8	188	—	—	—	—	8	0	—	—	—	—	8	25	—	—	—	—
SS 028167	11	11	152	—	—	—	—	11	0	—	—	—	—	11	26	—	—	—	—
SFS 4088	12	12	120	—	—	—	—	12	0	—	—	—	—	12	21	—	—	—	—
NS 4792	2	2	127	—	—	—	—	2	0	—	—	—	—	2	30	—	—	—	—
Other/Unknown	2	2	474	—	—	—	—	2	0	—	—	—	—	2	310	—	—	—	—

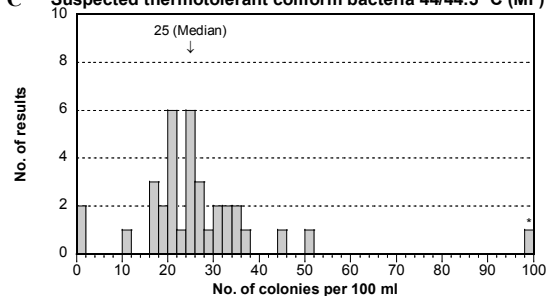
A Suspected thermotolerant coliform bacteria 44/44.5 °C (MF)



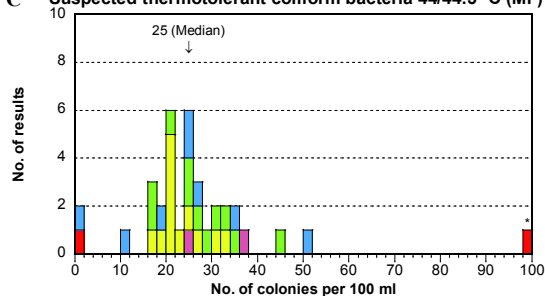
A Suspected thermotolerant coliform bacteria 44/44.5 °C (MF)



C Suspected thermotolerant coliform bacteria 44/44.5 °C (MF)



C Suspected thermotolerant coliform bacteria 44/44.5 °C (MF)



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 three laboratories using Norwegian standard has this time incubated at 44.5 °C, the rest at 44.5 °C. All laboratories using Finnish standard has incubated at 44 °C, according to the standard.

No general correlation between standard, and thus indirectly temperature, and colony recovery can be seen from the table or the method histograms.

#### **Mixture A**

- The strain of *E. coli* appears with blue colonies on m-FC at 44/44.5 °C. The corresponding colonies are dark yellow on LTTC.
- The average result was in this mixture somewhat higher on LTTC than on m-FC.

#### **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 on both m-FC and LTTC.
- Seven laboratories have reported other results than zero cfu per 100 ml.

#### **Mixture C**

- The strain of *E. coli* appears with blue colonies on m-FC at 44/44.5 °C. The corresponding colonies are dark yellow on LTTC.
- Two zero results were also obtained from two different methods.

### ***Escherichia coli* (MF)**

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*E. coli* is quantified after confirmation of colonies that have grown either at 36±2 °C or at 44/44.5 °C. Depending on method, either test of indole production or  $\beta$ -glucuronidase activity is used as sufficient confirmation.

The primary growth media LTTC, LES and nowadays even 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 40 results with unclear incubation temperature are not separately shown but are included only in the table "All results".

Since almost half of the results could not be connected to method – although they belong to either temperature – it is not meaningful to discuss differences between method groups within the respective temperature.

#### **Mixture A**

- 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.

# All results

Medium	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total</b>	<b>83</b>	<b>80</b>	<b>163</b>	<b>20</b>	<b>2</b>	<b>0</b>	<b>1</b>	<b>79</b>	<b>0</b>	<b>–</b>	<b>4</b>	<b>–</b>	<b>–</b>	<b>81</b>	<b>27<sup>#</sup></b>	<b>14<sup>#</sup></b>	<b>0</b>	<b>1</b>	<b>1</b>

# Calculated without the 19 zero results

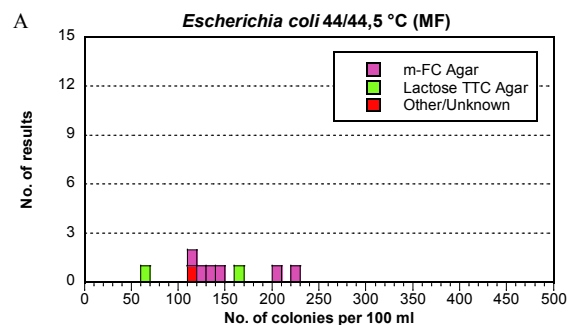
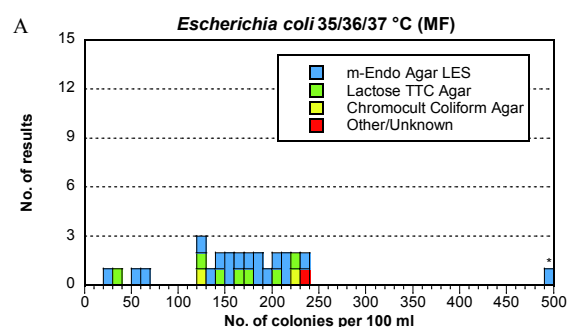
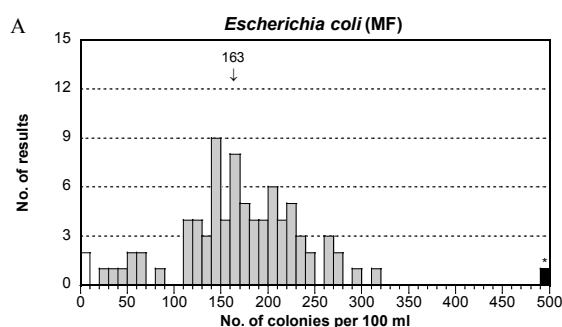
## From 36±2 °C

Medium	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total</b>	<b>34</b>	<b>33</b>	<b>152</b>	<b>21</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>32</b>	<b>0</b>	<b>–</b>	<b>2</b>	<b>–</b>	<b>–</b>	<b>33</b>	<b>8</b>	<b>90</b>	<b>0</b>	<b>0</b>	<b>1</b>
m-Endo Agar LES	18	17	144	23	0	0	1	16	0	–	2	–	–	17	11	72	0	0	1
Lactose TTC Agar	7	7	141	26	0	0	0	7	0	–	0	–	–	7	13	69	0	0	0
Chromocult C Agar	8	8	168	13	0	0	0	8	0	–	0	–	–	8	0	–	0	–	–
Other/Unknown	1	1	230	–	0	0	0	1	0	–	0	–	–	1	30	–	0	0	0

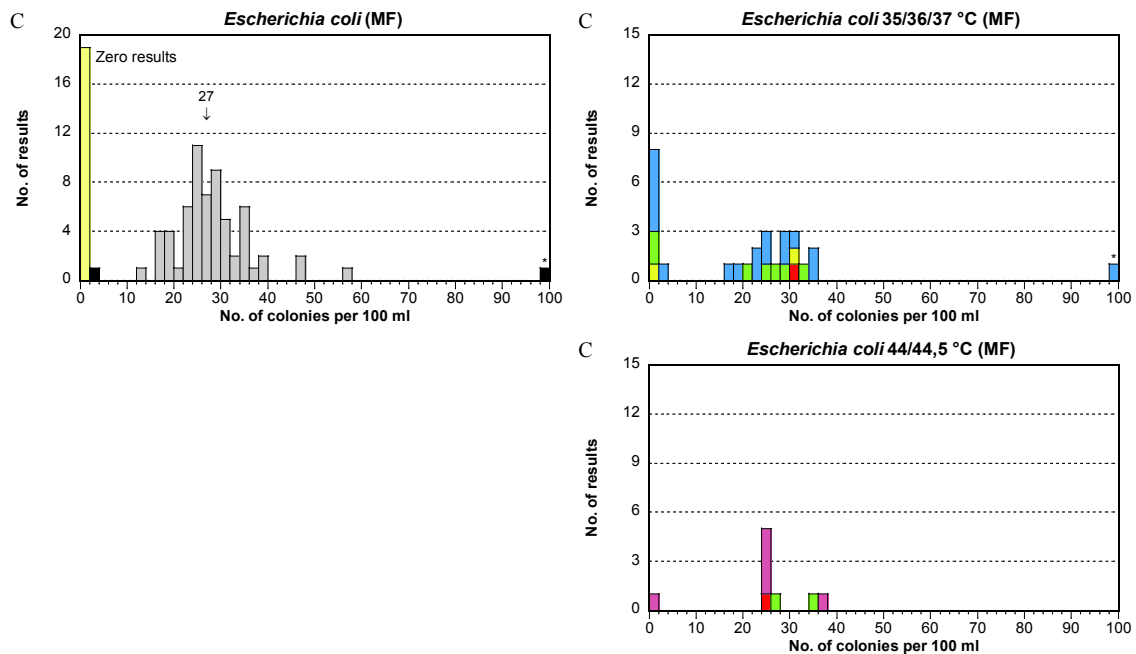
## From 44/44.5 °C

Medium/Standard	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total</b>	<b>9</b>	<b>9</b>	<b>137</b>	<b>18</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>9</b>	<b>0</b>	<b>–</b>	<b>0</b>	<b>–</b>	<b>–</b>	<b>9</b>	<b>22</b>	<b>38</b>	<b>0</b>	<b>0</b>	<b>0</b>
<u>Medium</u>																			
m-FC Agar	6	6	154	14	0	0	0	6	0	–	0	–	–	6	19	50	0	0	0
Lactose TTC Agar	2	2	104	–	0	0	0	2	0	–	0	–	–	2	30	–	0	0	0
Other/Unknown	1	1	110	–	0	0	0	1	0	–	0	–	–	1	25	–	0	0	0
<u>Standard</u>																			
EN ISO 9308-1	4	4	134*	–	0	0	0	4	0	–	0	–	–	4	25*	–	0	0	0
SS 028167	0	0	–	–	–	–	–	0	–	–	–	–	–	0	–	–	–	–	–
SFS 4088	2	2	178	–	0	0	0	2	0	–	0	–	–	2	25	–	0	0	0
NS 4792	2	1	126	–	0	0	0	2	0	–	0	–	–	2	30	–	0	0	0
Other/Unknown	1	1	119	–	0	0	0	1	0	–	0	–	–	1	25	–	0	0	0

\* Median instead of mean value







### Mixture B

- No *E. coli* was included in the mixture. On the other hand, there were four false positive results, out of which three had a colony number that is possible if colonies of *E. cloacae* are taken for *E. coli*.

### Mixture C

- One strain of *E. coli* with weak  $\beta$ -glucuronidase activity was present in the mixture, resulting in varying outcome on different primary media.
- Nineteen zero results were reported together with 64 results where presence of *E. coli* were reported. The zero results originate probably from media where test of  $\beta$ -glucuronidase activity has been decisive, since the strain is indole positive. The 4 laboratories that have used XX-EN ISO 9308-1:2014 and the medium CCA or corresponding must have interpreted the colonies as pink and reported only zero results.
- The other zero results are from different methods from different countries. The most probable is that test of  $\beta$ -glucuronidase activity has been used as confirmation, e.g. test in broth with MUG reagent, and that the fluorescence has been interpreted as negative. A weak enzyme activity is present and the incubation time before reading is crucial for the interpretation of the outcome. In our tests with the strain, the outcome is weakly positive but it is necessary to compare with a clearly positive and negative strain to state the result.
- The same average result was obtained as with the rapid method, 27 cfu per 100 ml, with the zero results excluded.
- The low result 3 cfu per 100 ml is an outlier when the zero results are separately handled. The distribution of accepted results looks good and has small dispersion.

## 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 either 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). The laboratories often analysed both diluted and undiluted samples. The only laboratory in the category Other/Unknown stated the use of "Colilert 24 hours".

For coliform bacteria in all mixtures and *E. coli* in mixture A there was a tendency that the trays with 51 wells give somewhat lower average recovery than trays with 97 wells (not shown). In the mixture B and C there is a small tendency to higher results after incubation at 35 °C compared to at 37 °C.

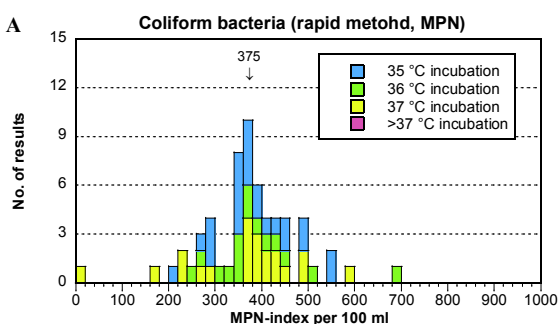
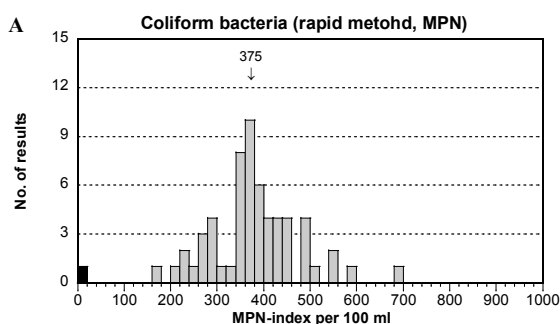
Individual outliers are seen in all these analyses. The 4 lowest of the 5 low outliers originate from only one laboratory that reported the results with common logarithms instead of in ordinary cfu scale. If reported properly they would have been correct. None of the analyses outcomes indicates any interpretation problem.

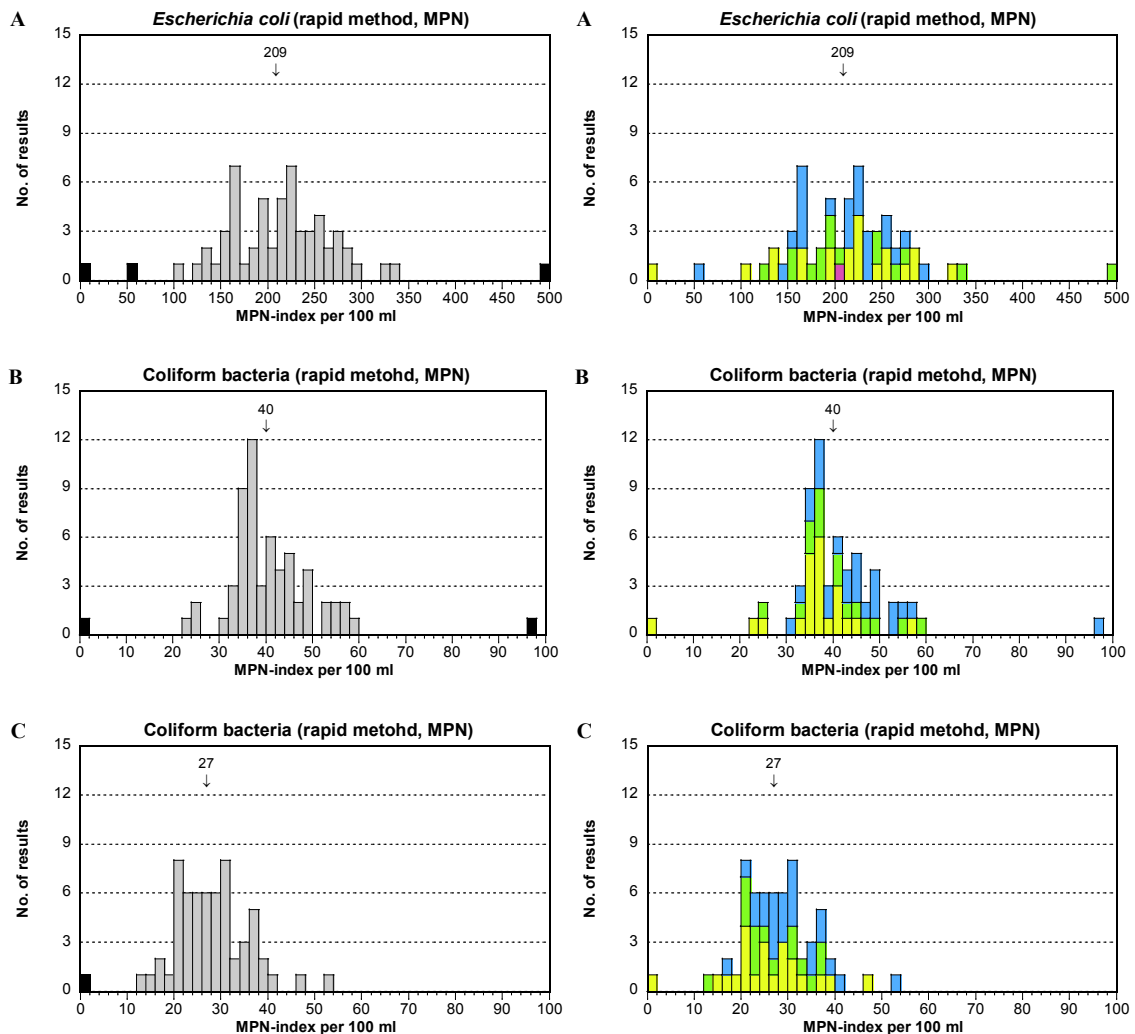
### Coliform bacteria, Rapid method with MPN

Medium	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total, Rapid meth.</b>	<b>61</b>	<b>59</b>	<b>375</b>	<b>13</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>59</b>	<b>40</b>	<b>10</b>	<b>0</b>	<b>1</b>	<b>1</b>	<b>60</b>	<b>27</b>	<b>14</b>	<b>0</b>	<b>1</b>	<b>0</b>
35 °C incubation	24	24	376	11	0	0	0	23	42	9	0	0	1	24	29	13	0	0	0
36 °C incubation	15	15	378	13	0	0	0	15	40	11	0	0	0	15	26	14	0	0	0
37 °C incubation	22	20	370	14	0	1	0	21	37	9	0	1	0	21	26	14	0	1	0
>37 °C incubation	0	0	–	–	0	0	0	0	–	–	0	0	0	0	–	–	0	0	0

### *E. coli*, Rapid method with MPN

Medium	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total, Rapid meth.</b>	<b>61</b>	<b>57</b>	<b>209</b>	<b>12</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>61</b>	<b>0</b>	<b>–</b>	<b>0</b>	<b>–</b>	<b>–</b>	<b>59</b>	<b>0</b>	<b>–</b>	<b>1</b>	<b>–</b>	<b>–</b>
35 °C incubation	23	22	210	10	0	1	0	23	0	–	0	–	–	23	0	–	0	–	–
36 °C incubation	15	14	204	14	0	0	1	15	0	–	0	–	–	15	0	–	0	–	–
37 °C incubation	22	20	213	14	0	1	0	22	0	–	0	–	–	20	0	–	1	–	–
>37 °C incubation	1	1	203	–	0	0	0	1	0	–	0	–	–	1	0	–	0	–	–





### Mixture A

- The strains of *E. coli* and *C. freundii* grow and possess  $\beta$ -galactosidase. They are thus detected as coliform bacteria by methods based on the activity of this enzyme (ONPG positive), e.g. Colilert®-18/24 Quanti-Tray® where ONPG is a substrate.
- The strain of *E. coli* possesses the enzyme  $\beta$ -glucuronidase and is also detected as *E. coli*.
- The averages are here somewhat higher than for the MF methods in general.

### Mixture B

- In this mixture were the coliform bacteria *E. cloacae* and *K. oxytoca* present. Both of them possess  $\beta$ -galactosidase but not  $\beta$ -glucuronidase and are thus detected as coliform bacteria but not as *E. coli*.
- The average result is somewhat higher than for the MF-methods in general.

### Mixture C

- The strain of *E. coli* is here detected as coliform bacterium only. It possesses  $\beta$ -galactosidase but has only very weak activity of the enzyme  $\beta$ -glucuronidase, leading to negative outcome for *E. coli* within stated incubation time.
- The zero results for *E. coli* are here reckoned as correct. There was one false positive result present.
- The average for coliform bacteria is the same as for the MF methods.

### Intestinal enterococci (MF)

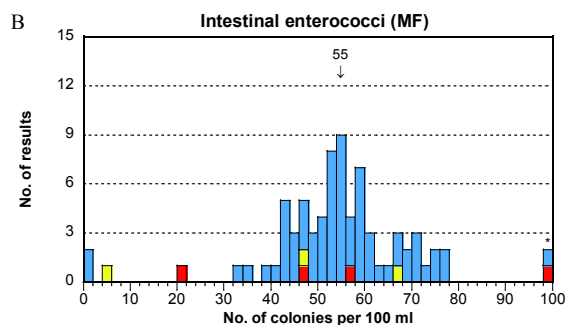
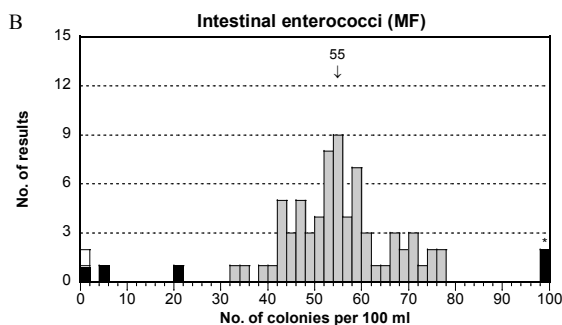
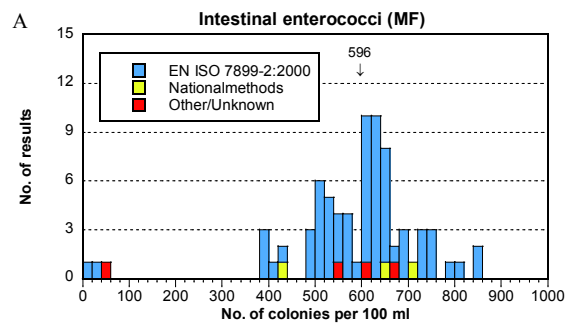
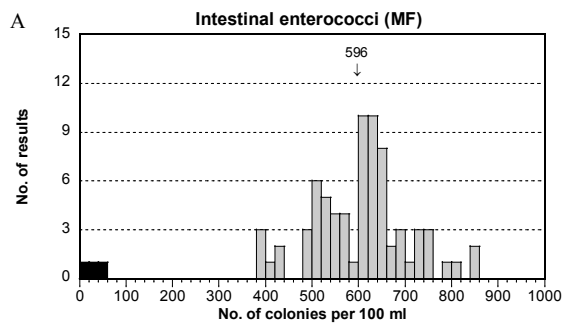
The method EN ISO 7899-2:2000 with m-Enterococcus Agar was almost always used. In only 6 cases another method reference, like national standards, has been stated. Also in these cases the medium m-Enterococcus Agar has been used as primary medium. Sometimes the medium is in the comments referred to as Slanetz & Bartley Agar, which is the same medium. Such comments are sometimes also found when EN ISO 7899-2:2000 is given as reference. In one laboratory "Enterolert" has been used, in spite of not being an MF method.

The reported temperature for incubation was always  $36 \pm 2$  °C and confirmation was performed in all cases. It was in 72% of the cases performed with Bile-esculine-azide agar (BEA Agar) as is stated in EN ISO 7899-2:2000 and in 16% performed on Bile-esculine agar (without azide; BE Agar). It is difficult to know if this difference is real or is due to terminology mixing-up. The temperature for confirmation was in 89% of the laboratories 44 °C, in 5% less than 44 °C and in 4% 44.5 °C.

Discussions about method differences are meaningless since the method for presumptive intestinal enterococci does not differ for the vast majority of the results reported. There was no difference in the confirmation outcome in relation to BEA Agar or BE Agar.

Standard	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total</b>	<b>76</b>	<b>73</b>	<b>596</b>	<b>9</b>	<b>0</b>	<b>3</b>	<b>0</b>	<b>70</b>	<b>55</b>	<b>9</b>	<b>1</b>	<b>3</b>	<b>2</b>	<b>75</b>	<b>0</b>	<b>–</b>	<b>1</b>	<b>–</b>	<b>–</b>
EN ISO 7899-2	69	67	596*	9	0	2	0	66	55	9	1	1	1	69	0	–	0	–	–
National standards	3	3	645*	–	0	0	0	2	56	–	0	1	0	2	0	–	1	–	–
Other/Unknown	4	3	603*	–	0	1	0	2	51	–	0	1	1	4	0	–	0	–	–

\* Median instead of mean value



### Mixture A

- A typical strain of *E. faecalis* was present in the mixture. The dispersion of the results was good. The colour of the colonies is often dark brow-red on m-Ent.
- Three low outliers were of unknown reason reported.

### Mixture B

- A strain of *E. durans* was present in the mixture. The dispersion of the results was generally good. The colour of the colonies is often light brow-red on m-Ent.
- Four low, out of which one false negative, and two high deviating results were obtained.
- It is known that the *E. durans* strain might give very low recovery on some membrane filters. If this has occurred, the filters need to be checked and recovery compared with that on a filter of a different batch or even brand.

### Mixture C

- No intestinal enterococcus strain was included but one false positive result was reported.

## *Pseudomonas aeruginosa* (MF)

The method EN ISO 16266:2008 – with or without modification – was used by 54 out of the 57 laboratories reporting results for this analysis. Some of the laboratories have reported the method by reference to the identical, since long time withdrawn, CEN standard EN 12780:2002, with or without modification. Incubation was always done at 36±2 °C. In 3 cases was *Pseudomonas* Isolation agar reported as primary medium. After checking the product number (OXOID, CM 559) it is evident that the medium used in fact is *Pseudomonas* Agar base/CN-agar according to the standard with added cetrимide and nalidixic acid (C/N-supplement). Even in the third case the OXOID brand is reported, but without a number. As Oxoid doesn't have a medium called *Pseudomonas* Isolation agar, the assumption that also this medium is *Pseudomonas* Agar base/CN-agar is made. However, in this case with only cetrимide added.

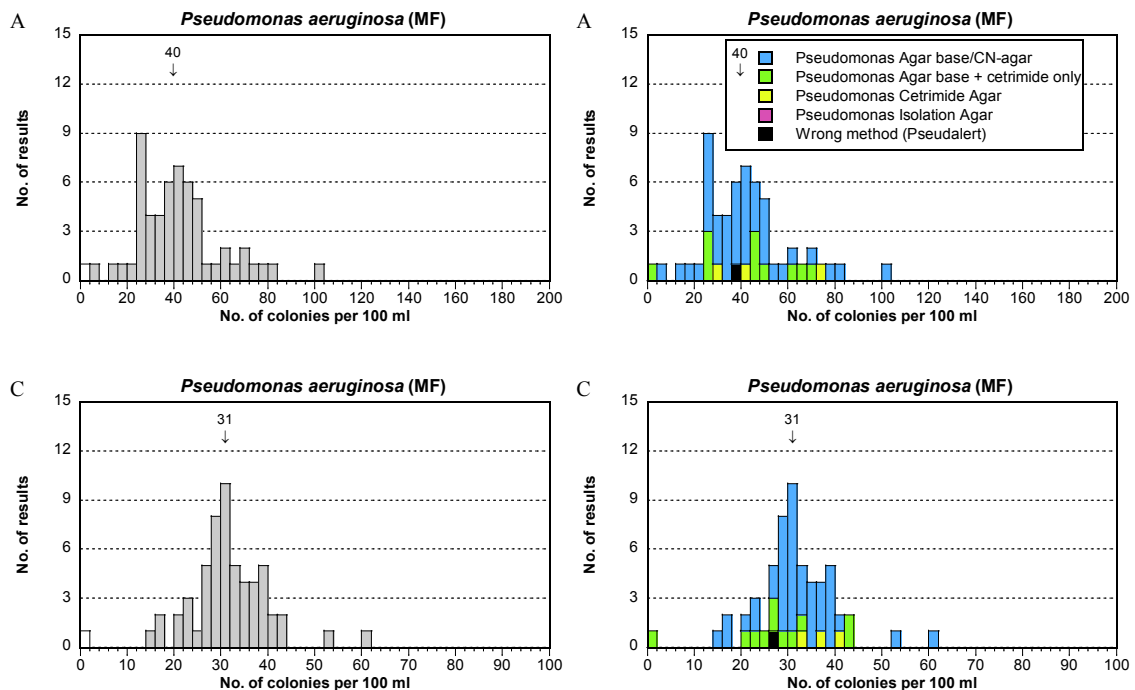
The base method and the primary cultivation medium for *P. aeruginosa* is the same for the majority of the results. Yet, the method differentiation is this time done in relation to base medium reported. The various supplements used, such as cetrимide (C) or nalidixic acid (N), are to some extent correlated to the medium stated. The medium *Pseudomonas* Cetrимide Agar reported by some laboratories is usually used in connection with methods for other matrices than drinking water.

In 42 of 53 cases have the laboratories that reported *Pseudomonas* Agar base/CN-agar used both cetrимide and nalidixic acid, while 11 laboratories used cetrимide only. All these 53 laboratories are referring to the standards EN ISO 16266:2008 or EN 12780:2002. Looking at mixture A it seems that laboratories using cetrимide only obtained somewhat higher average results than those using both cetrимide and nalidixic acid. A higher average recovery is also supported by the few results where *Pseudomonas* Cetrимide Agar is reported.

It is impossible to state any tendencies for those method properties not accounted for here, probably at least partly because the numbers of results are very few for some method variants.

Medium used	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total</b>	<b>57</b>	<b>56</b>	<b>40</b>	<b>22</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>56</b>	<b>0</b>	<b>–</b>	<b>1</b>	<b>–</b>	<b>–</b>	<b>56</b>	<b>31</b>	<b>13</b>	<b>1</b>	<b>0</b>	<b>0</b>
Ps. Agar base, C+N	42	42	39	23	0	0	0	42	0	–	0	–	–	42	31	13	0	0	0
Ps. Agar base, C	11	10	45	19	1	0	0	10	0	–	1	–	–	10	29	13	1	0	0
Ps. Cetrимide Agar	3	3	40*	–	0	0	0	3	0	–	0	–	–	3	37*	–	0	0	0
Ps. Isolation Agar	0	0	–	–	–	–	–	0	–	–	–	–	–	0	–	–	–	–	–
<b>Wrong method</b>	<b>1</b>	<b>1</b>	<b>36</b>	<b>–</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>–</b>	<b>0</b>	<b>–</b>	<b>–</b>	<b>1</b>	<b>27</b>	<b>–</b>	<b>0</b>	<b>0</b>	<b>0</b>

\* Median instead of mean value



### Mixture A

- One strain of *P. aeruginosa* with typical, blue-green colonies on PACN was included in the mixture. The colonies there also showed clear fluorescence under UV-light.
- The distribution of the results was good. One false negative result was present.

### Mixture B

- There was no *P. aeruginosa* in the mixture. One false positive result was reported.

### Mixture C

- One strain of *P. aeruginosa* was included in the mixture. The colonies were not typical as having both a blue-green and a red-brown pigment on PACN, but they still showed clear fluorescence under UV-light. The brownish colour was best visible from the reverse side of the plate, as well as in colonies transferred to an unselective medium.
- Because of the blue green pigmentation and fluorescence on PACN, no confirmation of the colonies was needed according to the standard.
- The distribution of the results was good. One false negative result was present also here.

## Culturable microorganisms 22 °C, 3 days

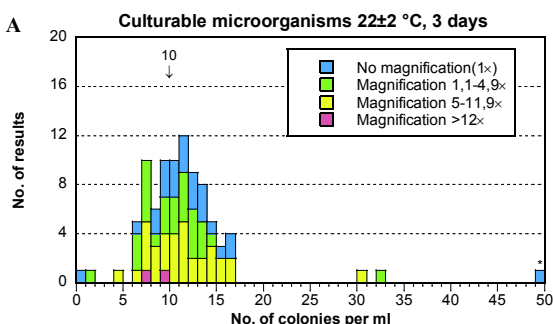
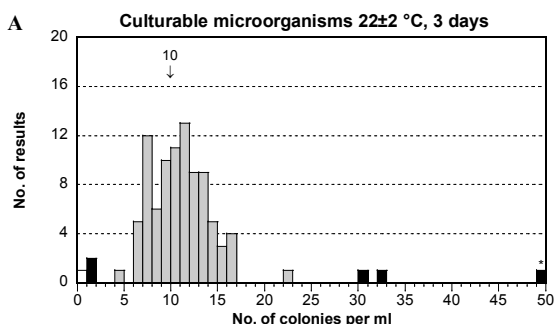
Eighty eight of the 95 laboratories performing the analysis reported EN ISO 6222:1999 as method, which prescribes the use of Yeast extract Agar. Nine laboratories used Plate Count Agar, of which 5 together with EN ISO 6222:1999. The other used national standards or "Standard methods" (5). Two laboratories used Nutrient Agar out of which one used spread plating together with EN ISO 6222:1999 and the other membrane filtration and "Nutrient pads". Four more laboratories reported spread plating, three of these in combination with 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 shown and discussed. Results are grouped for culture media and magnification for reading.

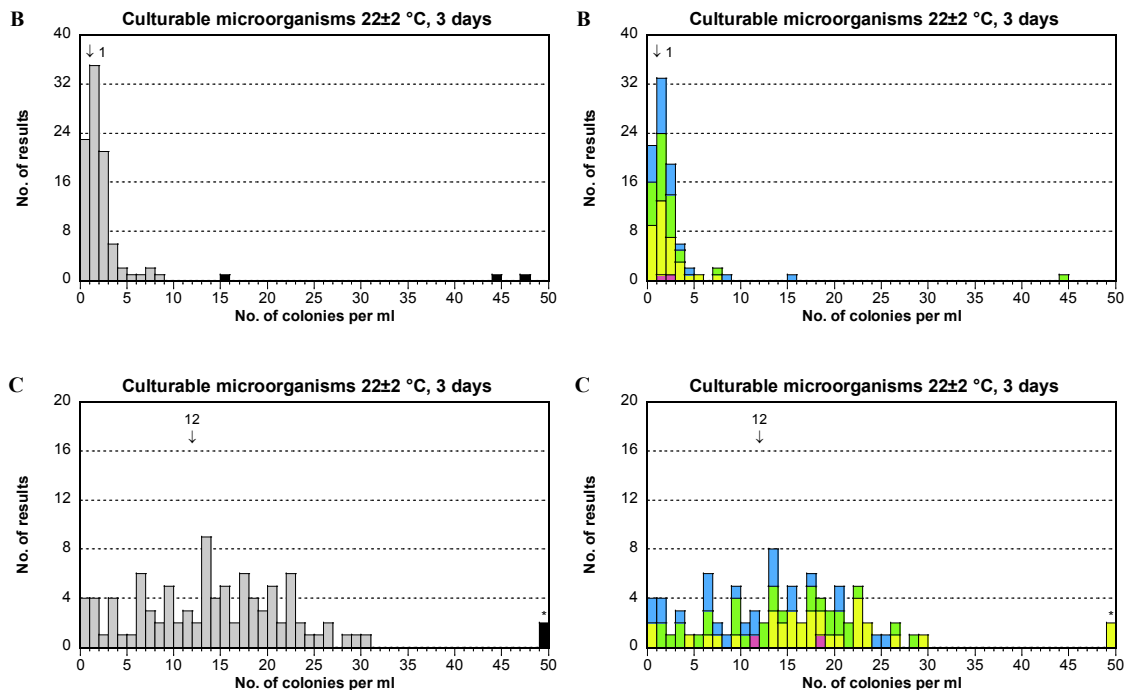
For mixture B there are too low group averages to state any differences. No method differences can be seen neither for mixture A. For mixture C the average result seems to be lower without magnification than with magnification used. Furthermore, the distribution is higher without magnification. The lowest results in average were obtained when PCA (erroneously?) was used on the basis of the standard EN ISO 6222:1999.

Group of results	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total, all results</b>	<b>95</b>	<b>89</b>	<b>0</b>	<b>108</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>92</b>	<b>1</b>	<b>70</b>	<b>-</b>	<b>-</b>	<b>3</b>	<b>93</b>	<b>12</b>	<b>38</b>	<b>0</b>	<b>0</b>	<b>2</b>
<b>EN ISO 6222</b>	<b>88</b>	<b>83</b>	<b>10</b>	<b>14</b>	<b>1</b>	<b>1</b>	<b>3</b>	<b>86</b>	<b>1</b>	<b>70</b>	<b>-</b>	<b>-</b>	<b>2</b>	<b>86</b>	<b>12</b>	<b>38</b>	<b>0</b>	<b>0</b>	<b>2</b>
<u>Medium</u>																			
Yeast extract Agar	81	78	10	14	0	1	2	80	1	70	-	-	1	79	12	34	0	0	2
Plate Count Agar	5	3	9*	-	1	0	1	4	1*	-	-	-	1	5	4	115	0	0	0
Other/Unknown	2	2	10	-	0	0	0	2	1	-	-	-	0	2	8	28	0	0	0
<u>Magnification</u>																			
None	24	22	11	12	1	0	1	23	1	74	-	-	1	24	9	47	0	0	0
1,1-4,9×	29	27	10	13	0	1	1	28	1	69	-	-	1	29	12	36	0	0	0
5-11,9×	33	32	10	15	0	0	1	33	1	74	-	-	0	31	14	33	0	0	2
> 12×	2	2	8	-	0	0	0	2	1	-	-	-	0	2	14	-	0	0	0
<b>Other method</b>	<b>7</b>	<b>6</b>	<b>11</b>	<b>23</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>6</b>	<b>1</b>	<b>66</b>	<b>-</b>	<b>-</b>	<b>1</b>	<b>7</b>	<b>12</b>	<b>36</b>	<b>0</b>	<b>0</b>	<b>0</b>

\* Median instead of mean value







### Mixture A

- All the four bacteria can grow as culturable microorganisms in low numbers. For *P. aeruginosa* even <1 cfu per ml.
- The distribution was good except for 3 low and 3 high deviating results.

### Mixture B

- The few colonies are made up of the coliform bacteria and *E. durans*.
- Due to the very low average, also a zero result is appropriate and acceptable.
- The distribution was good with only 3 high outliers.

### Mixture C

- The colonies are almost entirely made up of *P. fluorescens*. All other strains will also grow but only with low numbers.
- Unusually and unexpectedly many low results are seen from the distribution. The strain of *P. fluorescens* is known to sometimes, without good explanation, give quite scattered distribution, even though the colonies are not particularly small. Due to the many low results it was impossible to discern low outliers, only 2 high ones.

## Culturable microorganisms 36 °C, 2 days

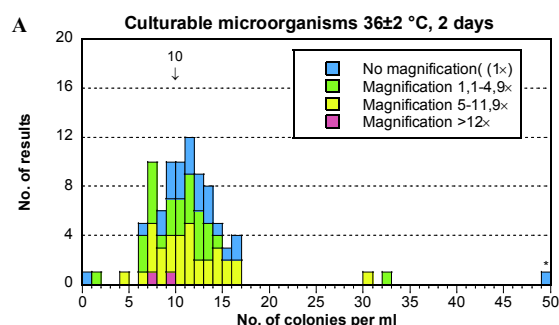
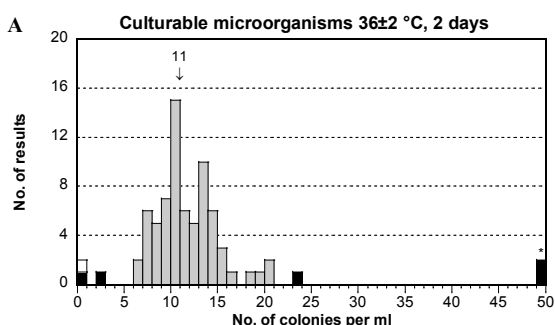
Only 4 out of 77 laboratories reported a method other than EN ISO 6222:1999. Among these 4 laboratories, one low and one high outlier were reported from one mixture each. Eight laboratories have reported Plate Count Agar, out of which 6 together with EN ISO 6222:1999, even though that standard states the use of Yeast extract Agar. The two remaining laboratories with other reference report the use of Nutrient Agar and Tryptic Soy Agar, respectively.

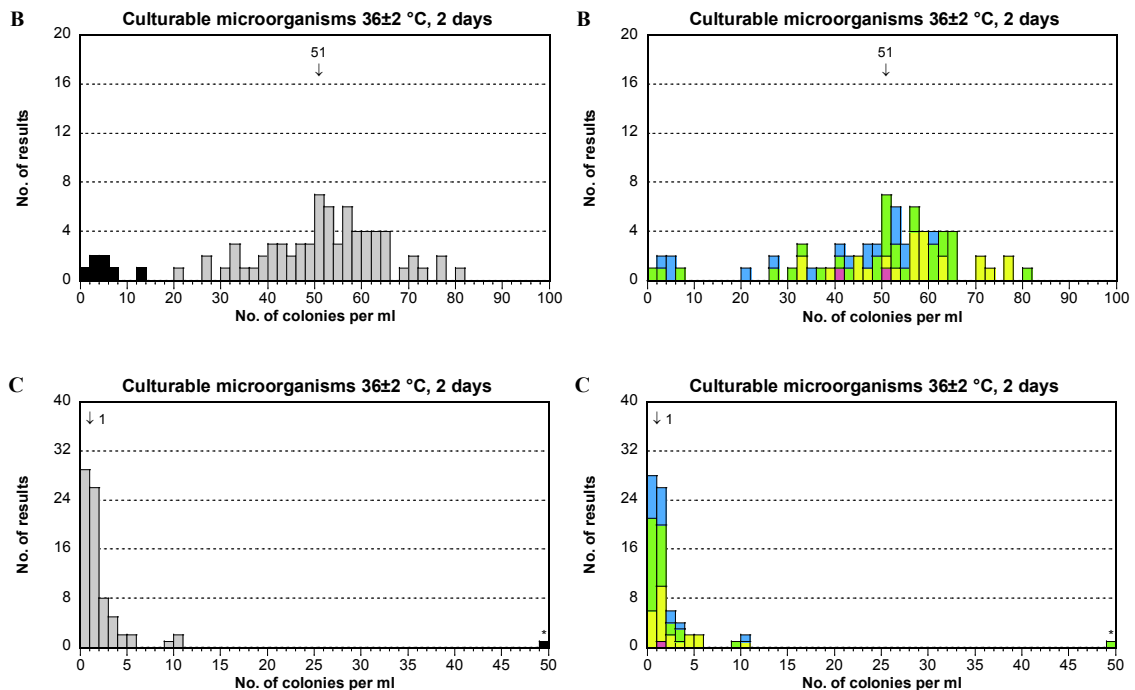
As for the analysis at 22 °C, comparisons of method variants are relevant to discuss only when EN ISO 6222:1999 was used. Also here, the results are presented in relation to culture media and magnification for reading. The 4 results with other method reference are, thus, not shown in the histogram for magnifications.

As for mixture C at 22 °C, the average result for mixture B seems to be somewhat lower when no magnification was used compared to when some magnification was used.

Group of results	Tot n	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
<b>Total, all results</b>	<b>77</b>	<b>70</b>	<b>11</b>	<b>14</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>70</b>	<b>51</b>	<b>13</b>	<b>0</b>	<b>7</b>	<b>0</b>	<b>75</b>	<b>1</b>	<b>96</b>	<b>–</b>	<b>–</b>	<b>1</b>
<b>EN ISO 6222</b>	<b>73</b>	<b>67</b>	<b>11</b>	<b>14</b>	<b>1</b>	<b>2</b>	<b>2</b>	<b>67</b>	<b>51</b>	<b>13</b>	<b>0</b>	<b>6</b>	<b>0</b>	<b>71</b>	<b>1</b>	<b>99</b>	<b>–</b>	<b>–</b>	<b>1</b>
<u>Medium</u>																			
Yeast extract Agar	65	61	11	13	0	2	2	60	51	12	0	5	0	64	1	101	–	–	1
Plate Count Agar	6	4	11*	–	1	0	0	5	54	14	0	1	0	5	0	91	–	–	0
Other/Unknown	2	2	15	–	0	0	0	2	59	–	0	0	0	2	1	–	–	–	0
<u>Magnification</u>																			
None	17	15	10	12	1	0	1	14	44	14	0	3	0	17	1	107	–	–	0
1,1–4,9×	31	28	12	13	0	2	1	28	52	12	0	3	0	30	0	118	–	–	1
5–11,9×	23	23	11	16	0	0	0	23	56	12	0	0	0	23	1	79	–	–	0
> 12×	2	1	10	–	0	0	0	2	46	–	0	0	0	1	1	–	–	–	0
<b>Other method</b>	<b>4</b>	<b>3</b>	<b>9*</b>	<b>–</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>3</b>	<b>43*</b>	<b>–</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>4</b>	<b>2*</b>	<b>–</b>	<b>–</b>	<b>–</b>	<b>0</b>

\* Median instead of mean value





### Mixture A

- All four bacteria can grow as culturable microorganisms in quite low numbers also at this temperature as they can at 22 °C. For *P. aeruginosa* <1 cfu per ml.
- The distribution was good and the dispersion the same as for the same analysis at 22 °C. Even here were 3 low and 3 high deviating results present.

### Mixture B

- All bacteria strains in the mixture appear at 36±2 °C and contribute to the total number of culturable microorganisms. The considerably higher average here compared to at 22 °C is because also the strain of *S. capitis*, present in highest concentration, grows at 36 but not at 22 °C.
- The distribution reveals unusually and unexpectedly many low results and usually doesn't look like this when *S. capitis* is used. Seven of the low results could here be identified as outliers, indicating that there might be certain circumstances in those laboratories that obtained such results. As a consequence, the dispersion (CV) for the accepted results still turned out to be small.

### Mixture C

- The few colonies originate from the other three strains except the strain of *P. fluorescens* that doesn't grow at 36±2 °C.
- Due to the very low average, also a zero result is appropriate and acceptable.
- The distribution was good with only one high outlier.

## **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 assessment is basically a clear indication of 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**

When whole samples seem to have been mixed up, the corresponding sample numbers are hatched in annex A. One laboratory (7282) seems to have mixed up the vials for mixture A and B. A couple of laboratories (3164, 8998) have probably mixed up sample/results for individual analyses. One laboratory has erroneously reported results with common logarithms, leading to several low outliers. Furthermore, a number of laboratories have several deviating results. No laboratory seems to have calculated the results for another volume than asked for.

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

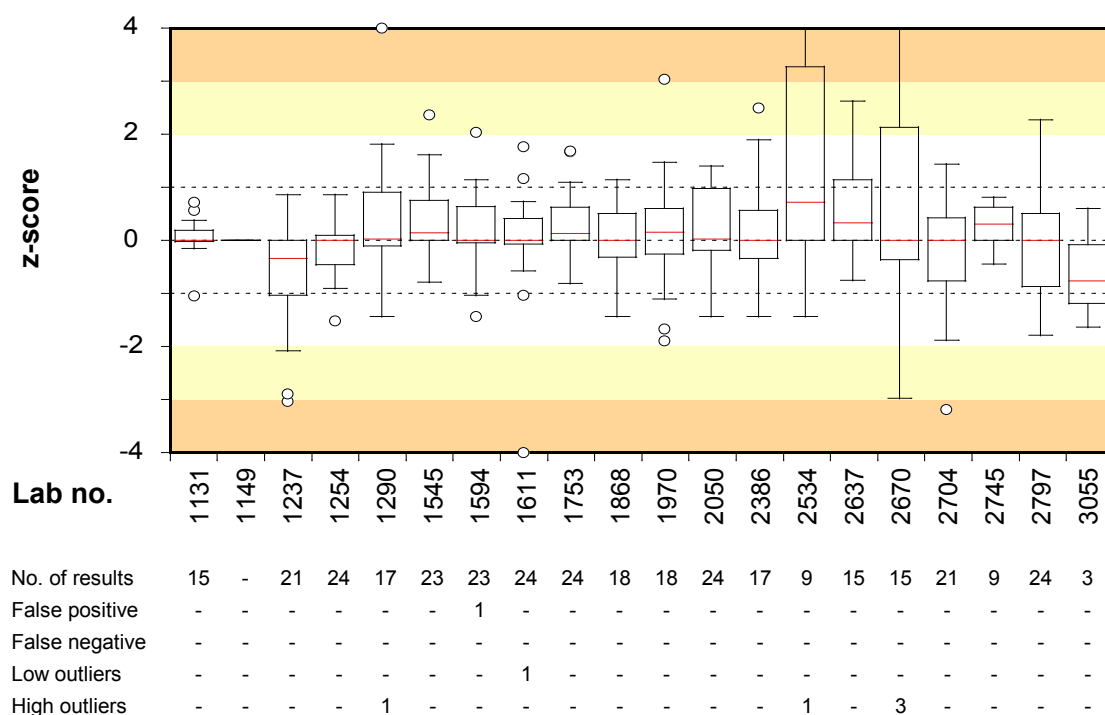
The square root transformed results of the laboratories are calculated to standard scores, z-scores, to be comparable between analyses. They are shown in annex B but not further evaluated. They are given explicitly to facilitate the follow-up process for laboratories using z-scores in control charts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

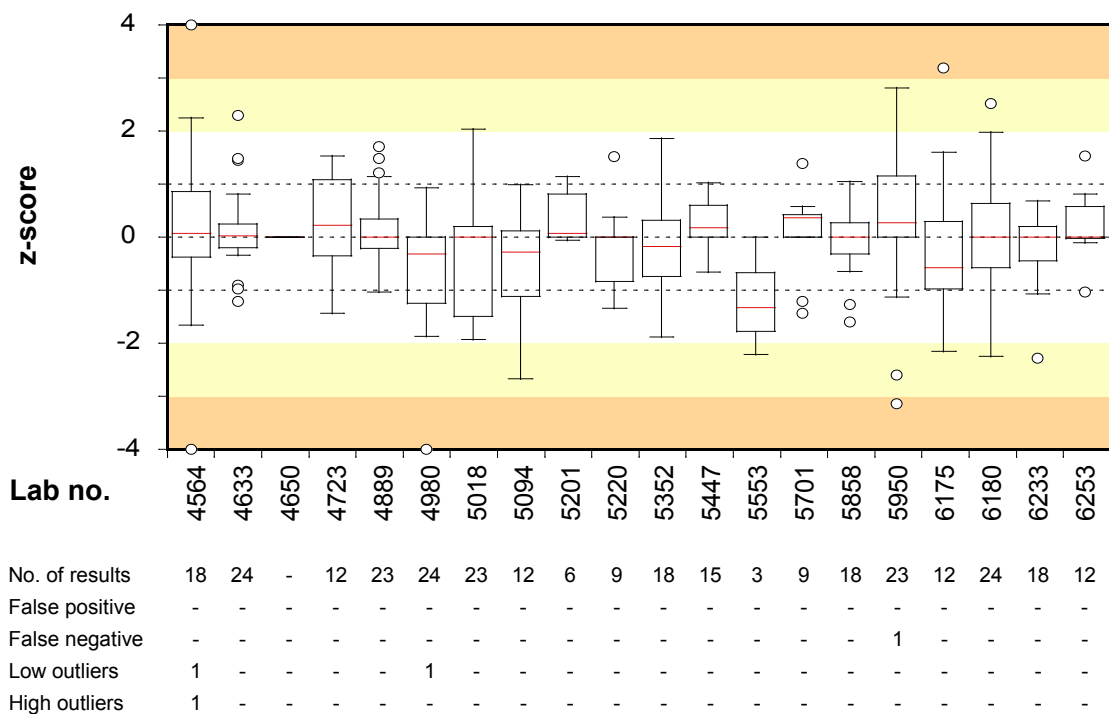
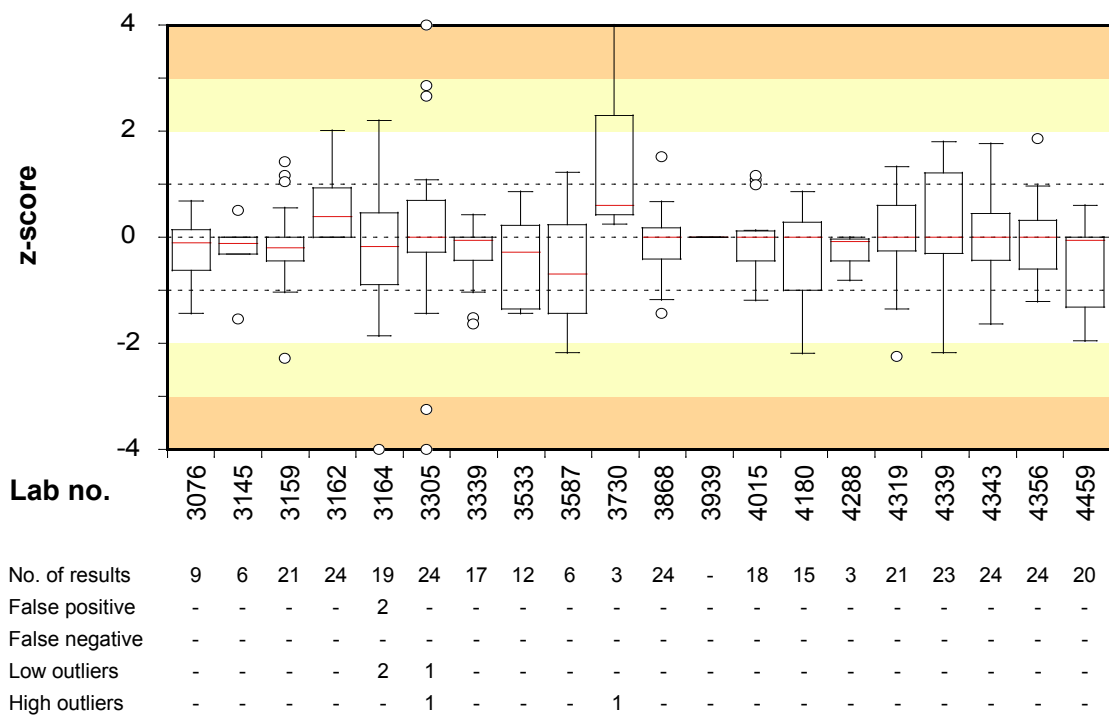
The z-scores are the base for the box plots. The range of the z-scores for each laboratory is shown by a rectangle (box) and lines and/or circles above and beneath the box. The smaller the range from lowest to highest value is in the plot and the more centred around zero the values are, the better is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

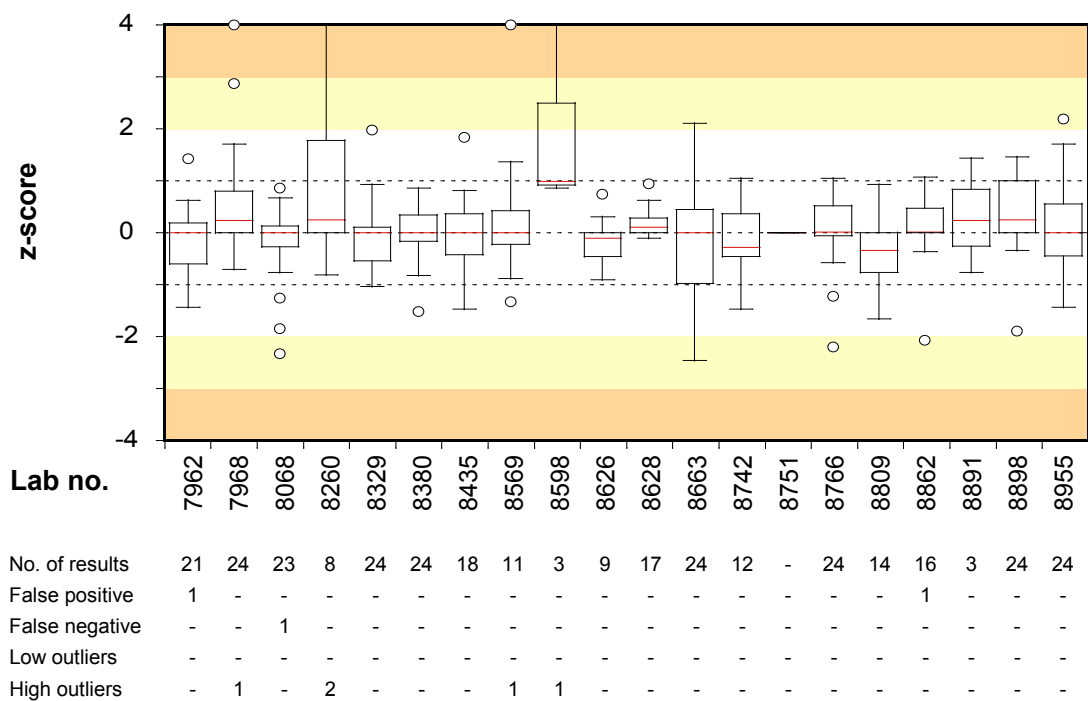
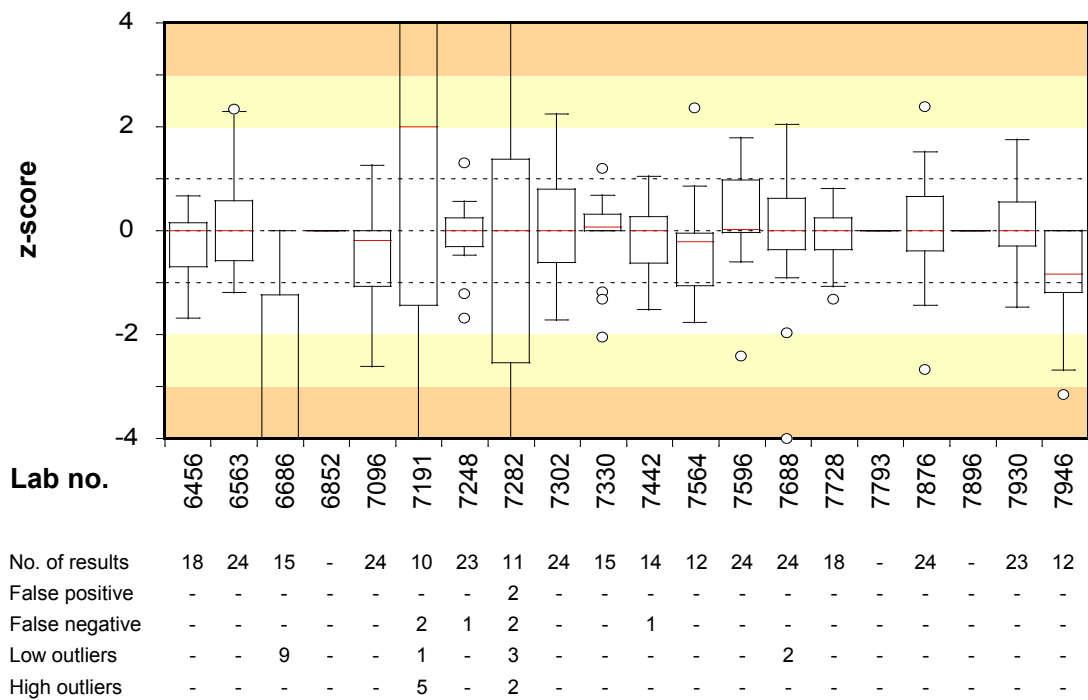
### Box plots and numbers of deviating results for each participating laboratory

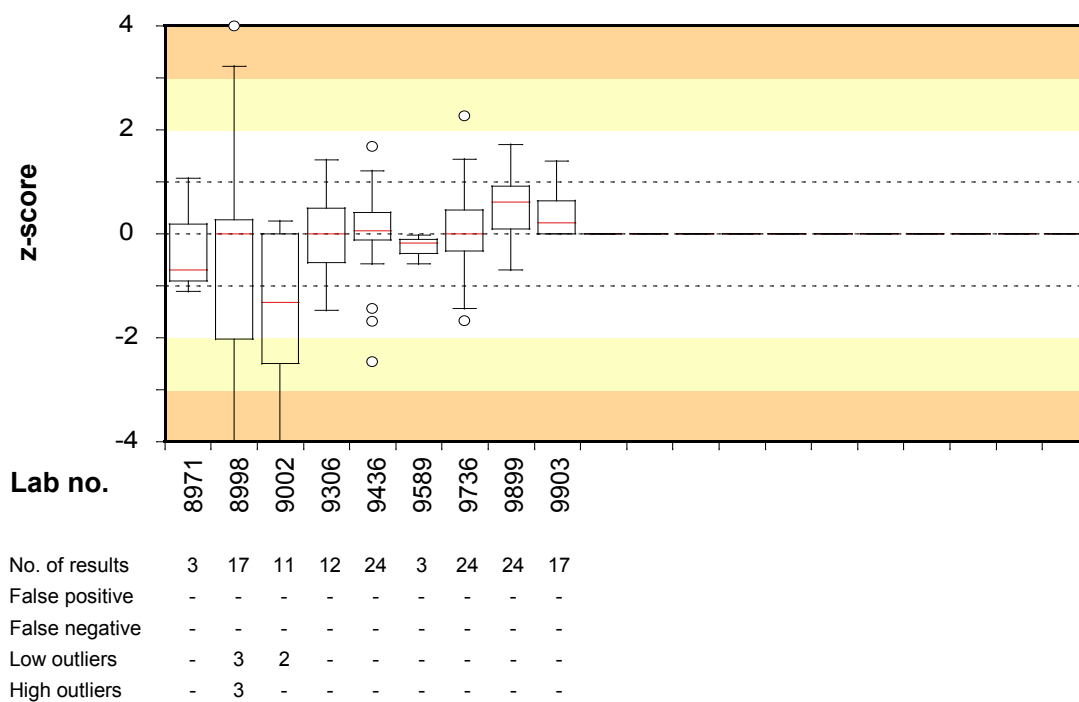
- Z-scores are calculated from the formula  $z = (x - mv) / s$  (see annex A).
- False results do not generate z-scores and are not included in 'No. of results'.
- The outliers are included in the plots after recalculation to standardised values with the same standard deviation (s) as the rest of the 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.

\*  $< [\text{smallest value of the box} - 1.5 \times (\text{largest value of the box} - \text{smallest value of the box})]$  or  $> [\text{largest value of the box} + 1.5 \times (\text{largest value of the box} - \text{smallest value of the box})]$











## 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 <sup>1</sup>	Microorganisms	Strain collection no.		cfu/100 ml <sup>2</sup>
		SLV (own)	CCUG <sup>3</sup>	
A	<i>Escherichia coli</i>	082	45097	200
	<i>Citrobacter freundii</i>	424	-	220
	<i>Enterococcus faecalis</i>	051	45101	680
	<i>Pseudomonas aeruginosa</i>	453	551	75
B	<i>Enterobacter cloacae</i>	451	30205	22
	<i>Klebsiella oxytoca</i>	553	–	20
	<i>Enterococcus durans</i>	078	44816	61
	<i>Staphylococcus capitis</i>	463	35173	89 *
C	<i>Escherichia coli</i>	295	–	32
	<i>Aeromonas hydrophila</i>	081	45103	16
	<i>Pseudomonas aeruginosa</i>	xxx <sup>4</sup>	–	51
	<i>Pseudomonas fluorescens</i>	535	45106	26 *

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 Culture Collection University of Gothenburg, Sweden

4 not yet included in the collection

\* 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 more than 10 dispensed aliquots in vials of each

mixture. The largest differences between vials were between 2 and 9 mg in the mixtures. The largest accepted difference is 15 mg (3%).

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.

**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<sup>1</sup>

Analysis parameter <i>Method standard for analysis</i>	Mixture								
	A			B			C		
	cfu	$I_2$	T	cfu	$I_2$	T	cfu	$I_2$	T
Coliform bacteria (MF) <i>m-Endo Agar LES according to SS 028167</i>	56 <sup>a</sup>	1.2	1.3	42	1.3	1.4	48	1.3	1.4
Suspected thermotolerant colif. bact. (MF) <i>m-FC Agar, 44 °C according to SS 028167</i>	23 <sup>a</sup>	0.8	1.4	0	–	–	27	1.0	1.5
<i>Escherichia coli</i> (MF) <i>m-Endo Agar LES according to SS 028167</i>	27 <sup>a</sup>	1.0	1.5	–	–	–	32	0.7	1.3
Intestinal enterococci (MF) <i>m-Enterococcus Agar acc. to SS-EN ISO 7899-2:2000</i>	91 <sup>a</sup>	2.5	1.4	61	1.2	1.3	–	–	–
<i>Pseudomonas aeruginosa</i> (MF) <i>Pseudomonas Agar base with cetrimide and nalidixic acid according to SS-EN ISO 16288:2008</i>	10 <sup>a</sup>	1.6	2.2	–	–	–	51	1.2	1.3
Culturable microorg., 2d 37 °C (pour plate) <i>Yeast extract Agar according to SS-EN ISO 6222:1999</i>	30 <sup>b</sup>	1.1	1.4	74	1.4	1.3	1 <sup>d</sup>	1.1	6.4
Culturable microorg., 3d 22 °C (pour plate) <i>Yeast extract Agar according to SS-EN ISO 6222:1999</i>	29 <sup>b</sup>	0.3	1.2	<1 <sup>c</sup>	1.2	– <sup>c</sup>	27	1.2	1.5

1 n=10 vials analysed in duplicate, normally 100 ml for MF and 1 ml for pour plate, 21, 14 and 11 weeks ahead of the testing round start for the mixtures A, B and C, respectively

a Determined for the volume 5 ml after reconstitution of the vial content in 300 ml diluent

b Determined per ml after reconstitution of the vial content in 300 ml diluent

c One zero result from the two analyses in each of six of the ten vials, and also zero results from both of the two analyses in one vial implying that no T value can be calculated; with these duplicate zero results excluded we get  $I_2 = 0.9$  and T = 5.9 – that is a high T value due to the six remaining single zero results

d One zero result from the two analyses in each of four of the ten vials – resulting in the high T value – No target organism and thus no analysis

## 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](http://www2.slv.se/absint).

## References

1. Anonymous 2014. Scheme protocol, Microbiology, Drinking water & Food, 3<sup>rd</sup> 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. This is also valid for results in **shaded columns**. 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

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
1131	3 1 2	310	38	33	310	38	26	-	-	-	213	0	26	411	32	28	214	0	0
1149	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1237	3 2 1	-	-	-	115	32	20	40	1	25	30	0	20	-	37	30	-	0	-
1254	2 3 1	280	40	25	280	40	25	-	-	-	140	0	25	330	33	21	180	0	0
1290	1 2 3	-	-	-	265	34	25	-	-	-	123	0	<u>0</u>	-	-	-	-	-	-
1545	3 1 2	460	28	46	460	28	28	230	0	28	230	0	<u>0</u>	394	43	29	243	0	0
1594	1 2 3	360	53	28	360	53	28	145	0	21	185	<b>28</b>	28	366	49	22	260	0	0
1611	1 2 3	370	50	30	350	50	30	138	0	31	150	0	30	387	43	27	248	0	0
1753	2 1 3	410	49	30	410	49	30	-	-	-	200	0	30	435	45	31	261	0	0
1868	3 2 1	317	30	25	317	30	25	-	-	-	162	<1	25	342	48	25	164	<1	<1
1970	1 2 3	400	34	50	230	34	30	400	34	50	230	0	30	-	-	-	-	-	-
2050	2 1 3	-	-	-	400	38	25	-	-	-	245	0	25	343	49	35	161	0	0
2386	3 1 2	440	38	49	440	38	49	260	0	0	260	0	<u>0</u>	-	-	-	-	-	-
2534	1 3 2	376	81	101	376	<b>81</b>	57	-	-	-	310	<1	57	-	-	-	-	-	-
2637	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	360	36	29	250	<1	<1
2670	2 1 3	-	-	-	270	44	26	-	-	-	270	0	26	-	-	-	-	-	-
2704	2 3 1	-	-	-	330	11	25	-	-	-	160	0	25	288	34	21	164	<1	<1
2745	2 1 3	340	34	32	340	34	32	220	0	32	220	0	32	-	-	-	-	-	-
2797	3 2 1	240	29	33	240	29	19	230	<1	34	160	<1	34	226	34	47	136	<1	<1
3055	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3076	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3145	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	345	38	17	236	0	0
3159	1 3 2	-	-	-	290	16	22	-	-	-	140	0	22	429	36.4	25.4	288	<1	<1
3162	3 1 2	390	40	29	390	40	29	-	-	-	175	0	29	488	52	28	236	0	0
3164	2 1 3	286	38	46	286	38	46	-	-	-	152	<b>14</b>	19	365	48	26	228	0	0
3305	3 1 2	-	-	-	<b>45</b>	30	25	-	-	-	21	<1	25	690	46	36	<b>490</b>	<1	<1
3339	2 1 3	-	-	-	280	35	17	-	-	-	140	0	<u>0</u>	-	-	-	-	-	-
3533	1 3 2	-	-	-	340	22	18	-	-	-	200	0	18	-	-	-	-	-	-
3587	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3730	3 2 1	300	36	40	-	-	-	210	0	35	-	-	-	-	-	-	-	-	-
3868	1 3 2	450	39	31	450	39	31	180	0	19	180	0	19	380	41	24	220	0	0
3939	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4015	2 3 1	300	34	42	300	34	26	-	-	-	118	0	26	276	31	36	155	0	0
4180	1 3 2	-	-	-	235	35	34	-	-	-	175	0	32	-	-	-	-	-	-
4288	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4319	1 2 3	360	32	32	330	32	18	120	0	22	147	0	13	509	34	20	277	0	0
4339	3 2 1	420	42	41	420	42	25	174	11	33	210	0	<u>0</u>	344.8	55.4	22.8	193.5	0	0
4343	3 1 2	279	40	29	279	40	24	-	-	-	137	0	24	291	55	28	225	0	0
4356	2 1 3	360	37	24	360	37	22	71	0	20	220	0	22	340	36	35	170	0	0
4459	1 2 3	309	20	21	309	20	21	-	-	-	145	0	<u>0</u>	261	41	21	122	0	0
4564	3 1 2	-	-	-	350	20	34	-	-	-	140	0	34	-	-	-	-	-	-
4633	2 3 1	-	-	-	336	35	39	80	0	24	173	0	39	379	38	21	199	0	0
4650	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4723	3 1 2	400	44	22	400	44	22	-	-	-	214	0	22	-	-	-	-	-	-
4889	3 2 1	-	-	-	320	40	37	-	-	-	160	0	<u>0</u>	490	36	26	220	0	0
4980	1 2 3	700	19	25	180	19	25	120	0	24	120	0	24	453	41	18	222	<1	<1
5018	3 1 2	220	38	21	176	38	21	-	-	-	154	0	<u>0</u>	236	41	17	135	0	0
5094	3 1 2	400	35	24	400	35	24	60	0	26	60	0	26	-	-	-	-	-	-
5201	2 1 3	190	34	28	-	-	-	-	-	-	160	0	28	-	-	-	-	-	-
5220	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	410.6	32.3	39.9	147	0	0
5352	3 2 1	327	31	52	237	31	25	119	31	25	119	<1	25	-	-	-	-	-	-
5447	3 2 1	-	-	-	370	39	35	-	-	-	190	0	35	-	-	-	-	-	-
5553	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5701	1 3 2	350	46	30	350	46	30	-	-	-	203	0	30	-	-	-	-	-	-
5858	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	240	45	25	150	<1	<1
5950	3 2 1	110	47	<1	110	47	<b>&lt;1</b>	121	<1	26	246	<1	29	276	35	32	276	<1	<1
6175	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	200	36	22	165	0	0
6180	2 3 1	300	37	30	300	37	23	160	0	21	210	0	23	400	24	22	150	0	0
6233	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	376	34	21	221	0	0
6253	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	370	45	40	160	0	0
6456	2 1 3	-	-	-	350	33	26	-	-	-	85	0	16	420	41	31	245	0	0
6563	1 3 2	270	37	47	270	37	47	-	-	-	270	0	47	386	39	20	237	0	0
6686	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	<b>2.58</b>	<b>1.66</b>	<b>1.49</b>	<b>2.32</b>	<1	<1
6852	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7096	3 2 1	230	31	30	230	31	26	-	-	-	140	<1	26	170	25	24	109	<1	<1
7191	3 1 2	780	300	620	<b>780</b>	<b>300</b>	<b>620</b>	780	0	620	<b>780</b>	0	<b>620</b>	-	-	-	-	-	-
7248	1 3 2	430	38	29	430	38	24	<1	<1	16	<b>&lt;1</b>	<1	16	349	37	31	214	<1	<1
7282	<del>1 3 2</del>	-	-	-	-	-	-	-	-	-	<b>0</b>	<b>155</b>	29	-	-	-	-	-	-
7302	2 3 1	342	41	58	342	41	46	152	<1	21	205	<1	46	309	36	36	187	<1	<1
7330	2 1 3	-	-	-	-	-	-	-	-	-	58	0	19	-	-	-	-	-	-
7442	2 1 3	278	21	29	278	21	<b>0</b>	-	-	-	181	0	29	295	35	34	164	0	0
Mean					<b>314</b>	<b>33</b>	<b>27</b>				<b>163</b>	<b>0</b>	<b>16</b>	<b>375</b>	<b>40</b>	<b>27</b>	<b>209</b>	<b>0</b>	<b>0</b>
CV (%)					13	13	14				20	-	58	13	10	14	12	-	-

are excluded, as well as other outliers, in the summarizing 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 are obtained as the square roots of the 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.

Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. <i>Pseudomonas aeruginosa</i> (MF)			<i>Pseudomonas aeruginosa</i> (MF)			Total plate count 22 °C, 3 days			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	A	B	C	
-	-	-	-	-	-	-	-	-	-	-	-	11	1	13	-	-	-	1131
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1149
-	-	-	400	40	0	-	-	-	25	0	20	13	1	20	10	63	0	1237
520	53	0	520	53	0	18	0	31	18	0	31	13	2	17	11	57	1	1254
-	-	-	782	55	0	-	-	34	78	0	34	12	0	21	15	50	60	1290
600	47	0	600	47	0	65	0	27	65	0	27	14	7	17	9	63	1	1545
720	49	0	720	49	0	40	0	35	40	0	35	10	0	19	11	65	0	1594
610	49	0	610	49	0	48	0	41	48	0	41	10	1	18	2	49	0	1611
600	55	0	600	55	0	75	0	32	75	0	32	8	1	13	10	50	3	1753
649	63	<1	649	63	<1	-	-	-	-	-	-	14	0	22	-	-	-	1868
630	52	0	630	52	0	70	0	60	70	0	60	9	2	18	6	32	1	1970
-	-	-	727	55	0	-	-	-	31	0	37	10	0	17	15	71	1	2050
480	52	0	480	52	0	80	0	30	80	0	30	8	0	17	10	52	0	2386
-	-	-	-	-	-	-	-	-	-	-	-	11	<1	3	-	-	-	2534
-	-	-	720	58	<1	-	-	-	-	-	-	16	8	24	20	42	3	2637
-	-	-	630	42	0	-	-	-	-	-	-	80	15	0	260	20	10	2670
-	-	-	640	65	0	-	-	-	-	-	-	9	4	1	13	60	3	2704
-	-	-	-	-	-	-	-	-	-	-	-	9	2	9	-	-	-	2745
740	53	<1	740	53	<1	48	<1	39	48	<1	39	7	2	15	12	61	<1	2797
-	-	-	-	-	-	-	-	-	-	-	-	6	2	6	-	-	-	3055
-	-	-	-	-	-	30	0	29	30	0	29	10	0	13	9	57	2	3076
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3145
-	-	-	600	67	0	-	-	-	-	-	-	9	3	10	10	51	0	3159
600	73	0	600	73	0	54	0	31	54	0	31	16	1	22	18	58	2	3162
420	4	60	420	4	60	-	-	-	-	-	-	13	2	6	9	4	0	3164
620	53	<1	620	53	<1	-	-	-	100	<1	30	11	<1	22	12	60	<1	3305
-	-	-	550	59	0	-	-	-	38	0	28	6	1	12	10	53	0	3339
-	-	-	500	49	0	-	-	-	-	-	-	13	0	13	-	-	-	3533
-	-	-	-	-	-	-	-	-	-	-	-	11	<1	25	10	27	<1	3587
-	-	-	-	-	-	-	-	-	-	-	-	30	2	14	-	-	-	3730
500	51	0	500	51	0	40	0	29	40	0	29	10	0	15	10	42	0	3868
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3939
608	67	0	608	67	0	-	-	-	-	-	-	9	1	22	-	-	-	4015
-	-	-	500	55	0	-	-	-	15	0	16	-	-	-	12	35	2	4180
-	-	-	-	-	-	-	-	-	-	-	-	8	1	11	-	-	-	4288
560	54	0	560	54	0	-	-	-	-	-	-	14	2	17	13	65	1	4319
570	70	0	570	70	0	70	0	42	70	0	42	7	2	26	15	27	0	4339
532	55	0	532	55	0	27	0	29	27	0	29	6	2	13	13	71	4	4343
490	75	0	490	75	0	27	0	32	27	0	32	7	1	19	11	51	1	4356
655	39	0	655	39	0	-	-	-	-	-	-	11	2	2	10	33	1	4459
-	-	-	850	140	0	-	-	-	28	0	22	11	3	13	10	4	1	4564
-	-	-	855	55	0	-	-	-	25	0	32	7	2	20	10	49	1	4633
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4650
636	56	0	627	56	0	-	-	-	-	-	-	15	0	29	-	-	-	4723
-	-	-	510	58	0	-	-	-	33	0	29	16	1	15	16	48	0	4889
660	44	0	660	44	0	23	0	21	23	0	21	6	1	9	14	6	<1	4980
620	77	0	620	77	0	26	0	36	26	0	36	6	0	1	14	65	1	5018
800	60	0	-	-	-	-	-	-	-	-	-	8	1	0	14	37	0	5094
-	-	-	-	-	-	-	-	-	-	-	-	14	1	20	-	-	-	5201
-	-	-	547.5	46.5	0	24.6	0	21.6	-	-	-	-	-	-	-	-	-	5220
560	75	<1	560	75	<1	46	<1	50	46	<1	30	12	2	1	14	38	<1	5352
-	-	-	530	51	0	-	-	-	-	-	-	12	1	13	10	55	1	5447
-	-	-	390	42	0	-	-	-	-	-	-	-	-	-	-	-	-	5553
-	-	-	-	-	-	-	-	-	-	-	-	7	0	12	-	-	-	5701
545	54	<1	545	54	<1	45	<1	26	45	<1	26	12	3	14	11	57	1	5858
636	61	<1	636	61	<1	63	<1	29	63	<1	29	4	1	19	19	72	10	5950
-	-	-	-	-	-	-	-	-	-	-	-	22	2	30	7	43	0	6175
500	76	0	500	76	0	40	0	40	40	0	40	13	2	5	20	80	1	6180
655	34	0	655	34	0	35	0	23	35	0	23	9	1	13	13	54	2	6233
-	-	-	630	60	0	-	-	-	-	-	-	10	1	20	-	-	-	6253
-	-	-	-	-	-	-	-	-	-	-	-	7	1	13	9	46	0	6456
480	53	0	480	53	0	27	0	24	27	0	24	13	1	4	13	44	3	6563
-	-	-	2.75	1.6	<1	-	-	-	-	-	-	1.18	0	1.26	0.85	1.75	0	6686
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6852
570	68	<1	570	68	<1	24	<1	16	24	<1	16	11	1	7	7	52	2	7096
-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	0	2	0	7191
646	50	<1	646	50	<1	46	<1	30	46	<1	30	7	1	16	10	51	1	7248
-	-	-	54	700	0	-	-	-	0	46	23	1	6	8	70	12	2	7282
432	42	<1	432	42	<1	63	<1	37	63	<1	37	10	<1	23	8	59	<1	7302
-	-	-	603	56	0	-	-	-	47	0	33	11	2	3	11	68	2	7330
736	75	0	-	-	-	48	0	30	-	-	-	10	3	20	-	-	-	7442
			596	55	0				40	0	31	10	1	12	11	51	1	Mean
			9	9	-				22	-	13	15	70	38	14	13	96	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
7564	2	1	3	-	-	-	230	31	34	-	-	-	150	<1	26	-	-	-	-	-	-
7596	2	1	3	390	34	31	390	34	31	133	0	36	133	0	36	490	23	36	250	0	0
7688	2	1	3	-	-	-	300	18	23	-	-	-	140	0	3.07	580	57	21	326	0	0
7728	3	2	1	-	-	-	320	25	29	-	-	-	220	0	29	-	-	-	-	-	-
7793	2	1	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7876	1	3	2	281	39	38	281	39	38	50	<1	25	112	<1	38	454	45	27	224	<1	<1
7896	3	1	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7930	2	1	3	370	39	23	370	39	23	-	-	-	296	0	0	429	36	31	288	0	0
7946	3	1	2	150	51	27	133	26	19	170	35	10	125	0	0	-	-	-	-	-	-
7962	2	3	1	330	36	36	330	36	25	110	0	17	130	4	0	365	44	23	161	0	0
7968	1	2	3	360	27	25	360	27	25	97	0	21	220	0	25	551	97	53	298	0	0
8068	2	1	3	-	-	-	220	35	28	-	-	-	66	0	28	440	34	22	210	0	0
8260	3	1	2	367	78	29	360	76	29	167	52	<1	167	<1	<1	-	-	-	-	-	-
8329	3	1	2	274	30	23	274	30	23	-	-	-	171	0	23	387	57	28	192	0	0
8380	2	1	3	290	21	33	290	21	26	-	-	-	198	0	26	359	37	31	200	0	0
8435	2	1	3	-	-	-	310	32	30	-	-	-	220	0	30	-	-	-	-	-	-
8569	3	1	2	360	37	40	215	37	21	190	0	30	190	0	0	-	-	-	-	-	-
8598	3	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8626	3	1	2	380	32	41	340	29	33	110	0	25	110	0	25	-	-	-	-	-	-
8628	1	2	3	-	-	-	330	35	30	-	-	-	160	0	0	-	-	-	-	-	-
8663	3	1	2	460	37	20	370	37	17	27	0	20	230	0	17	440	34	12	330	0	0
8742	3	1	2	-	-	-	390	30	25	-	-	-	200	<1	25	-	-	-	-	-	-
8751	2	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8766	2	1	3	318	28	35	318	28	35	236	10	45	191	0	35	367	40	27	210	0	0
8809	1	3	2	270	20	23	257	20	23	-	-	-	140	0	0	-	-	-	-	-	-
8862	2	3	1	319	36	26	319	36	26	-	-	-	164	0	0	392	37	14	210	0	2
8891	2	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8898	3	2	1	445	31	50	445	31	34	-	-	-	264	0	34	484	42	31	203	0	0
8955	1	3	2	-	-	-	330	38	22	120	0	26	170	0	22	370	59	32	190	0	0
8971	3	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8998	2	3	1	98	26	20	98	26	12	-	-	-	59	0	0	285.1	42	27.5	58	0	0
9002	3	1	2	-	-	-	72	15	13	-	-	-	125	0	0	-	-	-	-	-	-
9306	2	1	3	-	-	-	-	-	-	-	-	-	-	-	-	417	34	39	195	0	0
9436	1	3	2	336	34	23	336	34	23	43	0	16	43	0	16	367	36	30	275	0	0
9589	1	2	3	-	-	-	300	28	27	-	-	-	-	-	-	-	-	-	-	-	-
9736	2	1	3	527	37	51	527	37	28	-	-	-	264	0	28	357	52	24	252	0	0
9899	2	1	3	380	45	34	380	45	34	-	-	-	180	0	34	544	46	36	254	0	0
9903	1	3	2	368	33	50	368	33	30	205	0	19	205	0	0	-	-	-	-	-	-

n	58	58	58	81	81	81	35	35	35	83	83	83	60	61	61	60	61	60
Min	98	19	0	45	11	0	0	0	0	0	0	0	2.58	1.66	1.49	2.32	0	0
Max	780	300	620	780	300	620	780	52	620	780	155	620	690	97	53	490	0	2
Median	346	37	30	330	34.5	26	138	0	25	168.5	0	26	370	38	27.5	214	0	0
Mean				314	33	27				163	0	27	375	40	27	209	0	0
CV (%)				13	13	14				20	-	14	13	10	14	12	-	-
False positive				0	0	0				0	4	0	0	0	0	0	0	1
False negative				0	0	2				2	0	0	0	0	0	0	0	0
Outliers, low				3	0	0				0	0	1	1	1	1	2	0	0
Outliers, high				1	3	1				1	0	1	0	1	0	1	0	0
Low limit OK	98	19	0	110	11	12	0	0	0	21	0	13*	170	23	12	109	0	0
High limit OK	780	300	620	527	53	57	780	52	620	310	0	57	690	59	53	330	0	0

mv ( $\sqrt{\text{Mean}}$ )			17.721	5.731	5.212		12.784	0.000	5.192	19.353	6.310	5.226	14.466	0.000	0.000
s ( $\text{CV} \cdot \text{mv} / 100$ )			2.305	0.759	0.715		2.529	0.000	0.708	2.422	0.627	0.716	1.751	0.000	0.000
$U_{rel,mv}$ (%) ( $100 \cdot s / \sqrt{n_{mv}} / mv$ )			1.5	1.5	1.6		2.2		1.5	1.6	1.3	1.8	1.6		
x ( $\sqrt{\text{Result}}$ )															
z ( $(x - mv) / s$ )															

\* The calculated results and acceptance limits are calculated without the 19 zero results. However, also these zero results are judged as acceptable and not false negative.



Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. <i>Pseudomonas aeruginosa</i> (MF)			<i>Pseudomonas aeruginosa</i> (MF)			Total plate count 22 °C, 3 days			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	A	B	C	
-	-	-	-	-	-	-	-	-	-	-	-	10	7	6	8	31	<1	7564
590	55	0	590	55	0	36	0	27	36	0	27	15	1	7	13	77	5	7596
-	-	-	660	20	0	-	-	-	40	0	38	11	1	21	10	60	1	7688
-	-	-	650	51	0	-	-	-	38	0	33	12	1	3	8	41	1	7728
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7793
558	71	<1	558	71	<1	35	<1	53	35	<1	53	11	<1	<1	9	57	<1	7876
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7896
600	45	0	600	45	0	30	0	38	30	0	38	12	1	6	7	50	1	7930
507	54	0	500	44	0	122	24	34	4	0	14	-	-	-	-	51	-	7946
620	43	0	620	43	0	25	0	35	25	0	0	15	0	8	13	53	0	7962
600	68	0	600	68	0	43	0	36	43	0	36	9	2	9	12	62	2	7968
380	0	0	380	0	0	39	0	30	39	0	30	13	2	10	10	52	1	8068
-	-	-	-	-	-	-	-	-	-	-	-	8	5	79	-	-	-	8260
530	46	0	530	46	0	-	-	-	36	0	27	8	1	14	14	59	0	8329
630	58	0	630	58	0	27	0	35	27	0	35	13	1	16	12	56	1	8380
-	-	-	800	56	0	-	-	-	48	0	26	9	1	6	7	46	1	8435
745	57	0	745	57	0	-	-	-	-	-	-	9	1	95	-	-	-	8569
-	-	-	-	-	-	-	-	-	-	-	-	13	47	22	-	-	-	8598
-	-	-	-	-	-	-	-	-	-	-	-	10	1	7	-	-	-	8626
-	-	-	600	58	0	-	-	-	43	0	39	10	1	11	13	55	1	8628
530	59	0	520	59	0	48	0	30	48	0	30	7	1	28	8	40	0	8663
-	-	-	-	-	-	35	<1	39	-	-	-	7	3	9	7	44	1	8742
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8751
391	43	0	391	43	0	57	0	29	57	0	29	9	3	15	13	63	1	8766
700	50	0	695	47	0	13	0	10	-	-	-	7	1	11	10	41	1	8809
645	66	0	645	66	0	-	-	-	-	-	-	12	2	23	-	-	-	8862
-	-	-	-	-	-	-	-	-	-	-	-	11	4	6	-	-	-	8891
755	53	0	755	53	0	45	0	43	45	0	43	11	2	26	6	47	1	8898
-	-	-	700	46	0	-	-	-	32	0	28	16	0	17	13	56	0	8955
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9	38	3	8971
-	-	-	-	-	-	-	-	-	-	-	-	32	44	3	23	2	9	8998
-	-	-	30	32	0	-	-	-	-	-	-	7	0	14	-	-	-	9002
-	-	-	-	-	-	-	-	-	-	-	-	12	1	9	7	65	0	9306
681	53	0	681	53	0	43	0	35	43	0	35	11	0	15	14	59	5	9436
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9589
645	59	0	645	59	0	38	0	30	38	0	30	7	0	18	8	32	0	9736
622	70	0	622	70	0	45	0	39	45	0	39	12	2	18	9	76	1	9899
685	60	0	685	60	0	49	0	31	49	0	31	14	1	22	11	52	4	9903

52	52	52	76	76	76	44	44	45	57	57	57	95	95	95	76	77	76	n
380	0	0	2.75	0	0	13	0	10	0	0	0	0	0	0	0	1.75	0	Min
800	77	60	855	700	60	122	24	60	100	46	60	80	47	95	260	80	60	Max
604	54	0	603	55	0	41.5	0	31	40	0	30	10	1	13	10.5	52	1	Median
			596	55	0				40	0	31	10	1	12	11	51	1	Mean
			9	9	-				22	-	13	15	70	38	14	13	96	CV (%)
			0	0	1				0	1	0	0	0	0	0	0	0	False pos.
			0	1	0				1	0	1	1	0	0	1	0	0	False neg.
			3	3	0				0	0	0	2	0	0	2	7	0	Outliers <
			0	2	0				0	0	0	3	3	2	3	0	1	Outliers >
380	0	0	380	32	0	13	0	10	4	0	14	4	0	0	6	20	0	Low limit
800	77	60	855	77	0	122	24	60	100	0	60	22	8	30	20	80	10	High limit

	24.405	7.389	0.000			6.334	0.000	5.567	3.208	0.999	3.422	3.318	7.161	0.850		mv
	2.112	0.682	0.000			1.376	0.000	0.718	0.466	0.697	1.286	0.458	0.903	0.820		s
	1.0	1.1				2.9		1.7	1.5	7.3	3.9	1.6	1.5	11.1		u <sub>rel,mv</sub> (%)
																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		
1131				-0.049	0.571	-0.158				0.716	0.000	-0.131	0.380	-1.042	0.092	0.093	0.000	0.000		
1149																				
1237				-3.035	-0.097	-1.034				-2.890	0.000	-1.016			-0.363	0.352			0.000	
1254				-0.428	0.782	-0.296				-0.376	0.000	-0.271	-0.490	-0.902	-0.898	-0.600	0.000	0.000		
1290				-0.626	0.132	-0.296				-0.670	0.000									
1545				1.617	-0.579	0.112				0.942	0.000		0.205	0.394	0.223	0.641	0.000	0.000		
1594				0.544	2.041	0.112				0.323		0.140	-0.092	1.100	-0.747	0.947	0.000	0.000		
1611				0.428	1.766	0.371				-0.212	0.000	0.403	0.132	0.394	-0.041	0.732	0.000	0.000		
1753				1.096	1.672	0.371				0.537	0.000	0.403	0.621	0.635	0.478	0.965	0.000	0.000		
1868				0.036	-0.334	-0.296				-0.022	0.000	-0.271	-0.355	0.985	-0.315	-0.948	0.000	0.000		
1970				-1.108	0.132	0.371				0.942	0.000	0.403								
2050				0.989	0.571	-0.296				1.135	0.000	-0.271	-0.344	1.100	0.965	-1.015	0.000	0.000		
2386				1.412	0.571	2.500				1.321	0.000									
2534				0.724	4.000	3.268				1.907	0.000	3.328								
2637													-0.157	-0.495	0.223	0.768	0.000	0.000		
2670				-0.559	1.189	-0.158				1.443	0.000	-0.131								
2704				0.193	-3.180	-0.296				-0.053	0.000	-0.271	-0.984	-0.764	-0.898	-0.948	0.000	0.000		
2745				0.312	0.132	0.622				0.810	0.000	0.656								
2797				-0.967	-0.455	-1.192				-0.053	0.000	0.902	-1.784	-0.764	2.277	-1.601	0.000	0.000		
3055																				
3076																				
3145													-0.322	-0.232	-1.540	0.512	0.000	0.000		
3159				-0.300	-2.280	-0.729				-0.376	0.000	-0.708	0.561	-0.442	-0.259	1.430	0.000	0.000		
3162				0.880	0.782	0.243				0.176	0.000	0.273	1.130	1.436	0.092	0.512	0.000	0.000		
3164				-0.351	0.571	2.196				-0.180		-1.176	-0.103	0.985	-0.177	0.362	0.000	0.000		
3305				-4.000	-0.334	-0.296				-3.243	0.000	-0.271	2.855	0.753	1.082	4.000	0.000	0.000		
3339				-0.428	0.244	-1.522				-0.376	0.000									
3533				0.312	-1.370	-1.355				0.537	0.000	-1.340								
3587																				
3730																				
3868				1.515	0.677	0.498				0.250	0.000	-1.176	0.058	0.148	-0.456	0.209	0.000	0.000		
3939																				
4015				-0.174	0.132	-0.158				-0.760	0.000	-0.131	-1.132	-1.184	1.082	-1.151	0.000	0.000		
4180				-1.037	0.244	0.866				0.176	0.000	0.656								
4288																				
4319				0.193	-0.097	-1.355				-0.261	0.000	-2.239	1.325	-0.764	-1.052	1.243	0.000	0.000		
4339				1.203	0.988	-0.296				0.675	0.000		-0.324	1.806	-0.629	-0.317	0.000	0.000		
4343				-0.441	0.782	-0.437				-0.427	0.000	-0.414	-0.948	1.763	0.092	0.305	0.000	0.000		
4356				0.544	0.464	-0.729				0.810	0.000	-0.708	-0.378	-0.495	0.965	-0.815	0.000	0.000		
4459				-0.062	-1.658	-0.879				-0.294	0.000		-1.321	0.148	-0.898	-1.953	0.000	0.000		
4564				0.428	-1.658	0.866				-0.376	0.000	0.902								
4633				0.264	0.244	1.445				0.146	0.000	1.486	0.047	-0.232	-0.898	-0.205	0.000	0.000		
4650																				
4723				0.989	1.189	-0.729				0.730	0.000	-0.708								
4889				0.073	0.782	1.218				-0.053	0.000		1.149	-0.495	-0.177	0.209	0.000	0.000		
4980				-1.867	-1.807	-0.296				-0.723	0.000	-0.414	0.797	0.148	-1.373	0.247	0.000	0.000		
5018				-1.932	0.571	-0.879				-0.148	0.000		-1.648	0.148	-1.540	-1.626	0.000	0.000		
5094				0.989	0.244	-0.437				-1.992	0.000	-0.131								
5201										-0.053	0.000	0.140								
5220													0.376	-0.999	1.524	-1.337	0.000	0.000		
5352	-1.009	-0.215	-0.296				-0.742	0.000	-0.271											
5447	0.657	0.677	0.985				0.396	0.000	1.022											
5553																				
5701	0.428	1.385	0.371				0.579	0.000	0.403											
5858										-1.595	0.635	-0.315	-1.267	0.000	0.000					
5950	-3.137	1.482					1.147	0.000	0.273	-1.132	-0.628	0.602	1.226	0.000	0.000					
6175										-2.152	-0.495	-0.747	-0.926	0.000	0.000					
6180	-0.174	0.464	-0.581				0.675	0.000	-0.559	0.267	-2.250	-0.747	-1.267	0.000	0.000					
6233										0.016	-0.764	-0.898	0.228	0.000	0.000					
6253										-0.049	0.635	1.535	-1.038	0.000	0.000					
6456	0.428	0.018	-0.158				-1.410	0.000	-1.683	0.677	0.148	0.478	0.677	0.000	0.000					
6563	-0.559	0.464	2.298				1.443	0.000	2.348	0.121	-0.104	-1.052	0.530	0.000	0.000					
6686										-4.000	-4.000	-4.000	-4.000	0.000	0.000					
6852																				
7096	-1.108	-0.215	-0.158				-0.376	0.000	-0.131	-2.608	-2.089	-0.456	-2.299	0.000	0.000					
7191	4.000	4.000	4.000				4.000	0.000	4.000											
7248	1.308	0.571	-0.437					0.000	-1.683	-0.277	-0.363	0.478	0.093	0.000	0.000					
7282									0.273											
7302	0.335	0.886	2.196				0.607	0.000	2.245	-0.733	-0.495	1.082	-0.452	0.000	0.000					
7330							-2.044	0.000	-1.176											
7442	-0.454	-1.512					0.265	0.000	0.273	-0.899	-0.628	0.846	-0.948	0.000	0.000					
7564	-1.108	-0.215	0.866				-0.212	0.000	-0.131											
7596	0.880	0.132	0.498				-0.495	0.000	1.140	1.149	-2.414	1.082	0.768	0.000	0.000					
7688	-0.174	-1.960	-0.581				-0.376	0.000	-4.000	1.953	1.976	-0.898	2.049	0.000	0.000					
7728	0.073	-0.963	0.243				0.810	0.000	0.273											
7793																				
7876	-0.416	0.677	1.332				-0.870	0.000	1.372	0.807	0.635	-0.041	0.286	0.000	0.000					
7896																				
7930	0.657	0.677	-0.581				1.748	0.000		0.561	-0.495	0.478	1.430	0.000	0.000					
7946	-2.684	-0.832	-1.192				-0.634	0.000												
7962	0.193	0.355	-0.296																	

positive results can no z-scores be calculated. Z-scores from 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.

Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. <i>Pseudomonas aeruginosa</i> (MF)			<i>Pseudomonas aeruginosa</i> (MF)			Total plate count 22 °C, 3 days			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	A	B	C	
												0.233	0.002	0.143				1131
																		1149
			-2.086	-1.561	0.000				-0.969	0.000	-1.525	0.854	0.002	0.817	-0.339	0.859	-1.037	1237
			-0.759	-0.159	0.000				-1.520	0.000	0.001	0.854	0.596	0.545	-0.002	0.430	0.183	1254
			1.685	0.040	0.000				1.815	0.000	0.367	0.550	-1.433	0.903	1.212	-0.100	4.000	1290
			0.042	-0.782	0.000				1.256	0.000	-0.517	1.146	2.363	0.545	-0.693	0.859	0.183	1545
			1.150	-0.570	0.000				-0.007	0.000	0.486	-0.098	-1.433	0.729	-0.002	0.998	-1.037	1594
			0.139	-0.570	0.000				0.432	0.000	1.164	-0.098	0.002	0.638	-4.000	-0.178	-1.037	1611
			0.042	0.040	0.000				1.690	0.000	0.125	-0.815	0.002	0.143	-0.339	-0.100	1.075	1753
			0.507	0.805	0.000							1.146	-1.433	0.987				1868
			0.329	-0.260	0.000				1.477	0.000	3.034	-0.447	0.596	0.638	-1.895	-1.665	0.183	1970
			1.211	0.040	0.000				-0.557	0.000	0.718	-0.098	-1.433	0.545	1.212	1.400	0.183	2050
			-1.182	-0.260	0.000				1.896	0.000	-0.125	-0.815	-1.433	0.545	-0.339	0.055	-1.037	2386
												0.233	-1.433	-1.315				2534
												1.701	2.625	1.149	2.519	-0.753	1.075	2637
			1.150	0.333	0.000							4.000	4.000	-2.662	4.000	-2.976	2.819	2670
			0.329	-1.332	0.000							-0.447	1.436	-1.884	0.628	0.647	1.075	2704
			0.423	0.988	0.000							-0.447	0.596	-0.329				2745
									0.432	0.000	0.944	-1.208	0.596	0.351	0.319	0.719	-1.037	2797
												-1.629	0.596	-0.757				3055
									-0.623	0.000	-0.253	-0.098	-1.433	0.143	-0.693	0.430	0.688	3076
																		3145
			0.042	1.169	0.000							-0.447	1.052	-0.202	-0.339	-0.022	-1.037	3159
			0.042	1.695	0.000				0.737	0.000	0.001	1.701	0.002	0.987	2.018	0.503	0.688	3162
			-1.852	-4.000								0.854	0.596	-0.757	-0.693	-4.000	-1.037	3164
			0.234	-0.159	0.000				2.663	0.000	-0.125	0.233	-1.433	0.987	0.319	0.647	-1.037	3305
			-0.451	0.429	0.000				-0.123	0.000	-0.384	-1.629	0.002	0.033	-0.339	0.132	-1.037	3339
			-0.968	-0.570	0.000							0.854	-1.433	0.143				3533
												0.233	-1.433	1.227	-0.339	-2.175	-1.037	3587
												4.000	0.596	0.248				3730
			-0.968	-0.363	0.000				-0.007	0.000	-0.253	-0.098	-1.433	0.351	-0.339	-0.753	-1.037	3868
																		3939
			0.120	1.169	0.000							-0.447	0.002	0.987				4015
			-0.968	0.040	0.000				-1.788	0.000	-2.182				0.319	-1.378	0.688	4180
												-0.815	0.002	-0.082				4288
												1.146	0.596	0.545	0.628	0.998	0.183	4319
			-0.351	-0.059	0.000							-1.208	0.596	1.304	1.212	-2.175	-1.037	4339
			-0.251	1.435	0.000				1.477	0.000	1.272	-1.629	0.596	0.143	0.628	1.400	1.402	4343
			-0.635	0.040	0.000				-0.827	0.000	-0.253	-1.629	0.596	0.143	-0.002	-0.022	0.183	4356
			-1.075	1.865	0.000				-0.827	0.000	0.125	-1.208	0.002	0.729	-0.339	-1.568	0.183	4459
			0.562	-1.678	0.000							0.233	0.596	-1.562	-0.339	-1.568	0.183	4459
			2.249	4.000	0.000				-0.758	0.000	-1.221	0.233	1.052	0.143	-0.339	-4.000	0.183	4564
			2.290	0.040	0.000				-0.969	0.000	0.125	-1.208	0.596	0.817	-0.339	-0.178	0.183	4633
																		4650
												1.428	-1.433	1.527				4723
			0.301	0.139	0.000				-0.428	0.000	-0.253	1.701	0.002	0.351	1.489	-0.258	-1.037	4889
			-0.863	0.333	0.000				-1.118	0.000	-1.371	-1.629	0.002	-0.329	0.925	-4.000	-1.037	4980
			0.609	-1.108	0.000				-0.897	0.000	0.603	-1.629	-1.433	-1.884	0.925	0.998	0.183	5018
			0.234	2.034	0.000							-0.815	0.002	-2.662	0.925	-1.194	-1.037	5094
												1.146	0.002	0.817				5201
																		5220
			-0.477	-0.836	0.000													5352
			-0.351	1.865	0.000				0.326	0.000	-0.125	0.550	0.596	-1.884	0.925	-1.103	-1.037	5447
			-0.655	-0.363	0.000							0.550	0.002	0.143	-0.339	0.282	0.183	5553
			-2.205	-1.332	0.000							-1.208	-1.433	0.033				5701
												0.272	0.000	-0.652	-0.002	0.430	0.183	5858
			-0.502	-0.059	0.000				1.165	0.000	-0.253	-2.595	0.002	0.729	2.272	1.466	2.819	5950
			0.385	0.619	0.000							3.184	0.596	1.599	-1.466	-0.668	-1.037	6175
												0.854	0.596	-0.923	2.519	1.974	0.183	6180
			-0.968	1.950	0.000				-0.007	0.000	1.055	-0.447	0.002	0.143	0.628	0.207	0.688	6233
			0.562	-2.285	0.000				-0.304	0.000	-1.074	-0.098	0.002	0.817				6253
			0.329	0.524	0.000							-1.208	0.002	0.143	-0.693	-0.419	-1.037	6456
									-0.827	0.000	-0.930	0.854	0.002	-1.106	0.628	-0.584	1.075	6563
			-1.182	-0.159	0.000							-4.000	-1.433	-1.789	-4.000	-4.000	-1.037	6686
			-4.000	-4.000	0.000													6852
									-1.043	0.000	-2.182	0.233	0.002	-0.604	-1.466	0.055	0.688	7096
												-1.433	-2.662		-4.000	-1.037		7191
			0.479	-0.466	0.000				0.326	0.000	-0.125	-1.208	0.002	0.449	-0.339	-0.022	0.183	7248
			-4.000	4.000	0.000						-1.074	-4.000	2.081	-0.462	4.000	-4.000	0.688	7282
									1.165	0.000	0.718	-0.098	-1.433	1.069	-1.068	0.576	-1.037	7302
			-1.715	-1.332	0.000				0.379	0.000	0.247	0.233	0.596	-1.315	-0.002	1.201	0.688	7330
			0.071	0.139	0.000							-0.098	1.052	0.817				7442
												-0.098	2.363	-0.757	-1.068	-1.764	-1.037	7564
			-0.055	0.040	0.000				-0.243	0.000	-0.517	1.428	0.002	-0.604	0.628	1.786	1.690	7596
			0.609	-4.000	0.000				-0.007	0.000	0.832	0.233	0.002	0.903	-0.339	0.647	0.183	7688
			0.516	-0.363	0.000				-0.123	0.000	0.247	0.550	0.002	-1.315	-1.068	-0.839	0.183	7728
																		7793
									-0.304	0.000	2.385	0.233	-1.433	-2.662	-0.693	0.430	-1.037	7876
																		7896
									-0.623	0.000	0.832	0.550	0.002	-0.757	-1.466	-0.100	0.183	7930
			-0.968	-1.108	0.000				-3.149	0.000	-2.542				-0.022			7946
									-0.969	0.000		1.428	-1.433	-0.462	0.628	0.132	-1.037	7962
			0.234	-1.219	0.000				0.162	0.000	0.603	-0.447	0.596	-0.329	0.319	0.789	0.688	7968
			0.042	1.258	0.000				-0.065	0.000	-0.125	0.854	0.596	-0.202	-0.339	0.055	0.183	8068
			-2.326		0.000							-0.815	1.775	4.000				8260

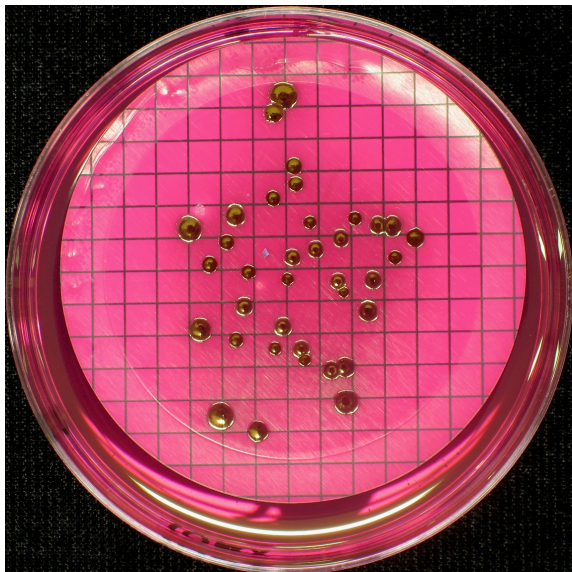
Lab no.	Sample	Suspected coliform bacteria (MF)			Coliform bacteria (MF)			Susp. thermotolerant coliform bact. (MF)			<i>E. coli</i> (MF)			Coliform bacteria ("rapid" MPN)			<i>E. coli</i> ("rapid" MPN)		
		A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
8329					-0.507	-0.334	-0.581				0.116	0.000	-0.559	0.132	1.976	0.092	-0.348	0.000	0.000
8380					-0.300	-1.512	-0.158				0.509	0.000	-0.131	-0.168	-0.363	0.478	-0.185	0.000	0.000
8435					-0.049	-0.097	0.371				0.810	0.000	0.403						
8569					-1.327	0.464	-0.879				0.396	0.000							
8598																			
8626					0.312	-0.455	0.745				-0.908	0.000	-0.271						
8628					0.193	0.244	0.371				-0.053	0.000							
8663					0.657	0.464	-1.522				0.942	0.000	-1.509	0.670	-0.764	-2.460	2.112	0.000	0.000
8742					0.880	-0.334	-0.296				0.537	0.000	-0.271						
8751																			
8766					0.049	-0.579	0.985				0.410	0.000	1.022	-0.081	0.023	-0.041	0.014	0.000	0.000
8809					-0.733	-1.658	-0.581				-0.376	0.000							
8862					0.061	0.355	-0.158				0.009	0.000		0.184	-0.363	-2.072	0.014	0.000	
8891																			
8898					1.464	-0.215	0.866				1.370	0.000	0.902	1.093	0.272	0.478	-0.125	0.000	0.000
8955					0.193	0.571	-0.729				0.101	0.000	-0.708	-0.049	2.186	0.602	-0.390	0.000	0.000
8971																			
8998					-3.393	-0.832	-2.443				-2.018	0.000		-1.019	0.272	0.026	-3.912	0.000	0.000
9002					-4.000	-2.447	-2.245				-0.634	0.000							
9306														0.441	-0.764	1.424	-0.287	0.000	0.000
9436					0.264	0.132	-0.581				-2.462	0.000	-1.683	-0.081	-0.495	0.352	1.209	0.000	0.000
9589					-0.174	-0.579	-0.022												
9736					2.271	0.464	0.112				1.370	0.000	0.140	-0.190	1.436	-0.456	0.804	0.000	0.000
9899					0.769	1.288	0.866				0.250	0.000	0.902	1.640	0.753	1.082	0.840	0.000	0.000
9903					0.634	0.018	0.371				0.607	0.000							
n		0	0	0	81	81	79	0	0	0	81	79	64	60	61	61	60	61	59
Min					-4.000	-3.180	-2.443				-3.243	0.000	-4.000	-4.000	-4.000	-4.000	-4.000	0.000	0.000
Max					4.000	4.000	4.000				4.000	0.000	4.000	2.855	4.000	2.870	4.000	0.000	0.000
Median					0.073	0.244	-0.158				0.101	0.000	-0.131	-0.049	-0.232	-0.041	0.054	0.000	0.000
Mean					-0.091	0.147	0.051				0.049	0.000	0.000	-0.067	0.000	-0.066	-0.065	0.000	0.000
SD					1.298	1.239	1.091				1.089	0.000	1.215	1.118	1.225	1.116	1.322	0.000	0.000
z<-3					5	1	0				1	0	1	1	1	1	2	0	0
-3≤z<-2					1	2	2				4	0	1	2	3	2	1	0	0
2<z≤3					1	1	4				0	0	2	1	1	2	2	0	0
z>3					1	3	2				1	0	2	0	1	0	1	0	0

Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. <i>Pseudomonas aeruginosa</i> (MF)			<i>Pseudomonas aeruginosa</i> (MF)			Total plate count 22 °C, 3 days			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	A	B	C	
			-0.655	-0.889	0.000				-0.243	0.000	-0.517	-0.815	0.002	0.248	0.925	0.576	-1.037	8329
			0.329	0.333	0.000				-0.827	0.000	0.486	0.854	0.002	0.449	0.319	0.357	0.183	8380
			1.837	0.139	0.000				0.432	0.000	-0.652	-0.447	0.002	-0.757	-1.466	-0.419	0.183	8435
			1.368	0.237	0.000							-0.447	0.002	4.000				8569
												0.854	4.000	0.987				8598
												-0.098	0.002	-0.604				8626
			0.042	0.333	0.000				0.162	0.000	0.944	-0.098	0.002	-0.082	0.628	0.282	0.183	8628
			-0.759	0.429	0.000				0.432	0.000	-0.125	-1.208	0.002	1.454	-1.068	-0.926	-1.037	8663
												-1.208	1.052	-0.329	-1.466	-0.584	0.183	8742
			-2.193	-1.219	0.000				0.883	0.000	-0.253	-0.447	1.052	0.351	0.628	0.859	0.183	8751
			0.927	-0.782	0.000							-1.208	0.002	-0.082	-0.339	-0.839	0.183	8766
			0.470	1.079	0.000							0.550	0.596	1.069				8809
												0.233	1.436	-0.757				8862
			1.455	-0.159	0.000				0.272	0.000	1.379	0.233	0.596	1.304	-1.895	-0.338	0.183	8891
			0.972	-0.889	0.000				-0.492	0.000	-0.384	0.233	0.596	1.304	0.628	0.357	-1.037	8898
												1.701	-1.433	0.545	-0.693	-1.103	1.075	8955
															4.000	4.000	-1.315	8971
			-4.000	-2.541	0.000							-1.208	-1.433	0.248	3.225	-4.000	2.621	8998
												0.550	0.002	-0.329	-1.466	0.998	-1.037	9002
			0.801	-0.159	0.000				0.162	0.000	0.486	0.233	-1.433	0.351	0.925	0.576	1.690	9306
																		9436
			0.470	0.429	0.000				-0.123	0.000	-0.125	-1.208	-1.433	0.638	-1.068	-1.665	-1.037	9589
			0.253	1.435	0.000				0.272	0.000	0.944	0.550	0.596	0.638	-0.693	1.723	0.183	9736
			0.837	0.524	0.000				0.484	0.000	0.001	1.146	0.002	0.987	-0.002	0.055	1.402	9899
																		9903
0	0	0	76	75	75	0	0	0	56	56	56	94	95	95	75	77	76	n
			-4.000	-4.000	0.000				-3.149	0.000	-2.542	-4.000	-1.433	-2.662	-4.000	-4.000	-1.037	Min
			2.290	4.000	0.000				2.663	0.000	3.034	4.000	4.000	4.000	4.000	1.974	4.000	Max
			0.042	0.040	0.000				-0.007	0.000	-0.125	0.068	0.002	0.248	-0.002	-0.022	0.183	Median
			-0.158	-0.053	0.000				0.000	0.000	0.000	0.043	0.126	0.084	0.043	-0.364	0.053	Mean
			1.255	1.418	0.000				1.000	0.000	1.000	1.343	1.209	1.145	1.391	1.499	1.094	SD
			3	3	0				1	0	0	2	0	0	2	7	0	Sum
			4	2	0				0	0	3	1	0	4	0	3	0	31
			2	1	0				1	0	1	0	4	0	4	0	3	35
			0	2	0				0	0	1	4	3	2	3	0	1	30
																		27



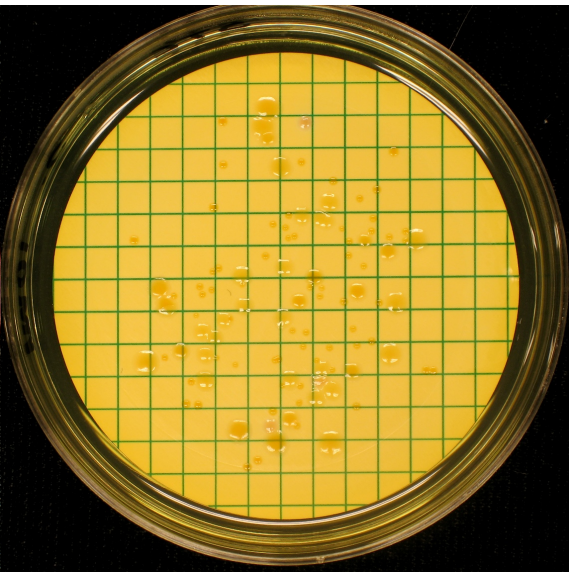
Mixture A

m-Endo Agar LES, 37 °C



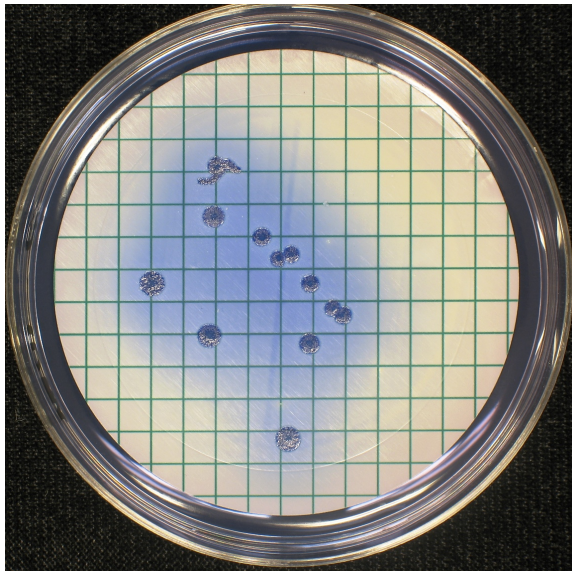
10 ml

m-Lactose TTC Agar, 37 °C



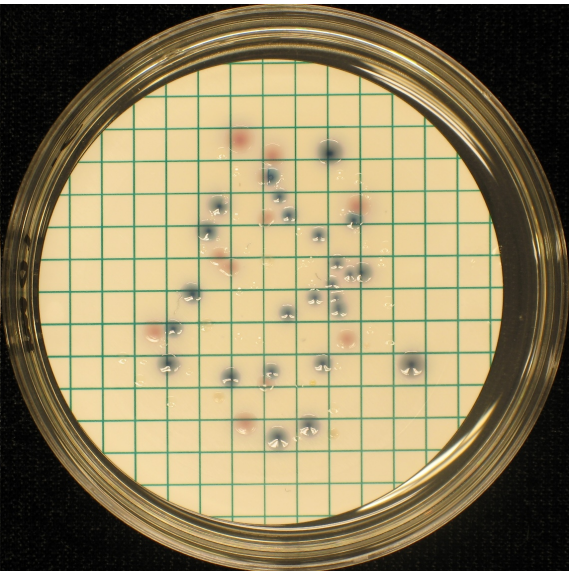
10 ml

m-FC Agar, 44 °C



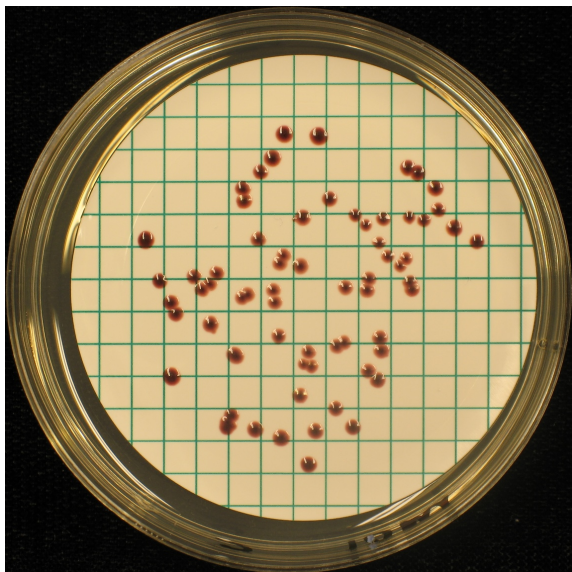
10 ml

Chromocult Coliform Agar, 37 °C



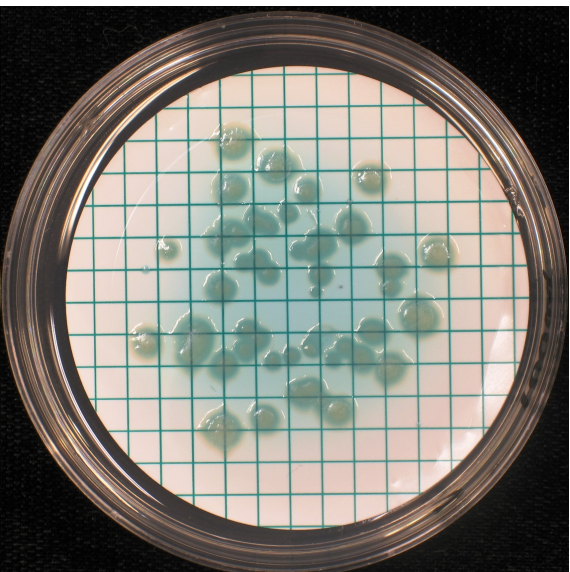
10 ml

m-Enterococcus Agar, 37 °C



10 ml, 2 days

m-Pseudomonas CN Agar, 37 °C

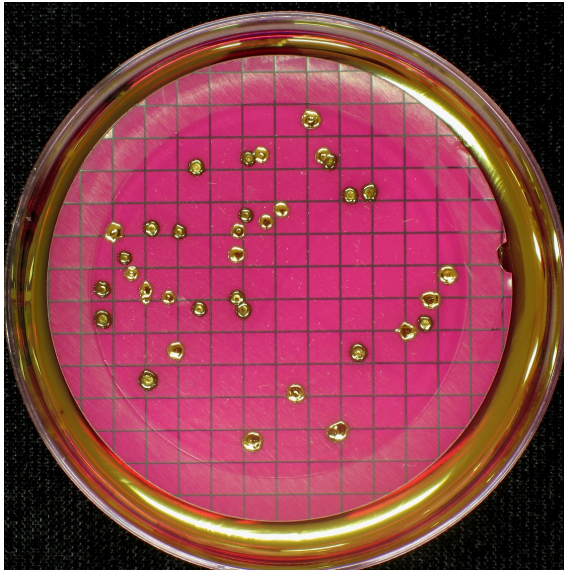


100 ml, 2 days



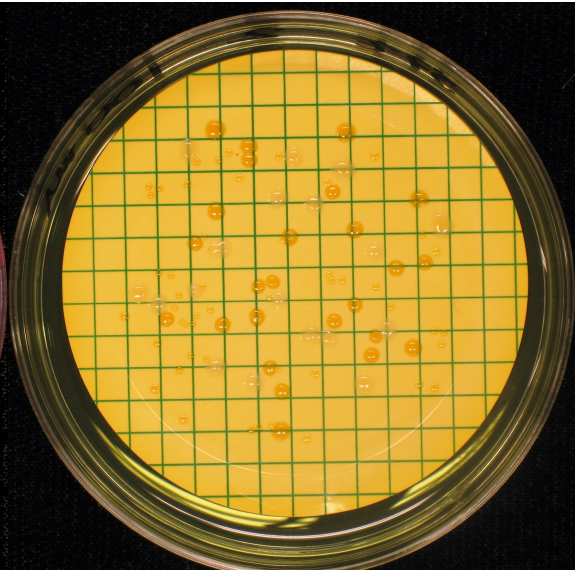
## Mixture B

m-Endo Agar LES, 37 °C



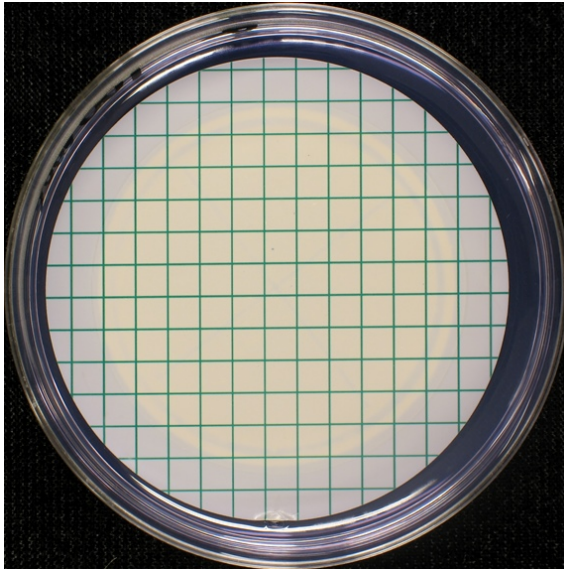
100 ml

m-Lactose TTC Agar, 37 °C



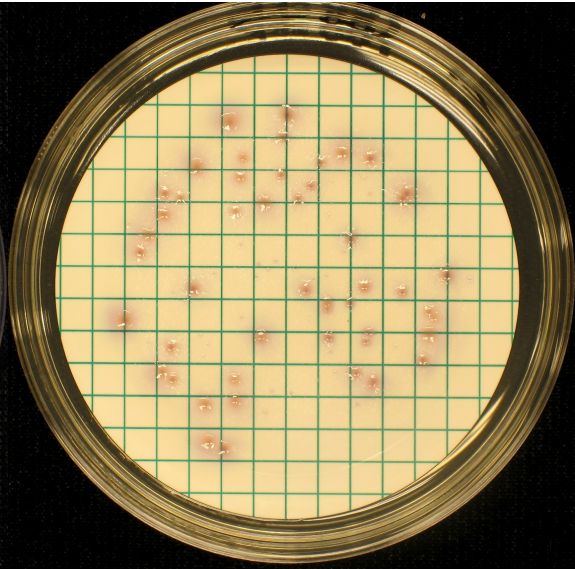
100 ml

m-FC Agar, 44 °C



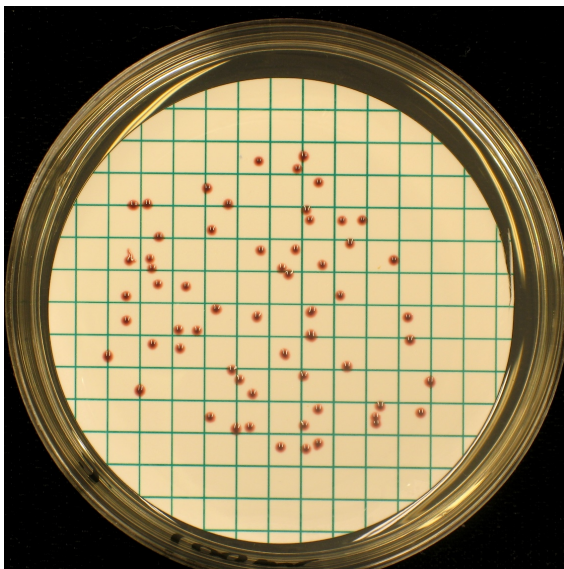
100 ml

Chromocult Coliform Agar, 37 °C



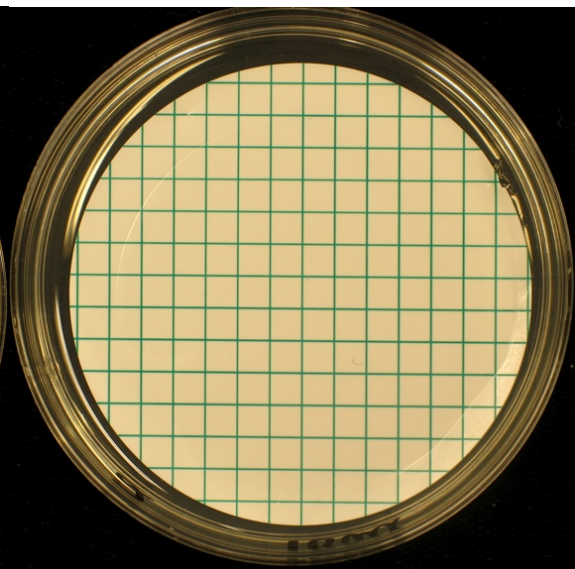
100 ml

m-Enterococcus Agar, 37 °C



10 ml, 2 days on BEAA

m-Pseudomonas CN Agar, 37 °C

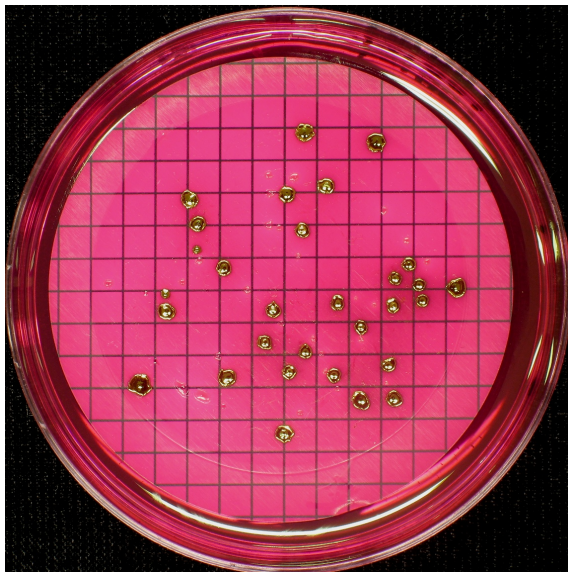


100 ml, 2 days



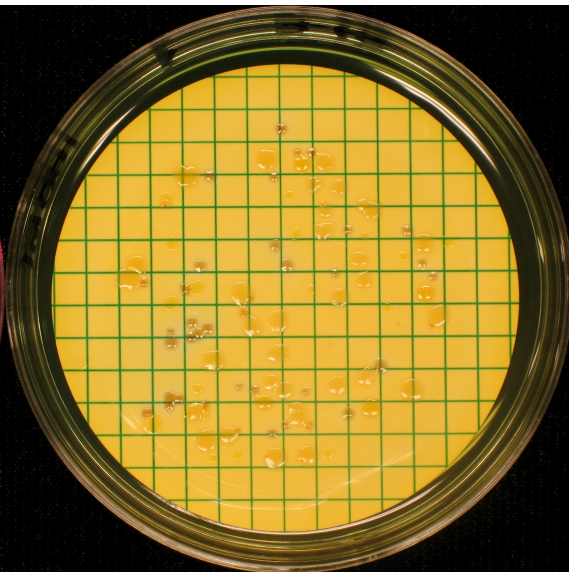
## Mixture C

m-Endo Agar LES, 37 °C



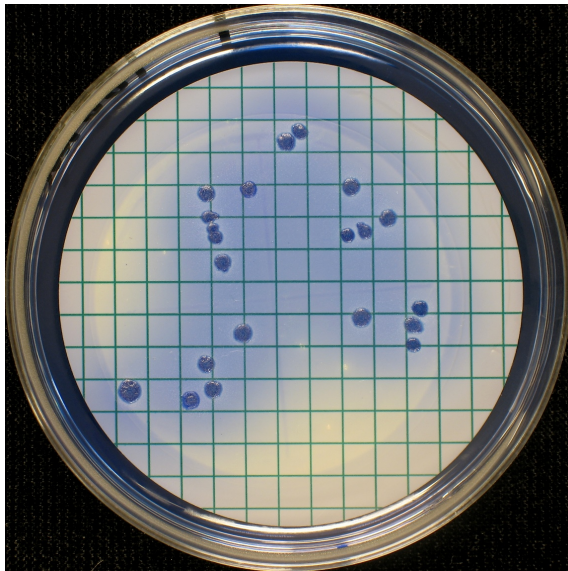
100 ml

m-Lactose TTC Agar, 37 °C



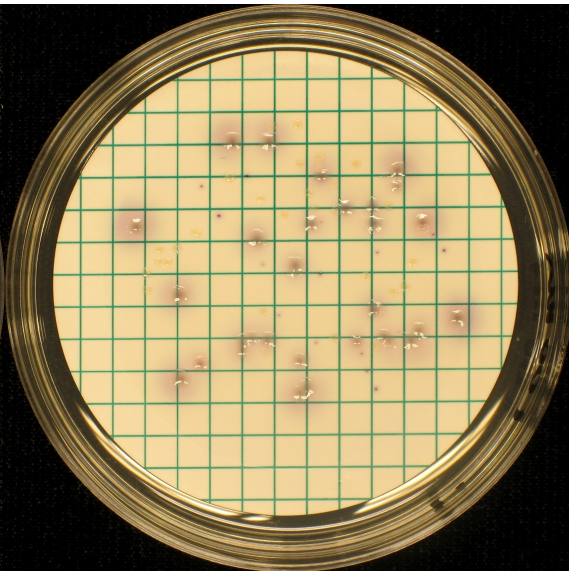
100 ml

m-FC Agar, 44 °C



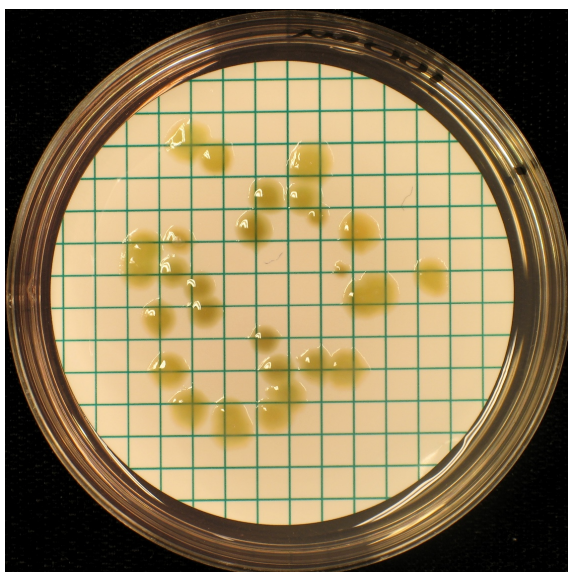
100 ml

Chromocult Coliform Agar, 37 °C



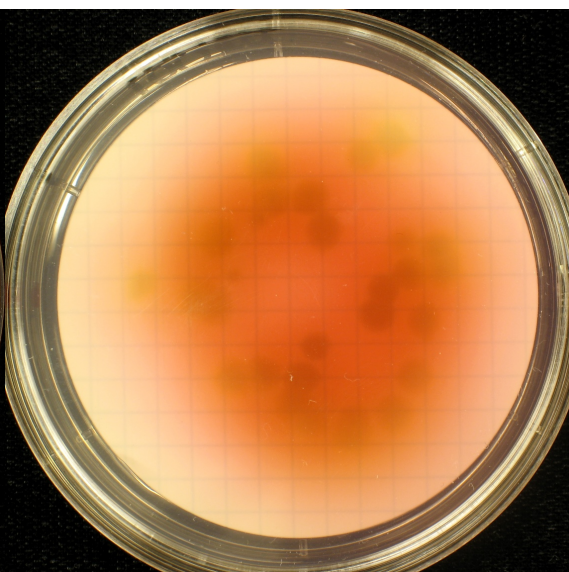
100 ml

m-Pseudomonas CN Agar, 37 °C



100 ml, 2 days

m-Pseudomonas CN Agar, 37 °C



100 ml, 2 days, from back side



## **PT reports published 2014**

Proficiency Testing – Food Microbiology, January 2014, by Laurence Nachin, Christina Normark and Irina Boriak

Proficiency Testing – Drinking Water Microbiology, March 2014, by Tommy Šlapokas and Kirsi Mykkänen

Proficiency Testing – Food Microbiology, April 2014, by Laurence Nachin and Irina Boriak

Proficiency Testing – Drinking Water Microbiology, September 2014, by Tommy Šlapokas and Kirsi Mykkänen

Proficiency Testing – Food Microbiology, October 2014, by Laurence Nachin and Irina Boriak

## **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 2014, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, October 2014

## **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](http://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](http://www.livsmedelsverket.se/en/RM-micro)