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Abbreviations

Media

ALOA	Agar for Listeria according to Ottaviani & Agosti
APW 2%	Alcaline peptone water, 2 % NaCl
BA	Blood agar
BcsA	*Bacillus cereus* selective agar
BEA	Bile esculin agar
BGA	Brilliant green agar
BGLB	Brilliant green lactose bile broth
BP	Baird-Parker agar
BPW	Buffered peptone water
BS	Bromthymol blue saccharose agar
CBC	Oxoid Brilliance™ *Bacillus cereus* agar
CIN	Cefsulodin irgasan novobiocin agar
Compact Dry EC	Compact Dry™ *E. coli* and coliforms
Compact Dry ETB	Compact Dry™ Enterobacteriaceae
Compact Dry ETC	Compact Dry™ Enterococcus
Compact Dry TC	Compact Dry™ Total Count
COMPASS	COMPASS® Enterococcus agar
CT-SMAC	Cefixime tellurite sorbitol MacConkey agar
DG18	Dikloran glycerol agar
DRBC	Dikloran Rose-Bengal chloramphenicol agar
EC	*E. coli* broth
ENT	Slanetz & Bartley *Enterococcus* agar
HEA	Hektoen enteric agar
IA	Iron agar
ISA	Iron sulphite agar
ITC	Irgasan ticarcillin potassium chlorate broth
KEAA	Kanamycin esculin azide agar
LMBA	*Listeria monocytogenes* blood agar
LSB	Lauryl sulphate broth
LTLSB	Lactose tryptone lauryl sulphate broth
mCCDA	Modified charcoal cephoperazone deoxycholate agar
mCP	Membrane *Clostridium perfringens* agar
MKTTn	Muller-Kauffmann tetrathionate/novobiocin broth
MPCA	Milk plate count agar
MRB	Modified Rappaport broth
MRS	de Man, Rogosa and Sharpe agar
MRS-aB	de Man, Rogosa and Sharpe agar with amphotericin
MRS-S	de Man, Rogosa and Sharpe agar with sorbic acid
MSRV	Modified semi-solid Rappaport-Vassiliadis enrichment media
mTSB	Modified tryptone soya broth

MYP	Mannitol egg yolk polymyxin agar
OCLA	Oxoid Brilliance™ Listeria agar
OGYE	Oxytetracyclin glucose yeast extract agar
OPSP	Oleandomycin, Polymixin, Sulphadiazine, Perfringens agar
PAB	Perfringens agar base
PDA	Potato dextrose agar
PALCAM	Polymyxin acriflavine lithium chloride ceftazidime aesculin mannitol agar
Petrifilm AC	3M™ Petrifilm™ Aerobic Count
Petrifilm CC	3M™ Petrifilm™ Coliform count
Petrifilm Disk	3M™ Petrifilm™ Staph Express Disk
Petrifilm EB	3M™ Petrifilm™ Enterobacteriaceae
Petrifilm EC/CC	3M™ Petrifilm™ *E. coli*/Coliform count
Petrifilm LAB	3M™ Petrifilm™ Lactic acid bacteria
Petrifilm RAC	3M™ Petrifilm™ Rapid Aerobic Count
Petrifilm REC	3M™ Petrifilm™ Rapid *E. coli*/Coliform count
Petrifilm SEC	3M™ Petrifilm™ Select *E. coli*
Petrifilm Staph	3M™ Petrifilm™ Staph Express
PEMBA	Polymyxin pyruvate egg yolk mannitol bromothymol blue agar
PSB	Peptone sorbitol bile salts broth
PCA	Plate count agar
RPFA	Baird-Parker agar with rabbit plasma fibrinogen
SFA	Sugar-free agar
RVS	Rappaport-Vassiliadis Soy peptone broth
Saubouraud	Saubouraud chloramphenicol agar
SC	Sulphite cycloserine agar
SFP	Shahidi-Ferguson Perfringens agar
SMAC	Sorbitol MacConkey agar
SP	Salt Polymyxin broth
SSDC	Salmonella/Shigella sodium deoxycholate calcium chloride agar
TBX	Tryptone bile X-glucuronide agar
TCBS	Thiosulphate citrate bile salts sucrose agar
TGE	Tryptone glucose extract agar
TEMPO AC	TEMPO® Aerobic count
TEMPO BC	TEMPO® *Bacillus cereus*
TEMPO CAM	TEMPO® Campylobacter
TEMPO CC	TEMPO® Coliform count
TEMPO EB	TEMPO® Enterobacteriaceae
TEMPO EC	TEMPO® E. coli
TEMPO RYM	TEMPO® Rapid Yeast/Mould
TEMPO STA	TEMPO® Coagulase-positive staphylocci
TEMPO YM	TEMPO® Yeast/Mould
TGE	Tryptone glucose extract agar
TS	Tryptose sulphite agar
TSA	Tryptic soya agar
TSC	Tryptose sulphite cycloserine agar

TSBY	Tryptone soya broth with yeast extract
XLD	Xylose lysine deoxycholate agar
VRB	Violet red bile agar
VRBG	Violet red bile glucose agar
YGC	Yeast extract glucose chloramphenicol agar

Organisations

AFNOR	French National Standardization Association
AOAC	AOAC INTERNATIONAL
ATCC	American Type Culture Collection
CBS	Centraalbureau voor Schimmelcultures (Westerdijk Institute)
CCUG	Culture Collection University of Gothenburg
IDF	International Dairy Foundation
ISO	International Organization for Standardization
NMKL	Nordic-Baltic Committee on Food Analyses
NordVal	NordVal International - NMKL
SLV	Livsmedelsverket/Swedish Food Agency, Sweden
Fohm	Public Health Agency of Sweden

Analyses in this PT round

Quantitative analyses

Aerobic microorganisms, 30 °C

Aerobic microorganisms, 20 °C

Contaminating microorganisms in dairy products

Enterobacteriaceae

Coliform bacteria 30 °C

Coliform bacteria 37 °C

Thermotolerant coliform bacteria

Escherichia coli

Presumptive *Bacillus cereus*

Coagulase-positive staphylococci

Enterococci

Gram-negative bacteria in pasteurised milk and cream

Method

Reporting of results and method information

It is the responsibility of the individual participants to correctly report results according to the instructions. Incorrectly reported results, for example results reported for the wrong sample, cannot be correctly processed. Incorrectly reported results are as a general rule excluded but may – after manual assessment by the Swedish Food Agency in each individual case – still be included and processed.

It is also mandatory for the participants to report method information for all analyses. This method information is sometimes contradictory or difficult to interpret. For example when participants state a medium that is not included in the standard method they refer to, or when manual comments by the participant contradict the reported method information. In such cases, the reported method information provided by the participants is generally used in method comparisons "as it is". Alternatively, method data that are difficult to interpret may be excluded or added to the group "Other", together with results from methods and media that are only used by 1–2 participants.

Standard deviation and assigned value

Evaluation of the participants' results and statistical calculations are carried out on the $\log_{10}$ transformed results. Results reported by participants as "> value" are not evaluated. Results reported as "< value" are treated as zero (negative result).

A robust statistical approach is used to determine the mean value and standard deviation. Algorithm A with iterated scale as described in ISO 13528:2015 [1] is used to determine the robust mean (m_{PT}) and robust standard deviation (s_{PT}) of the participants' results. Results that are obviously erroneous are excluded prior to determining m_{PT} and s_{PT} (blunder removal). For evaluated parameters, the assigned value consists of m_{PT}. It is regarded as the true, normative value. For parameters that are not statistically evaluated, the median (Med) of the participants results is instead used as the assigned value. This is also normally the case for parameters with fewer than 20 reported results.

Outliers

Outliers are results that deviate from the other results in a way that cannot be explained by normal variation. Results within $m_{PT} \pm 3s_{PT}$ are considered acceptable, whereas results outside this interval are considered as outliers. When fewer than 20 participants have reported results, as well as in some individual cases, subjective adjustments are made to set acceptance limits based on prior knowledge of the samples contents.

Results from different methods

Non-robust mean values (m) and standard deviations (s) and median values (Med) are calculated to assist in the evaluation of the results from different methods. These are shown in tables in the report, in connection with the respective analyses. In these instances, m, s and Med are calculated from the

respective method groups' results, with outliers and false results excluded. Normally, for method groups with fewer than 5 results, only the number of false results and outliers are provided.

Measurement uncertainty for the assigned value

The standard uncertainty (u_{PT}) of the assigned value (m_{PT}) is estimated from the standard deviation (s_{PT}) and the number of evaluated results (n):

$$u_{PT} = 1{,}25 \times \frac{s_{PT}}{\sqrt{n}}$$

The measurement uncertainty is considered negligible compared to the standard deviation (which is used for evaluating the participants' results) when:

$$u_{PT} < 0{,}3 s_{PT}$$

Z-scores

To allow comparison of the results from different analyses and samples, results are transformed into standard values (z-scores). Z-scores are calculated as:

$$z = \frac{x_{lab} - m_{PT}}{s_{PT}}$$

where x_{lab} is the result of the individual participant.

Z-scores for individual analyses are shown in Annex 2 and can be used as a tool by participants when following up on the results. For quantitative analyses, a z-score is either positive or negative, depending on whether the participants result is higher or lower than m_{PT}.

In evaluations of the analytical results, the following guidelines can be used:

$\|z\| \leq 2$	indicates that the result is acceptable
$2 < \|z\| < 3$	indicates a warning that the result may be deviating, and might motivate an action in the follow-up process
$\|z\| \geq 3$	indicates that the result is regarded as deviating and should lead to an action in the follow-up process

Table legends

N	number of participants that reported results for the analysis
n	number of participants with satisfactory result (false results and outliers excluded)
m_{PT}	assigned value, robust mean value in $\log_{10}$ cfu ml^{-1}
s_{PT}	robust standard deviation
u_{PT}	standard uncertainty of the assigned value
F	number of false positive or false negative results
<	number of low outliers
>	number of high outliers
	results deviating more than 1 s_{PT} from m, or unusually many deviating results.

Figure legends

- ▒ results within the interval of acceptance
- ■ outlier
- □ false negative result
- * value outside the x-axis scale

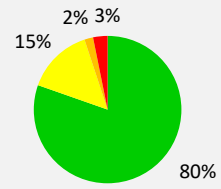
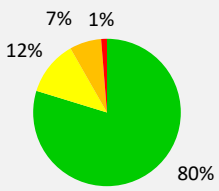
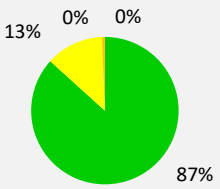
Results

General outcome

Samples were sent to 163 participants; 47 in Sweden, 104 in European countries, and 12 outside of Europe. Of the 158 participants that reported results, 59 (37 %) provided at least one result that received an annotation. In the previous PT round with similar analyses (October 2021) the proportion was 44 %.

Individual results are listed in Annex 1 and on the website: https://www2.slv.se/absint. Z-scores for individual results are listed in Annex 2.

Table 1. Composition of the test material and proportion of deviating results (N: number of reported results, F: false positive or false negative, X: outliers)

	Sample A				Sample B				Sample C			
% participants with 0 annotations 1 annotation 2 annotations >2 annotations												
Microorganisms	*Escherichia coli* *Serratia marcescens* *Staphylococcus aureus*				*Enterococcus faecium* *Escherichia coli* *Staphylococcus aureus* *Staphylococcus saprophyticus*				*Bacillus cereus* *Enterococcus durans* *Staphylococcus xylosus*			
Analysis	**Target organism**	**N**	**F**	**X**	**Target organism**	**N**	**F**	**X**	**Target organism**	**N**	**F**	**X**
Aerobic micro-organisms, 30 °C	**All**	148	0	7	**All**	146	0	11	**All**	149	0	3
Aerobic micro-organisms, 20 °C	**All**	21	0	1	**All**	21	0	0	**All**	21	0	1
Contaminating microorganisms	**All**	15	0	0	**All**	15	0	0	**All**	15	0	0
Enterobacteriaceae	***E. coli*** ***S. marcescens***	131	1	4	***E. coli***	130	1	5	-	131	0	0
Coliform bacteria, 30 °C	***E. coli*** *(S. marcescens)*	39	1	2	***E. coli***	38	0	3	-	40	0	0
Coliform bacteria, 37 °C	***E. coli*** *(S. marcescens)*	72	1	7	***E. coli***	71	4	5	-	72	0	0
Thermotol. coliform bacteria	***E. coli***	36	0	2	***E. coli***	36	0	4	-	36	0	0
Escherichia coli	***E. coli***	102	3	4	***E. coli***	100	0	6	-	105	1	0
Presumptive *Bacillus cereus*	*(S. marcescens)* *(S. aureus)*	104	3	0	-	102	2	0	***B. cereus*** *(S. xylosus)*	104	0	2
Coagulase-positive staphylococci	***S. aureus***	82	0	5	***S. aureus*** *(S. saprophyticus)*	80	1	4	*(S. xylosus)*	83	9	0
Enterococci	-	60	5	0	***E. faecium***	60	1	4	***E. durans***	60	3	3
Gram-negative bacteria	***E. coli*** ***S. marcescens***	12	0	0	***E. coli***	12	0	0	-	12	1	0

- no target organism or no value; **microorganism** = main target organism; (*microorganism*) = false positive before confirmation

The results are not evaluated

Aerobic microorganisms, 30 °C and 20 °C

Sample A

All strains in the sample were target organisms. The strain of *S. marcescens* was present in somewhat lower concentration than *S. aureus* and *E. coli*.

At 30 °C, 148 participants reported results. Three low and four high outliers were reported.

At 20 °C, 21 participants reported results. One high outlier was reported.

Sample B

All strains in the sample were target organisms. The strain of *S. saprophyticus* was present in somewhat lower concentration than *E. coli*, *E. faecium* and *S. aureus*.

At 30 °C, 146 participants reported results. Six low and five high outliers were reported.

At 20 °C, 21 participants reported results. No outliers or false negative results were reported.

Sample C

All strains in the sample were target organisms. The strain of *S. xylosus* was present in somewhat higher concentration than *B. cereus* and *E. durans*.

At 30 °C, 149 participants reported results. Two low and one high outliers were reported.

At 20 °C, 21 participants reported results. One high outlier was reported.

General remarks

The majority of the participants followed either NMKL 86:2013 or ISO 4833-1:2013, and thus incubated on PCA. Petrifilm AC was also used by a large number of participants. MPCA was mainly used by participants within the dairy industry, whereas incubation on TSA was mainly done by users of a company-specific method. ISO 4833-1:2013 was last reviewed by ISO in 2019 and remains current. NMKL 68:2013 was last reviewed by NMKL in 2022 and remains current.

A few participants used TEMPO AC, which is based on MPN (Most Probable Number). Users of this method often report slightly higher results compared to other methods, and the slight positive bias of this method for sample C can thus be considered normal.

At 20 °C, IA was used by participants that followed NMKL 184. This method is adapted for aerobic microorganisms and specific spoilage microorganisms in fish and fish products.

At 30 °C, three participants followed ISO 13559/IDF 153, which is adapted for the enumeration of contaminating microorganisms. However since the participants appear to have used media and

incubation conditions similar to the analysis of aerobic microorganisms, the results were still included in the evaluation.

Also at 30 °C, one participant followed IDF 100B:1991. This method has been withdrawn, and replaced by ISO 4833.

Table 2. Results from analysis of aerobic microorganisms, 30 °C.

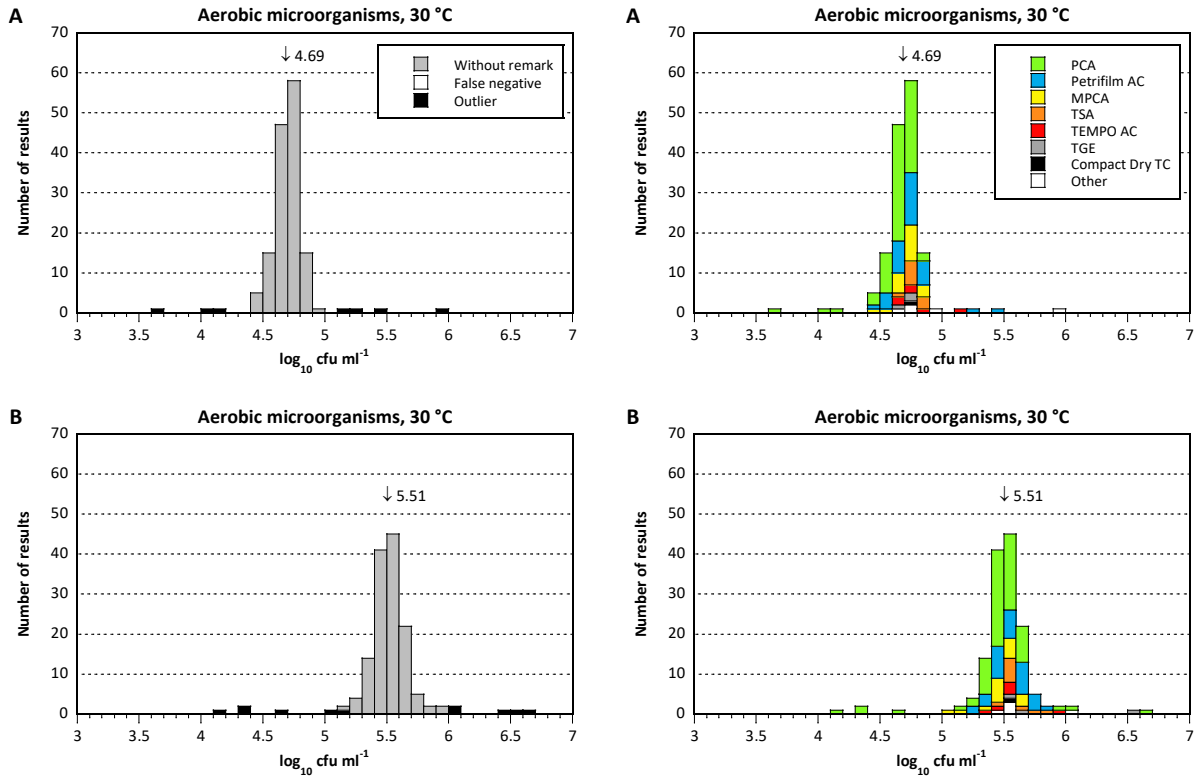
Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	M	s	F	<	>	N	n	m	s	F	<	>
All results	**148**	**141**	**4.69**	**0.10**	**0**	**3**	**4**	**146**	**135**	**5.51**	**0.13**	**0**	**6**	**5**	**149**	**146**	**5.13**	**0.14**	**0**	**2**	**1**
PCA	70	67	4.66	0.09	0	3	0	71	64	5.48	0.11	0	4	3	71	68	5.10	0.12	0	2	1
Petrifilm AC[1]	34	32	4.70	0.10	0	0	2	33	33	5.54	0.13	0	0	0	34	34	5.15	0.14	0	0	0
MPCA	19	19	4.70	0.11	0	0	0	17	15	5.51	0.10	0	2	0	19	19	5.12	0.14	0	0	0
TSA	10	10	4.76	0.06	0	0	0	10	10	5.58	0.11	0	0	0	10	10	5.23	0.19	0	0	0
TEMPO AC	6	5	4.72	0.09	0	0	1	6	6	5.54	0.20	0	0	0	6	6	5.26	0.12	0	0	0
TGE	3	3	-	-	0	0	0	3	2	-	-	0	0	1	3	3	-	-	0	0	0
Compact Dry TC[2]	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
Other	5	4	-	-	0	0	1	5	4	-	-	0	0	1	5	5	-	-	0	0	0

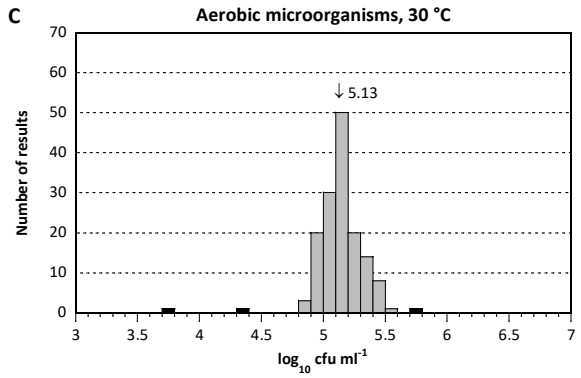
For "All results", m = robust m_{PT} and s = robust s_{PT}.

For individual media, m = mean value and s = standard deviation for the particular medium (outliers and false results excluded).

[1] "Petrifilm AC" includes two participants that incubated on Petrifilm RAC.

[2] One participant that incubated on Compact Dry TC followed ISO 11737-1:2018 ("Sterilization of health care products").





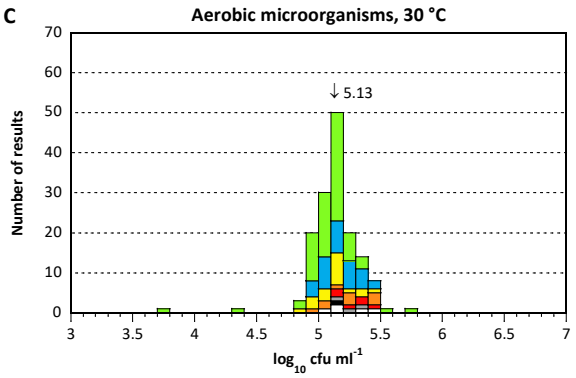
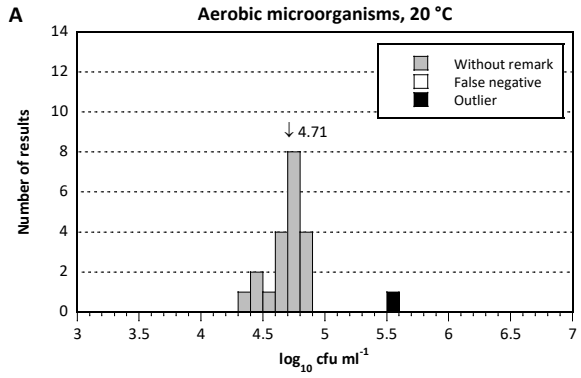


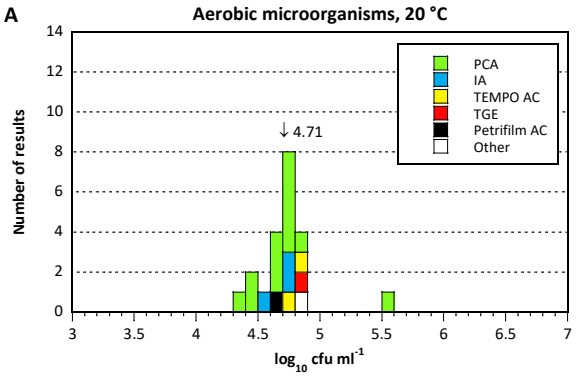
Table 3. Results from analysis of aerobic microorganisms, 20 °C.

Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**21**	**20**	**4.71**	**0.14**	**0**	**0**	**1**	**21**	**21**	**5.49**	**0.09**	**0**	**0**	**0**	**21**	**20**	**5.14**	**0.12**	**0**	**0**	**1**
PCA	13	12	4.65	0.14	0	0	1	13	13	5.50	0.09	0	0	0	13	12	5.11	0.11	0	0	1
IA	3	3	-	-	0	0	0	3	3	-	-	0	0	0	3	3	-	-	0	0	0
TEMPO AC	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
TGE	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
Petrifilm AC	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
Other	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0

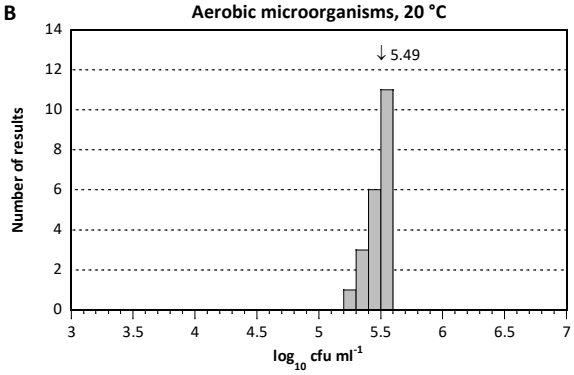
For “All results”, m = robust m_{PT} and s = robust s_{PT}.

For individual media, m = mean value and s = standard deviation for the particular medium (outliers and false results excluded).

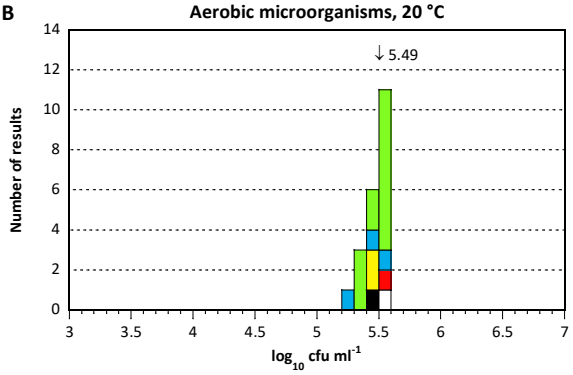




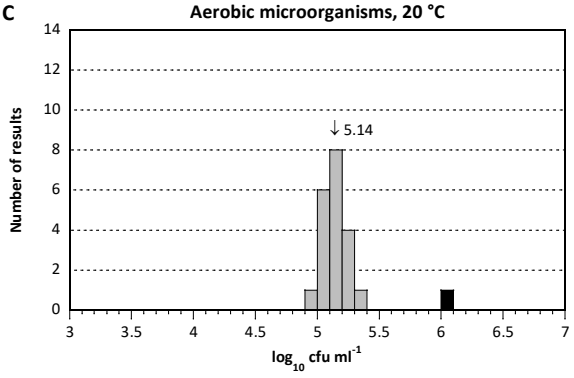
B


Aerobic microorganisms, 20 °C
↓5.49
Number of results
log10 cfu ml-1

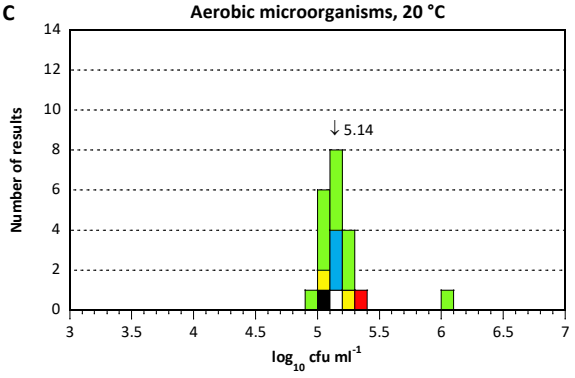
B


Aerobic microorganisms, 20 °C
↓5.49
Number of results
log10 cfu ml-1

C


Aerobic microorganisms, 20 °C
↓5.14
Number of results
log10 cfu ml-1

C


Aerobic microorganisms, 20 °C
↓5.14
Number of results
log10 cfu ml-1

Contaminating microorganisms

Sample A

In the quality control at the Swedish Food Agency, all strains in the sample formed colonies on SFA. The strain of *S. marcescens* was present in somewhat lower concentration than *S. aureus* and *E. coli*.

Due to the high measurement uncertainty of the assigned value, all results are considered acceptable. Participants with results lower than 4.0 cfu ml^{-1} are however encouraged to consider repeating the analysis.

Note: The measurement uncertainty of the assigned value is not negligible. The evaluation of the results could therefore be affected. As a consequence, the lower acceptance limit has been manually adjusted so that one value – initially assessed as a low outlier – is included among the accepted results.

Sample B

All strains in the sample were target organisms. The strain of *S. saprophyticus* was present in somewhat lower concentration than *E. coli*, *E. faecium* and *S. aureus*.

All results are considered acceptable.

Note: The measurement uncertainty of the assigned value is not negligible. The evaluation of the results could therefore be affected. All reported results are however within the acceptance limits.

Sample C

All strains in the sample were target organisms. The strain of *S. xylosus* was present in somewhat higher concentration than *B. cereus* and *E. durans*. Three different types of colonies were observed on SFA at the Swedish Food Agency. Two of these (*B. cereus* and *S. xylosus*) were catalase-positive, and one (*E. durans*) was catalase-negative.

Due to the high measurement uncertainty of the assigned value, all results are considered acceptable. Participants with results lower than 4.0 cfu ml^{-1} or higher than 6.0 cfu ml^{-1} are however encouraged to consider repeating the analysis.

Note: The measurement uncertainty of the assigned value is not negligible. The evaluation of the results could therefore be affected. As a consequence, the acceptance limits have been manually adjusted so that two values – initially assessed as a low and a high outlier, respectively – are included among the accepted results.

General remarks

Only 15 participants reported results, and the statistical analysis was therefore based on a somewhat limited dataset. As a consequence, and also considering that the measurement uncertainties of the assigned values were not negligible, no results are considered as outliers.

Ten of the 15 participants followed ISO 13559:2002 / IDF 153:2002. This was last reviewed by ISO in 2019 and remains current. One participant followed a modified version of the older IDF 153:1999. The remaining participants did not clearly specify which method they used. All participants except one incubated on SFA.

The goal of the analysis is to identify potential contaminating microorganisms in dairy products. For these products, lactic acid bacteria are generally not considered as contaminating microorganisms. Lactic acid bacteria are catalase-negative and some participants therefore use confirmation with a catalase test. Such a test is however not strictly necessary with ISO 13559:2002 / IDF 153:2002. Five of the 14 participants performed a confirmation with a catalase test, whereas eight participants stated they did not perform any confirmation. The remaining two participants did not specify whether a confirmation was performed or not. No apparent difference was seen between participants that performed a confirmation and those that did not.

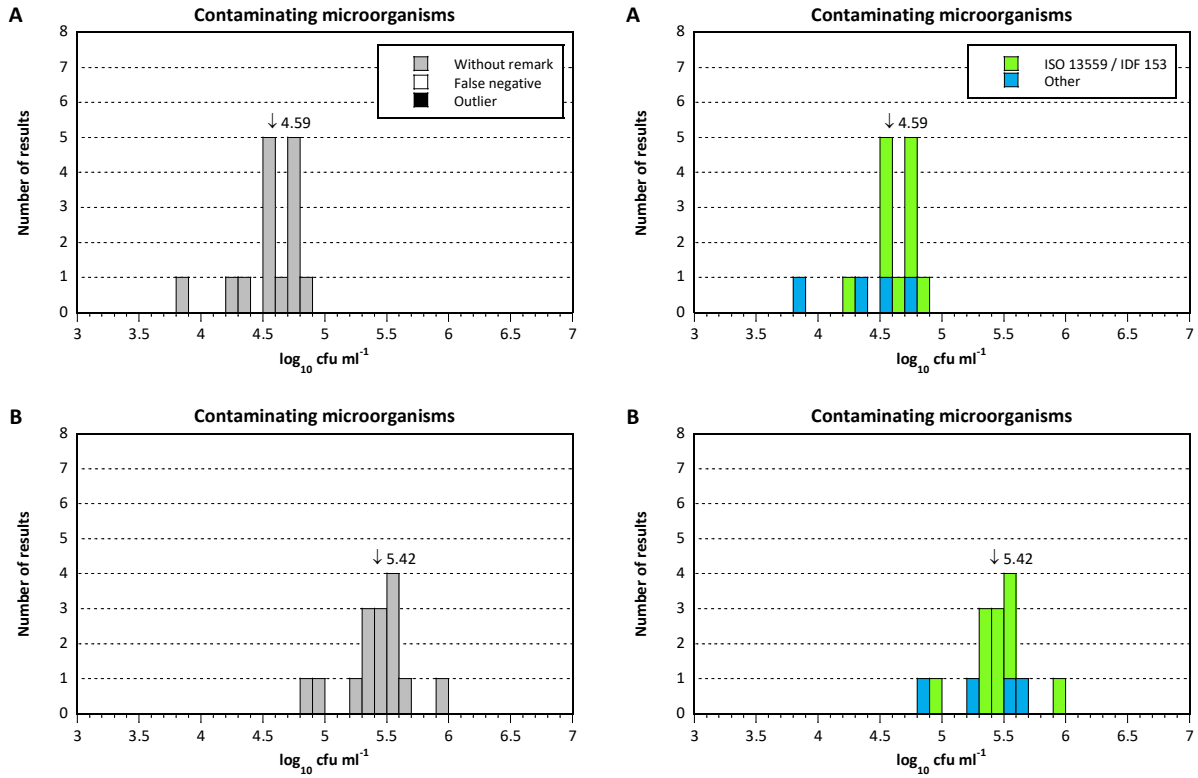
Table 4. Results from analysis of contaminating microorganisms.

Method	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**15**	**15**	**4.59**	**0.20**	**0**	**0**	**0**	**15**	**15**	**5.42**	**0.19**	**0**	**0**	**0**	**15**	**15**	**5.04**	**0.33**	**0**	**0**	**0**
ISO 13559:2002 / IDF 153:2002[a]	11	11	4.62	0.16	0	0	0	11	11	5.44	0.25	0	0	0	11	11	5.17	0.39	0	0	0
Other	4	4	-	-	0	0	0	4	4	-	-	0	0	0	4	4	-	-	0	0	0

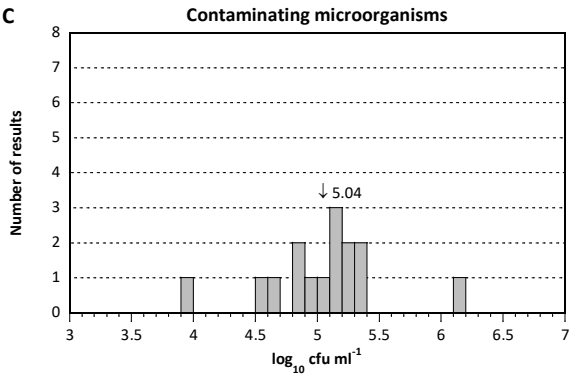
For "All results", m = robust m_{PT} and s = robust s_{PT}.

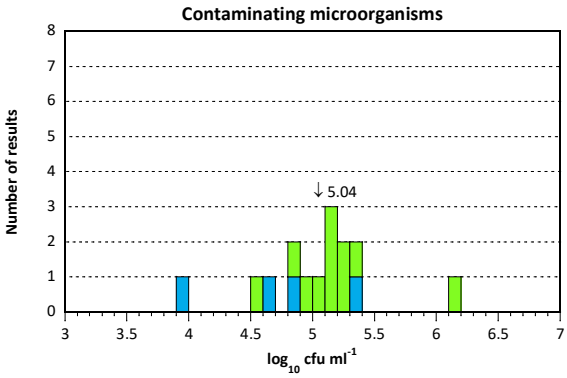
For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).

[a] Includes one participant that used a modified version of IDF 153:1991.



C


Contaminating microorganisms
Number of results
↓5.04
log10 cfu ml-1


Contaminating microorganisms
Number of results
↓5.04
log10 cfu ml-1

Enterobacteriaceae

Sample A

The strains of *E. coli* and *S. marcescens* were target organisms. In the Swedish Food Agency's quality control they both formed colonies on VRBG. The bile salt precipitation zone was less prominent for the colonies of *S. marcescens* compared to the colonies of *E. coli*. Both strains are oxidase-negative.

In total, 131 participants reported results. Two low and two high outliers were reported, as well as one false negative result.

Sample B

The strain of *E. coli* was target organism. On VRBG, it forms typical colonies surrounded by a bile salt precipitation zone. The strain is oxidase-negative.

In total, 130 participants reported results. Four low and one high outliers were reported, as well as one false negative result.

Sample C

No target organism was present in the sample.

In total, 131 participants reported results. No false positive results were reported.

General remarks

Enterobacteriaceae are Gram-negative and oxidase-negative bacteria that ferment glucose with the production of acid by-products. On VRBG they therefore form pink/red colonies, with or without a bile salt precipitation zone. The appearance is similar on Petrifilm EB, which also includes a colour indicator for acid by-products and a plastic film for detection of gas production.

Most participants followed either NMKL 144:2005 (45 %) or a method with Petrifilm EB (24 %). ISO methods were used by 21 % of the participants. Most followed ISO 21528-2:2017, which is based on colony-count. In comparison, ISO 21528-1:2017 is based on MPN. The latter method is recommended when the expected level of Enterobacteriaceae is lower than 100 cfu g^{-1}. Both ISO standards were last reviewed by ISO in 2022 and remain current. Ten participants still followed either of the previous – and now withdrawn – ISO 21528-2:2004 and ISO 21528-1:2004.

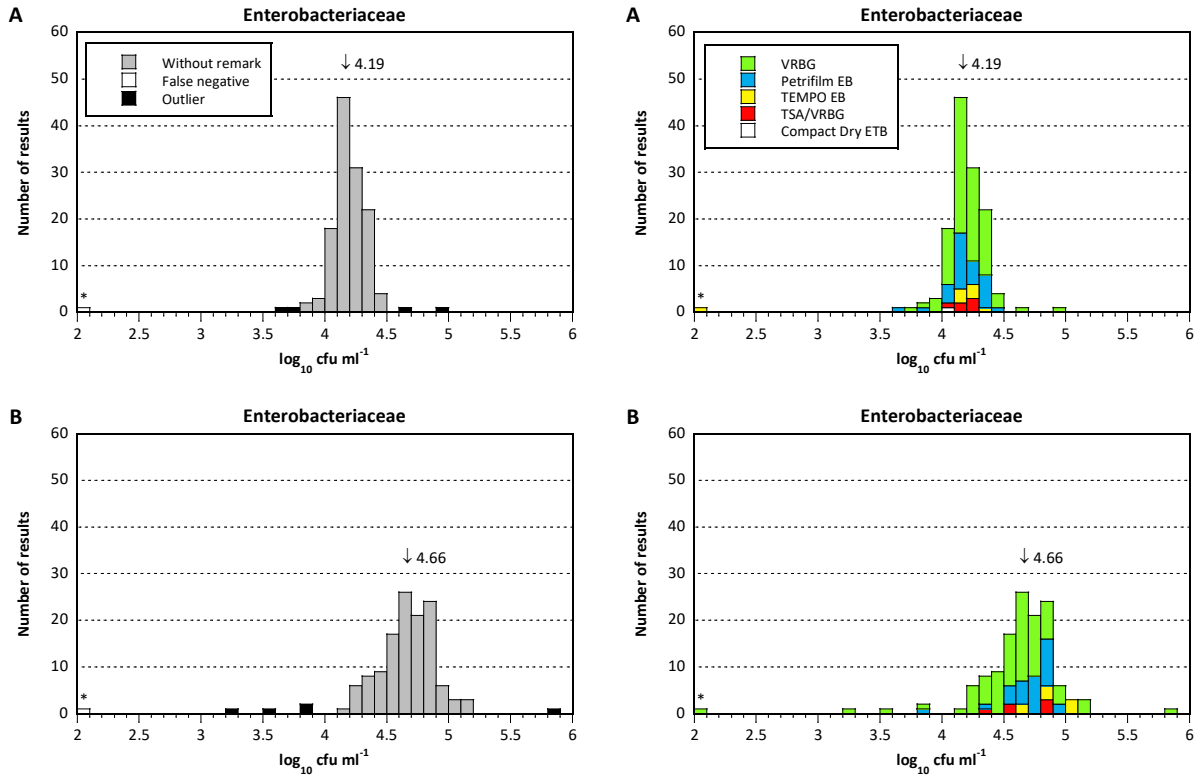
Confirmation was performed by 61 % of the participants, and most often consisted of an oxidase test.

Table 5. Results from analysis of Enterobacteriaceae.

Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**131**	**126**	**4.19**	**0.12**	**1**	**2**	**2**	**130**	**124**	**4.66**	**0.21**	**1**	**4**	**1**	**131**	**131**	**-**	**-**	**0**	**-**	**-**
VRBG	85	82	4.19	0.11	0	1	2	85	80	4.62	0.21	1	3	1	85	85	-	-	0	-	-
Petrifilm EB	31	30	4.19	0.13	0	1	0	31	30	4.74	0.13	0	1	0	31	31	-	-	0	-	-
TEMPO EB	8	7	4.22	0.07	1	0	0	8	8	4.86	0.18	0	0	0	8	8	-	-	0	-	-
TSA/VRBG	6	6	4.17	0.10	0	0	0	6	6	4.67	0.20	0	0	0	6	6	-	-	0	-	-
Compact Dry ETB	1	1	-	-	0	0	0	0	0	-	-	0	0	0	1	1	-	-	0	-	-

For “All results”, m = robust m_{PT} and s = robust s_{PT}.

For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).



Coliform bacteria, 37 °C and 30 °C

Sample A

The strain of *E. coli* was target organism. On VRB, it forms typical red colonies with a bile salt precipitation zone. In the Swedish Food Agency's quality control, *S. marcescens* also formed colonies on VRB. Both strains are oxidase-negative, but *S. marcescens* can be excluded after confirmation since in contrast to *E. coli*, it does not produce gas in BGLB.

At 37 °C, 72 participants reported results. Six low and one high outliers were reported, as well as one false negative result.

At 30 °C, 38 participants reported results. Two high outliers were reported, as well as one false negative result.

Sample B

The strain of *E. coli* (not identical to the one in sample A) was target organism. On VRB, it forms typical red colonies surrounded by a bile salt precipitation zone. The strain is oxidase-negative and produces gas from lactose fermentation in BGLB.

At 37 °C, 71 participants reported results. Five low outliers were reported, as well as four false negative results.

A 30 °C, 37 participants reported results. Three low outliers were reported.

Sample C

No target organism was present in the sample.

At 37 °C, 72 participants reported results. No false positive results were reported.

At 30 °C, 39 participants reported results. No false positive results were reported.

General remarks

Coliform bacteria are Gram-negative rods that ferment lactose with the production of gas and acid by-products. On VRB they form characteristic red colonies due to uptake of crystal violet and neutral red from the medium. The colonies are normally surrounded by a red/pink precipitation zone, which is formed due to the precipitation of bile salts when the pH decreases. Petrifilm CC and Petrifilm EC/CC are based on VRB, but also have a plastic film that facilitates detection of gas production.

Most participants followed NMKL 44:2004 or ISO 4832:2006, which both use VRB as the primary medium. At 37 °C, 3M™ Petrifilm™ was also used by many participants. Since these methods are based on media with a similar composition, differences in results are most often due to whether presumptive colonies and/or atypical colonies are confirmed or not. This varies between both methods and individual participants that use a particular method. In this PT however, no apparent differences could be seen

between results from the different methods and media. ISO 4832:2006 was last reviewed by ISO in 2021, and remains current.

LSB in combination with BGLB was used by participants that followed the MPN-based methods ISO 4831:2006 and NMKL 96:2009. They are adapted for use when the expected concentration of coliform bacteria is low, in the range of 100–300 cfu g^{-1}. This is normally not a problem, even though the concentrations of coliform bacteria in the PT samples is usually significantly higher. Users of these methods should however be aware of this, since it sometimes has an effect on the outcome. ISO 4831:2006 was last reviewed by ISO in 2021 and remains current.

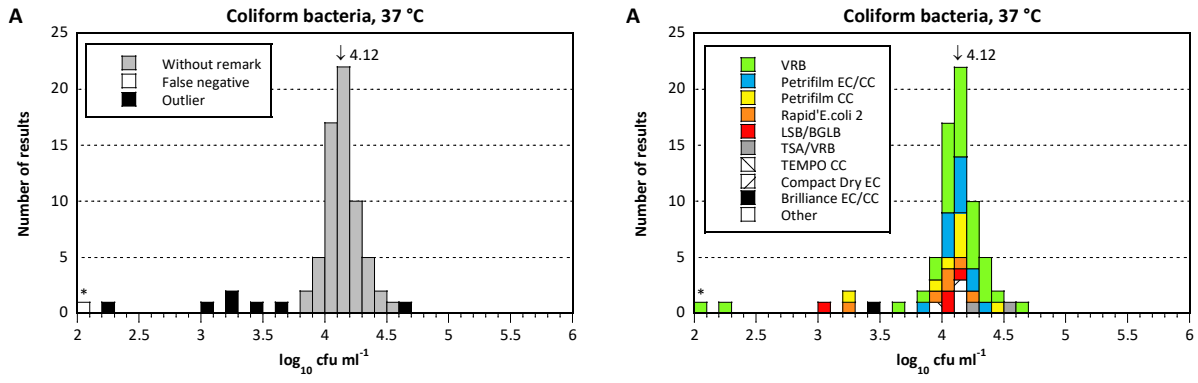
A few participants used methods/media that detect β-galactosidase and β-glucuronidase activity; RAPID'E.coli 2, Compact Dry EC and Brilliance EC/CC. For example on RAPID'E.coli 2 agar, coliform bacteria (Gal+/Gluc-) form blue/green colonies, while *E. coli* (Gal+/Gluc+) form pink/purple colonies. Two participants performed a pre-incubation on TSA prior to incubation on VRB, which is recommended by some methods if the sample is suspected to contain stressed coliform bacteria.

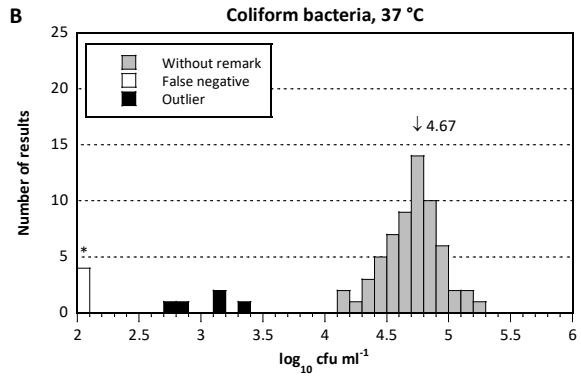
Table 6. Results from analysis of coliform bacteria, 37 °C.

Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**72**	**64**	**4.12**	**0.15**	**1**	**6**	**1**	**71**	**62**	**4.67**	**0.25**	**4**	**5**	**0**	**72**	**72**	**-**	**-**	**0**	**-**	**-**
VRB	34	30	4.14	0.13	1	2	1	34	29	4.61	0.19	1	4	0	34	34	-	-	0	-	-
Petrifilm EC/CC	13	13	4.11	0.13	0	0	0	13	13	4.78	0.22	0	0	0	13	13	-	-	0	-	-
Petrifilm CC	8	7	4.15	0.14	0	1	0	8	7	4.81	0.11	1	0	0	8	8	-	-	0	-	-
Rapid'E.coli 2	6	5	4.11	0.11	0	1	0	5	4	-	-	1	0	0	6	6	-	-	0	-	-
LSB/BGLB	4	3	-	-	0	1	0	4	3	-	-	0	1	0	4	4	-	-	0	-	-
TSA/VRB	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	-	-
TEMPO CC	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-
Compact Dry EC	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-
Brilliance EC/CC	1	0	-	-	0	1	0	1	0	-	-	1	0	0	1	1	-	-	0	-	-
Other	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	-	-

For "All results", m = robust m_{PT} and s = robust s_{PT}.

For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).





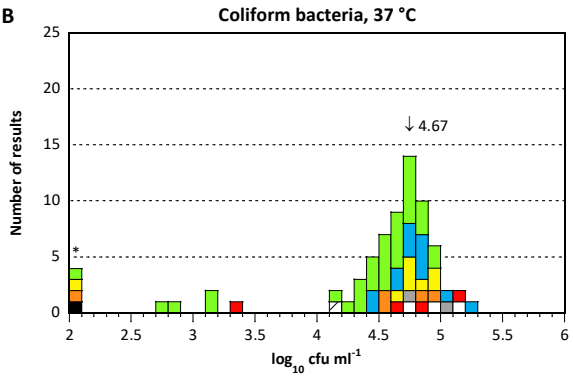


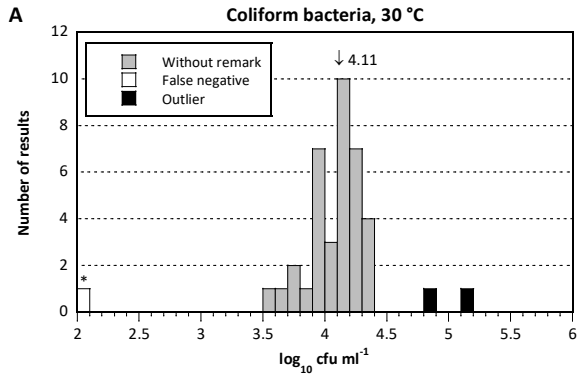
Table 7. Results from analysis of coliform bacteria, 30 °C.

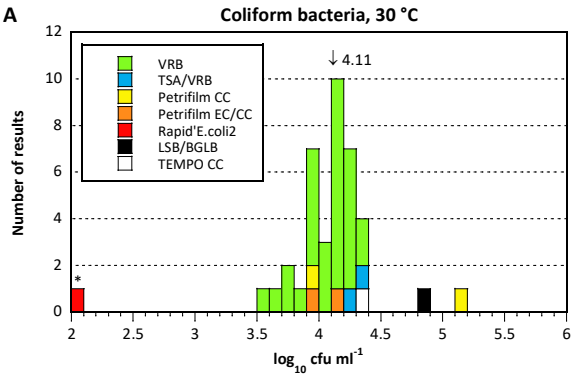
Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**39**	**36**	**4.11**	**0.19**	**1**	**0**	**2**	**38**	**35**	**4.58**	**0.30**	**0**	**3**	**0**	**40**	**40**	**-**	**-**	**0**	**-**	**-**
VRB	30	30	4.06	0.19	0	0	0	30	28	4.56	0.23	0	2	0	30	30	-	-	0	-	-
TSA/VRB	2	2	-	-	0	0	0	2	2	-	-	0	0	0	3	3	-	-	0	-	-
Petrifilm CC	2	1	-	-	0	0	1	2	1	-	-	0	1	0	2	2	-	-	0	-	-
Petrifilm EC/CC	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	-	-
Rapid'E.coli 2	1	0	-	-	1	0	0	0	0	-	-	0	0	0	1	1	-	-	0	-	-
LSB/BGLB	1	0	-	-	0	0	1	1	1	-	-	0	0	0	1	1	-	-	0	-	-
TEMPO CC	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-

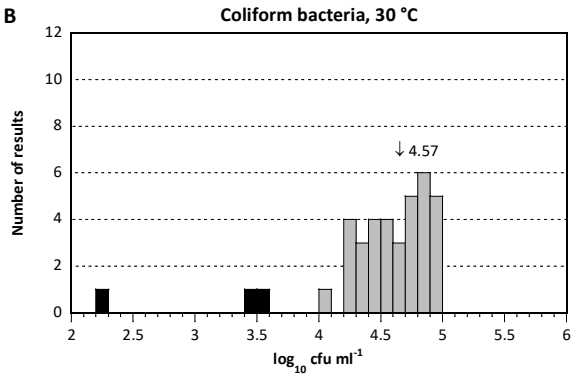
For “All results”, m = robust m_{PT} and s = robust s_{PT}.

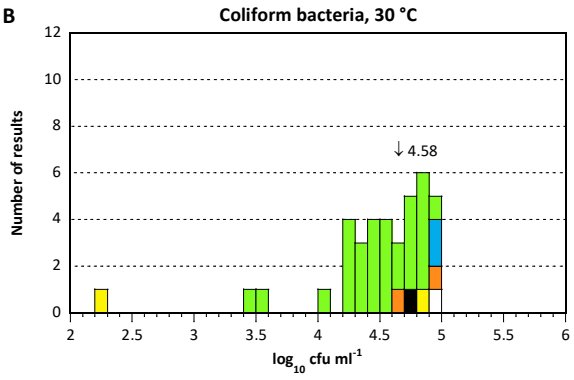
For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).

Comment: One participant that reported results at 30 °C, actually incubated at 37 °C. These results were as an exception included in the evaluation, as it was determined it did not in a significant way affect the assessment of the other participants’ results.






B
Coliform bacteria, 30 °C
Number of results
↓4.57
log10 cfu ml-1


B
Coliform bacteria, 30 °C
Number of results
↓4.58
log10 cfu ml-1

Thermotolerant coliform bacteria and *Escherichia coli*

Sample A

The strain of *E. coli* was the target organism for both analyses. On VRB, it forms typical red colonies with a bile salt precipitation zone. In the Swedish Food Agency's quality control, no other colonies were detected on VRB. The strain produces both gas and indole in LTLSB. The strain is oxidase-negative, and positive for β-glucuronidase.

For thermotolerant coliform bacteria, 36 participants reported results. Two low outliers were reported.

For *E. coli*, 102 participants reported results. Three low and one high outliers were reported, as well as three false negative results. The mean value for TEMPO EC was slightly higher compared to other methods/media. This has been seen in several previous PT rounds, and can thus be considered normal.

Sample B

The strain of *E. coli* (not identical to the one in sample A) was target organism. On VRB, it forms typical red colonies with a bile salt precipitation zone. The strain produces both gas and indole in LTLSB. The strain is oxidase-negative, and positive for β-glucuronidase.

For thermotolerant coliform bacteria, 36 participants reported results. Four low outliers were reported.

For *E. coli*, 100 participants reported results. Five low and one high outliers were reported. The mean value for TBX was lower compared to the mean value for other media. This has been seen in several previous PT rounds, and can thus be considered normal.

Sample C

No target organism was present in the sample.

For thermotolerant coliform bacteria, 36 participants reported results. No false positive results were reported.

For *E. coli*, 105 participants reported results. One false positive result was reported.

General remarks

On VRB, thermotolerant coliform bacteria form dark red colonies, surrounded by a red zone of bile salt precipitation. They also produce gas as a consequence of lactose fermentation. *E. coli* can be distinguished from other thermotolerant coliform bacteria by their production of indole, and since they possess the β-glucuronidase enzyme.

NMKL 125:2005 was by far the most commonly used method for the analysis of thermotolerant coliform bacteria (67 % of the participants). It is based on VRB and describes the analysis of both thermotolerant coliform bacteria and of *E. coli*. For *E. coli*, most participants used methods based on

3M™ Petrifilm™ (either Petrifilm EC/CC or Petrifilm SEC), or NMKL 125:2005. Both Petrifilm EC/CC and Petrifilm SEC include substrates that facilitate detection of β-glucuronidase, and therefore *E. coli* form blue-green colonies on these media. The plastic film in Petrifilm EC/CC and Petrifilm SEC also enables detection of gas production due to lactose fermentation.

The ISO 16649-2:2001 method is based on TBX, on which β-glucuronidase-positive *E. coli* form blue colonies. Participants that use TBX often get lower results compared to participants that use other media. This was clearly seen for sample B in this PT round. Lower results for TBX could be a consequence of participants not performing a pre-incubation at a lower temperature. ISO 16649-2:2001 was last reviewed by ISO in 2019 and remains current.

For *E. coli*, the mean value for the MPN-based TEMPO EC is often higher compared to other methods/media. This was apparent for sample A in this PT round, where the results for TEMPO EC was approximately one standard deviation higher compared to other methods/media. This has been seen in previous PT rounds and can be considered normal.

A few participants followed ISO 7251:2005 and NMKL 96:2009. ISO 7251 is an MPN-based method for the detection of *E. coli*. It was last reviewed by ISO in 2019 and remains current. NMKL 96 is also based on MPN, and is adapted for the analysis of coliform bacteria, thermotolerant coliform bacteria and *E. coli* in fish and seafood. Participants that followed these methods typically incubated in LSB/EC.

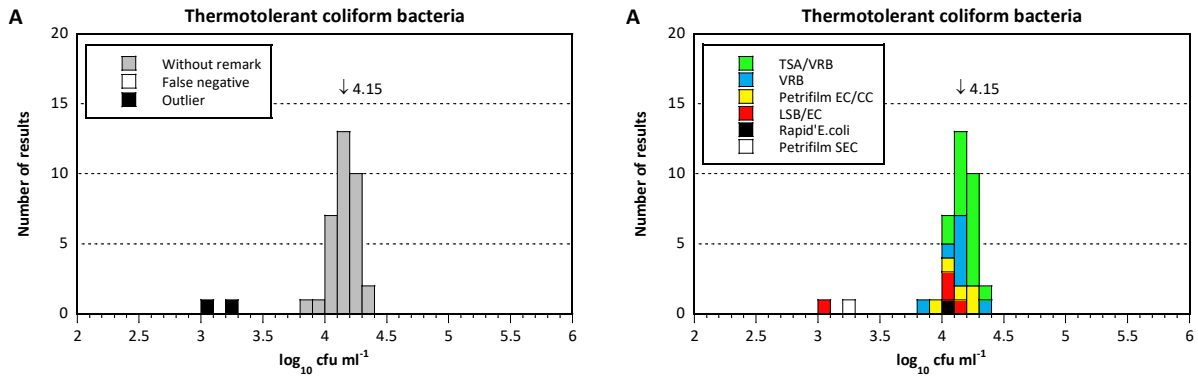
Table 8. Results from analysis of thermotolerant coliform bacteria.

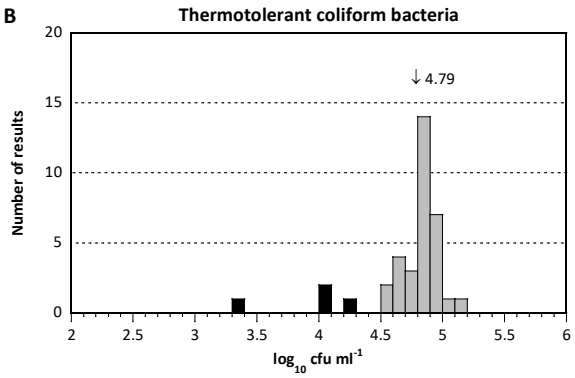
Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**36**	**34**	**4.15**	**0.11**	**0**	**2**	**0**	**36**	**32**	**4.79**	**0.16**	**0**	**4**	**0**	**36**	**36**	**-**	**-**	**0**	**-**	**-**
TSA/VRB	17	17	4.20	0.07	0	0	0	17	17	4.87	0.06	0	0	0	17	17	-	-	0	-	-
VRB	8	8	4.12	0.12	0	0	0	8	7	4.81	0.12	0	1	0	8	8	-	-	0	-	-
Petrifilm EC/CC	5	5	4.13	0.15	0	0	0	5	5	4.73	0.16	0	0	0	5	5	-	-	0	-	-
LSB/EC[1]	4	3	-	-	0	1	0	4	2	-	-	0	2	0	4	4	-	-	0	-	-
Rapid'E.coli	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-
Petrifilm SEC	1	0	-	-	0	1	0	1	0	-	-	0	1	0	1	1	-	-	0	-	-

For "All results", m = robust m_{PT} and s = robust s_{PT}.

For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).

[1] Represents participants that used MPN-based methods, where EC is normally used after a first enrichment in LSB.





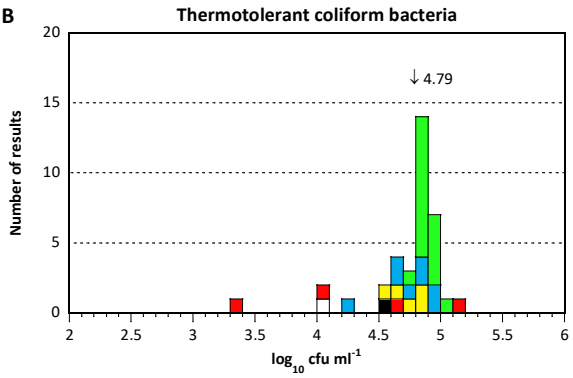


Table 9. Results from analysis of *Escherichia coli*.

Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**102**	**95**	**4.11**	**0.12**	**3**	**3**	**1**	**100**	**94**	**4.73**	**0.23**	**0**	**5**	**1**	**105**	**104**	**-**	**-**	**1**	**-**	**-**
Petrifilm EC/CC	22	21	4.09	0.11	0	0	1	22	21	4.79	0.18	0	0	1	22	22	-	-	0	-	-
TSA/VRB[1]	21	20	4.15	0.09	1	0	0	21	20	4.86	0.08	0	1	0	21	21	-	-	0	-	-
Petrifilm SEC	18	17	4.09	0.16	1	0	0	17	16	4.75	0.13	0	1	0	18	18	-	-	0	-	-
TBX	10	9	4.03	0.07	1	0	0	10	8	4.39	0.29	0	2	0	11	10	-	-	1	-	-
TEMPO EC	7	7	4.25	0.12	0	0	0	7	7	4.88	0.15	0	0	0	7	7	-	-	0	-	-
VRB	7	7	4.14	0.09	0	0	0	7	7	4.63	0.21	0	0	0	8	8	-	-	0	-	-
Compact Dry EC	4	4	-	-	0	0	0	4	4	-	-	0	0	0	4	4	-	-	0	-	-
Brilliance EC/CC	4	2	-	-	0	2	0	4	4	-	-	0	0	0	4	4	-	-	0	-	-
LSB/EC[2]	3	2	-	-	0	1	0	3	2	-	-	0	1	0	4	4	-	-	0	-	-
Other[3]	6	6	-	-	0	0	0	5	5	-	-	0	0	0	6	6	-	-	0	-	-

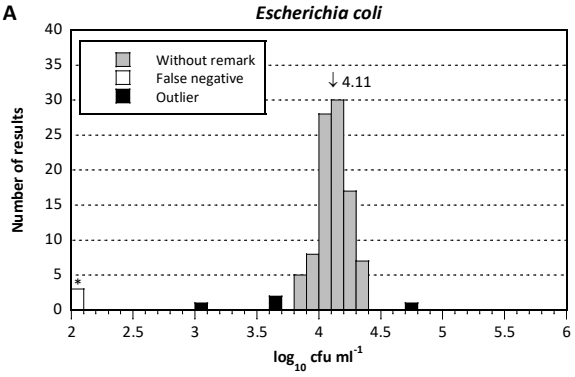
For "All results", m = robust m_{PT} and s = robust s_{PT}.

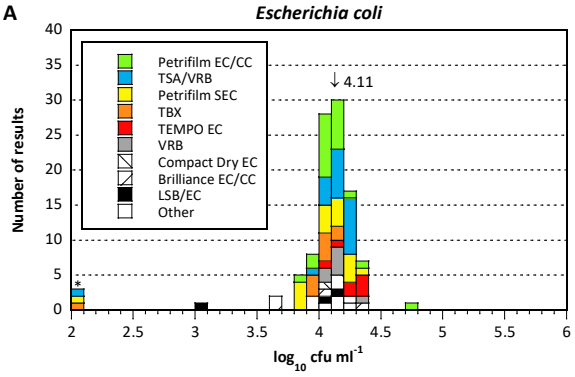
For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).

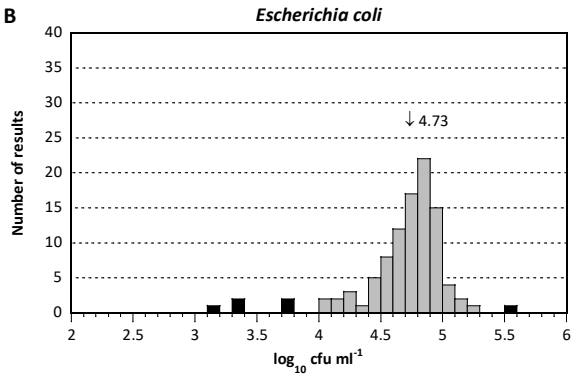
[1] Includes three participants that used TSA/VRBG.

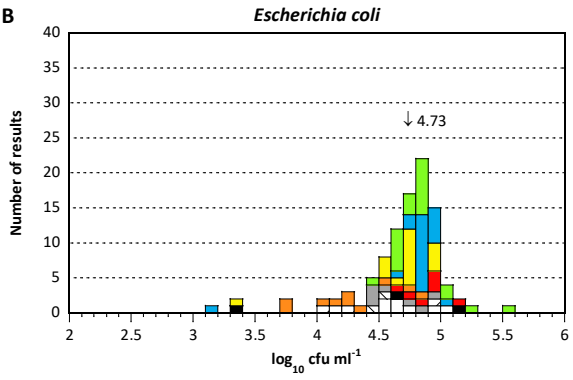
[2] Represents participants that used MPN-based methods, where EC is normally used after a first enrichment in LSB.

[3] Includes e.g. Rapid'E.coli 2 and Rebecca agar.






B
Escherichia coli
Number of results
↓4.73
log10 cfu ml-1


B
Escherichia coli
Number of results
↓4.73
log10 cfu ml-1

Presumptive *Bacillus cereus*

Sample A

No target organism was present in the sample. The strains of *S. marcescens* and *S. aureus* can however form colonies on BA. In the Swedish Food Agency's quality control, only atypical colonies were detected on BA. They could also easily be excluded after confirmation on BcsA.

In total, 104 participants reported results. Three false positive results were reported.

Sample B

No target organism was present in the sample. Several strains in the sample may form colonies on BA. They are however easily distinguished from *B. cereus*, since they are not surrounded by a zone of haemolysis.

In total, 102 participants reported results. Two false positive result were reported.

Sample C

The strain of *B. cereus* was target organism. On BA, it forms typical grey colonies with a zone of haemolysis. On BcsA, it forms typical blue colonies surrounded by a blue zone of precipitation. *S. xylosus* may also form colonies on BA, but is easily distinguished from *B. cereus* due to its atypical appearance on BA and BcsA.

In total, 104 participants reported results. Two high outliers were reported.

The mean value for Compact Dry X-BC was noticeably lower compared to other media, but within one standard deviation of the assigned value (m_{PT}).

General remarks

Most participants followed either NMKL 67:2010 (48 %) or ISO 7932:2004 (21 %). The new NMKL 67:2021 – which replaces NMKL 67:2010 – was in contrast only followed by ten participants (10 %). With NMKL 67:2021, primary incubation on BcsA is followed by confirmation on BA. With ISO 7932:2004, primary incubation on MYP is followed by confirmation on BA. An amendment is available for the ISO method (ISO 7932:2004/Amd 1:2020). It contains optional tests, including for PCR detection of cytK genes.

On BA, *B. cereus* forms large, irregular grey colonies, surrounded by a distinct zone of haemolysis. On BcsA, presumptive *B. cereus* form bluish colonies that are surrounded by a blue zone of precipitation, due to lecithinase activity on egg yolk present in the medium. On MYP, presumptive *B. cereus* form large pink colonies that are normally surrounded by a zone of precipitation, again as a consequence of lecithinase activity.

Compact Dry X-BC was used by five participants. The chromogenic and selective agents in this medium cause *B. cereus* to form blue/green colonies, whereas other bacteria normally form white colonies. Low results for Compact Dry X-BC – as in sample C – has been seen in previous PT rounds. That Compact

Dry X-BC may give somewhat lower results compared to the reference method ISO 7932:2004 is also mentioned in both the NordVal 045 and MicroVal 2011-LR41 validations. Slightly lower results for Compact Dry X-BC can therefore be considered normal.

The chromogenic medium CBC was used by five participants. CBC contains the substrate X-Gluc, which is cleaved by *B. cereus* β-glucuronidase. Colonies of *B. cereus* are therefore white with a blue/green centre on this medium.

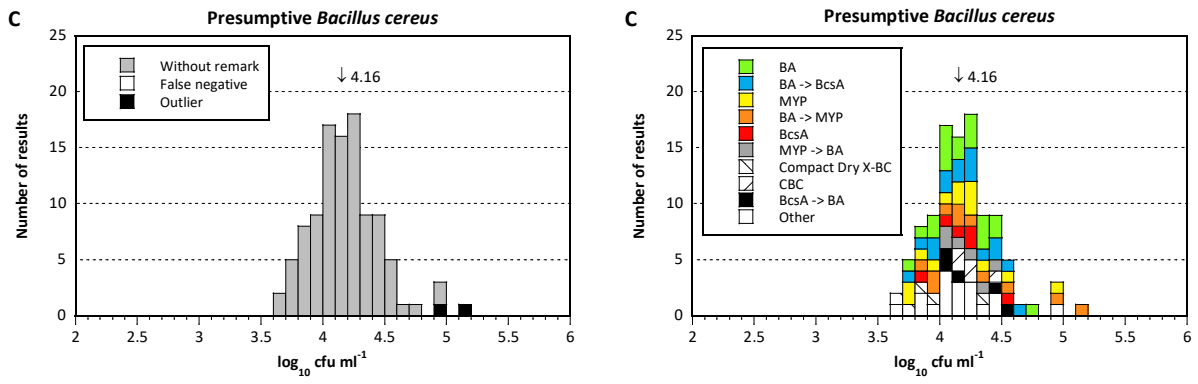
Table 10. Results from analysis of presumptive *Bacillus cereus*.

Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**104**	**101**	**-**	**-**	**3**	**-**	**-**	**102**	**100**	**-**	**-**	**2**	**-**	**-**	**104**	**102**	**4.16**	**0.26**	**0**	**0**	**2**
BA	18	18	-	-	0	-	-	18	18	-	-	0	-	-	19	19	4.17	0.25	0	0	0
BA → BcsA	17	16	-	-	1	-	-	17	16	-	-	1	-	-	16	16	4.18	0.25	0	0	0
MYP	13	13	-	-	0	-	-	12	12	-	-	0	-	-	13	12	4.11	0.25	0	0	1
BA → MYP	11	11	-	-	0	-	-	11	11	-	-	0	-	-	11	10	4.19	0.33	0	0	1
BcsA	6	5	-	-	1	-	-	6	5	-	-	1	-	-	6	6	4.19	0.24	0	0	0
MYP → BA	6	6	-	-	0	-	-	5	5	-	-	0	-	-	6	6	4.21	0.16	0	0	0
Compact Dry X-BC	5	4	-	-	1	-	-	5	5	-	-	0	-	-	5	5	3.91	0.27	0	0	0
CBC	5	5	-	-	0	-	-	5	5	-	-	0	-	-	5	5	4.24	0.11	0	0	0
BcsA → BA	5	5	-	-	0	-	-	5	5	-	-	0	-	-	5	5	4.26	0.25	0	0	0
Other[1]	18	18	-	-	0	-	-	18	18	-	-	0	-	-	18	18	-	-	0	0	0

For "All results", m = robust m_{PT} and s = robust s_{PT}.

For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).

[1] Includes COMPASS® Bacillus cereus agar, BACARA™, PEMBA, RAPID'B.cereus and TEMPO BC.



Coagulase-positive staphylococci

Sample A

The strain of *S. aureus* was the target organism. In the Swedish Food Agency's quality control, it formed typical colonies on RPFA. The surrounding coagulase zone was less prominent after 24 hours incubation, compared to after 48 hours incubation.

In total, 82 participants reported results. Four low and one high outliers were reported.

Sample B

The same strain of *S. aureus* as in sample A was target organism. On RPFA, it forms typical grey colonies surrounded by a coagulase zone. The coagulase-negative strain of *S. saprophyticus* was also present in the sample. On RPFA it forms grey colonies that are smaller compared to *S. aureus*, and that are not surrounded by a coagulase zone.

In total, 80 participants reported results. Three low and one high outliers were reported, as well as one false negative result.

Sample C

No target organism was present in the sample. The sample did however contain a coagulase-negative strain of *S. xylosus.* On RPFA, it forms grey colonies without a coagulase zone.

In total, 83 participants reported results. Nine of these reported a false positive result.

General remarks

The majority of the participants incubated on BP. On this medium, *S. aureus* form characteristic convex, shiny colonies that have a grey/black colour due to reduction of tellurite in the medium. The colonies are usually surrounded by a clear zone, due to proteolysis of egg yolk in the medium (lecithinase activity). An opaque halo may also form near the colony, due to precipitation caused by lipase activity. Participants that used BP typically performed a confirmation based on coagulase activity, for example a tube coagulase test or the use of RPFA as a secondary medium.

The second most common media were RPFA and Petrifilm Staph. With RPFA, the coagulase activity is tested directly in the medium. Petrifilm Staph is based on a modified Baird-Parker agar. It also contains a chromogenic indicator that causes *S. aureus* to form red/purple colonies. Participants that used Petrifilm Staph typically performed a confirmation with Petrifilm Staph Express Disk. This is based on detection of extracellular DNase, which is produced by the majority of coagulase-positive *S. aureus*, but also by the coagulase-positive staphylococci *S. intermedius* and *S. hyicus*. Toluidin blue O in the disks visualises DNase activity as a pink zone around the colonies.

Most participants (45 %) followed NMKL 66:2009, where incubation is done either with BP and/or RPFA. In comparison, ISO 6888-1:2021 stipulates BP, whereas 6888-2:2021 stipulates the use of RPFA. Most participants that followed an ISO method, referenced the withdrawn versions ISO 6888-1:1999 and ISO 6888-2:1999. One participant followed the MPN-based ISO 6888-3:2003, which is adapted for

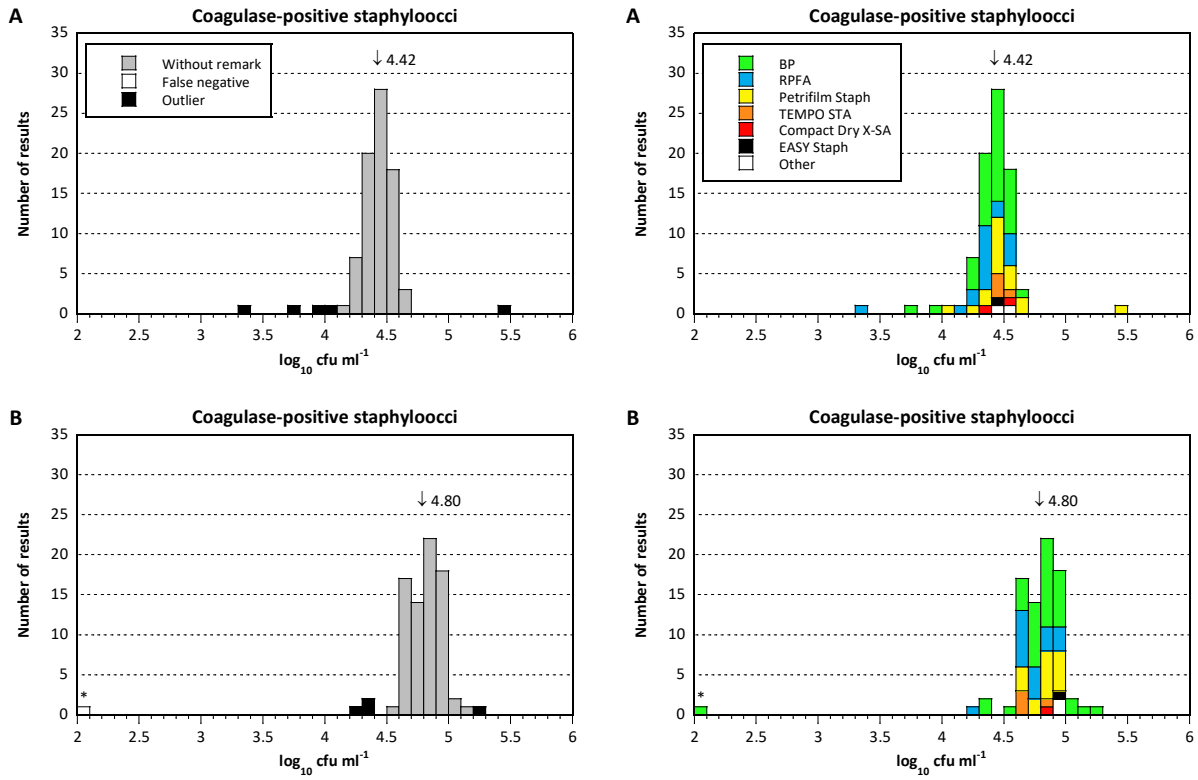
use when low numbers of stressed coagulase-positive staphylococci are expected. This was last reviewed by ISO in 2022 and remains current.

Table 11. Results from analysis of coagulase-positive staphylococci.

Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**82**	**77**	**4.42**	**0.12**	**0**	**4**	**1**	**80**	**75**	**4.80**	**0.14**	**1**	**3**	**1**	**83**	**74**	**-**	**-**	**9**	**-**	**-**
BP	38	36	4.43	0.10	0	2	0	38	34	4.83	0.13	1	2	1	39	35	-	-	4	-	-
RPFA	18	17	4.37	0.12	0	1	0	18	17	4.76	0.12	0	1	0	18	18	-	-	0	-	-
Petrifilm Staph	17	15	4.45	0.10	0	1	1	16	16	4.81	0.12	0	0	0	17	13	-	-	4	-	-
TEMPO STA	4	4	-	-	0	0	0	4	4	-	-	0	0	0	4	4	-	-	0	-	-
Compact Dry X-SA	2	2	-	-	0	0	0	1	1	-	-	0	0	0	2	1	-	-	1	-	-
EASY Staph	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-
Other	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	-	-

For "All results", m = robust m_{PT} and s = robust s_{PT}.

For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).



Enterococci

Sample A

No target organism was present in the sample. In the Swedish Food Agency's quality control, no colonies were detected on ENT.

In total, 60 participants reported results. Five of these reported a false positive result.

Sample B

The strain of *E. faecium* was target organism. On ENT, it forms typical brown-red raised colonies. On BEA, a distinct black colour is typically seen.

In total, 60 participants reported results. Three low and one high outliers were reported, as well as one false negative result.

Sample C

The strain of *E. durans* was target organism. On ENT, it forms typical brown-red raised colonies. On BEA, a distinct black colour is typically seen after both 2 h and 24 incubation. The strain is catalase-negative.

In total, 60 participants reported results. Three high outliers were reported, as well as three false negative results.

General remarks

Enterococci are normally defined as Gram-positive, catalase-negative and oval cocci that hydrolyse esculin at 44 °C. On ENT they reduce the colourless substrate 2,3,5-trifenyltetrazolium chloride to red formazan and form slightly raised colonies with a pink/red/maroon colour. They can sometimes also have a colourless edge. On BEA, which is often used for confirmation, enterococci cause a tan/black colour in the medium after 2–24 hours. The colour comes from β-glucosidase hydrolysis of esculin in BEA. This produces esculetin and glucose, which together with iron ions in the medium form a black precipitate.

The vast majority of the participants incubated on ENT, often with a pre-incubation on TSA. A pre-incubation on TSA can be preferable if the presence of stressed enterococci is expected. A smaller number of participants used COMPASS® Enterococcus agar, KEAA or Compact Dry ETC. KEAA was used by participants that followed IDF 149A:1997. With KEAA, hydrolysis of esculin is detected directly in the medium. Similar to BEA, COMPASS also detects β-glucosidase activity, but is instead based on the substrate X-Gluc. On this medium, enterococci therefore form blue colonies. Most participants that incubated on COMPASS also performed a confirmation on BEA.

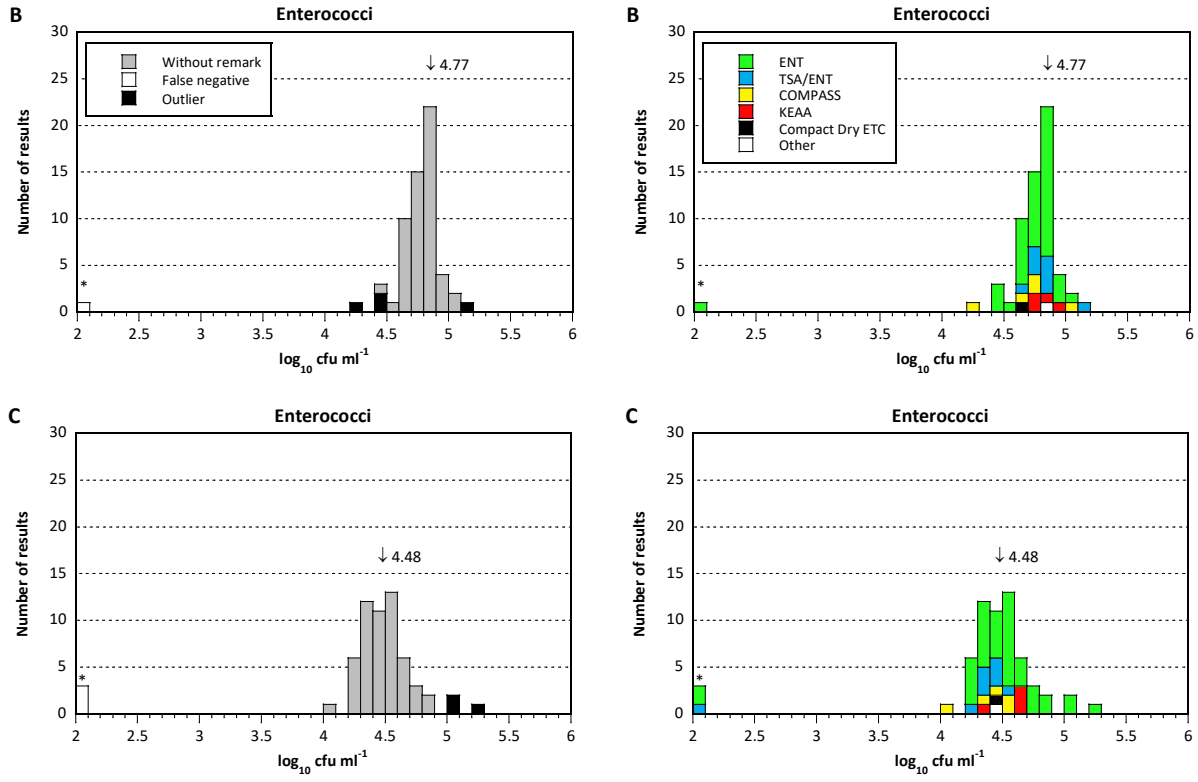
A clear majority of the participants (68 %) followed NMKL 68:2011. A few participants followed IDF 149A:1997 (7 %) or the drinking water method ISO 7899-2:2000 (7 %). ISO 7899-2:2000 was last reviewed by ISO in 2021 and remains current. IDF 149A:1997 has been replaced by ISO 27205:2010/IDF 149:2010. This was last reviewed by ISO in 2020 and remains current.

Table 12. Results from analysis of Enterococci.

Medium	Sample A							Sample B							Sample C						
	N	n	m	s	F	<	>	N	n	m	s	F	<	>	N	n	m	s	F	<	>
All results	**60**	**55**	**-**	**-**	**5**	**-**	**-**	**60**	**55**	**4.77**	**0.11**	**1**	**3**	**1**	**60**	**54**	**4.48**	**0.18**	**3**	**0**	**3**
ENT	40	38	-	-	2	-	-	40	37	4.77	0.11	1	2	0	40	35	4.49	0.17	2	0	3
TSA/ENT	9	6	-	-	3	-	-	9	8	4.78	0.08	0	0	1	9	8	4.40	0.07	1	0	0
COMPASS	5	5	-	-	0	-	-	5	4	-	-	0	1	0	5	5	4.39	0.19	0	0	0
KEAA	4	4	-	-	0	-	-	4	4	-	-	0	0	0	4	4	-	-	0	0	0
Compact Dry ETC	1	1	-	-	0	-	-	1	1	-	-	0	0	0	1	1	-	-	0	0	0
Other	1	1	-	-	0	-	-	1	1	-	-	0	0	0	1	1	-	-	0	0	0

For “All results”, m = robust m_{PT} and s = robust s_{PT}.

For individual methods, m = mean value and s = standard deviation for the particular method (outliers and false results excluded).



Gram-negative bacteria in pasteurised milk and cream

Sample A

The strains of *E. coli* and *S. marcescens* are Gram-negative.

In total, 12 participants reported results. All of these reported a correct positive result.

Sample B

The strain of *E. coli* is Gram-negative.

In total, 12 participants reported results. All of these reported a correct positive result.

Sample C

No target organism was present in the sample.

In total, 12 participants reported results. One of these reported a false positive result.

General remarks

NMKL 192:2011 is a qualitative method for detecting recontamination by Gram-negative bacteria in pasteurised milk and cream. These bacteria do not survive high temperature/short time pasteurisation (HTST), where the temperature is raised to 72 °C for at least 15 seconds. Presence of Gram-negative bacteria therefore indicates recontamination, something that may limit the shelf-life of the product.

Nine of the 12 participants followed NMKL 192:2011. One participant followed the ISO method for Enterobacteriaceae; ISO 21528-2:2017. This was last reviewed by ISO in 2022 and remains current. The two remaining participants followed a company-specific method.

Eleven of the 12 participants incubated on VRBG, while one used MacConkey agar.

All reported results were correct, except for one false positive result for sample C.

Table 13. Results from analysis of Gram-negative bacteria in pasteurised milk and cream.

Medium	Sample A			Sample B			Sample C		
	N	n	F	N	n	F	N	n	F
All results	**12**	**12**	**0**	**12**	**12**	**0**	**12**	**11**	**1**
NMKL 192:2011	9	9	0	9	9	0	9	9	0
ISO 21528-2:2017	1	1	0	1	1	0	1	1	0
Other	2	2	0	2	2	0	2	1	1

Outcome of the results of individual participants - assessment

Reporting and evaluation of results

The results of all participants are listed in Annex 1, together with the minimum and maximum accepted values for each analytical parameter. Outliers and false results are highlighted in yellow and red, respectively, with bold font.

Participants are not grouped or ranked based on their results. The performance of an individual participant can be broadly assessed by the numbers of outliers and false results, and by the z-scores.

Information on the results processing and recommendations for follow-up work are given in the Scheme Protocol [2].

Samples for follow-up analyses can be ordered at: www.livsmedelsverket.se/en/PT-extra

Box plots and numbers of deviating results for each participant

Box plots are based on the z-scores listed in Annex 2, and give a comprehensive view of the performance of each participant. The range of z-scores is indicated by the size of the box and, for most participants, by lines and/or circles above and beneath the box. A small range of values, centred around zero, indicates that the results of the individual participant are in general close to m_{PT} for the different analyses. For each participant, the number of false results and outliers are also listed in the tables below the box plots.

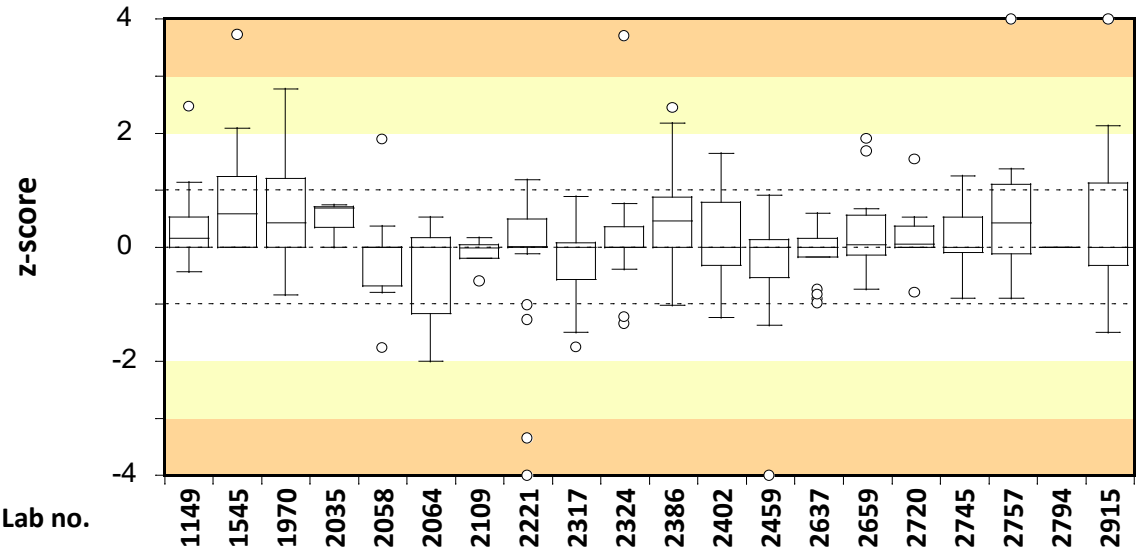
Outliers are included in the figures after being calculated to z-scores in the same way as for other results. Correct results for qualitative analyses and correct negative results for quantitative analyses without target organism are given a z-score of 0. False results do not generate any z-scores, and are not included in "No. of results".

The participant's median value is illustrated by a horizontal line in the box. Each box includes 50 % of a participant's results (25 % of the results above the median and 25 % of the results below the median). The remaining 50 % are illustrated by lines and circles outside the box. A circle is for technical reasons shown in the plot when a value deviates to certain degree* from the other values. This does not by itself indicate that the value is an outlier.

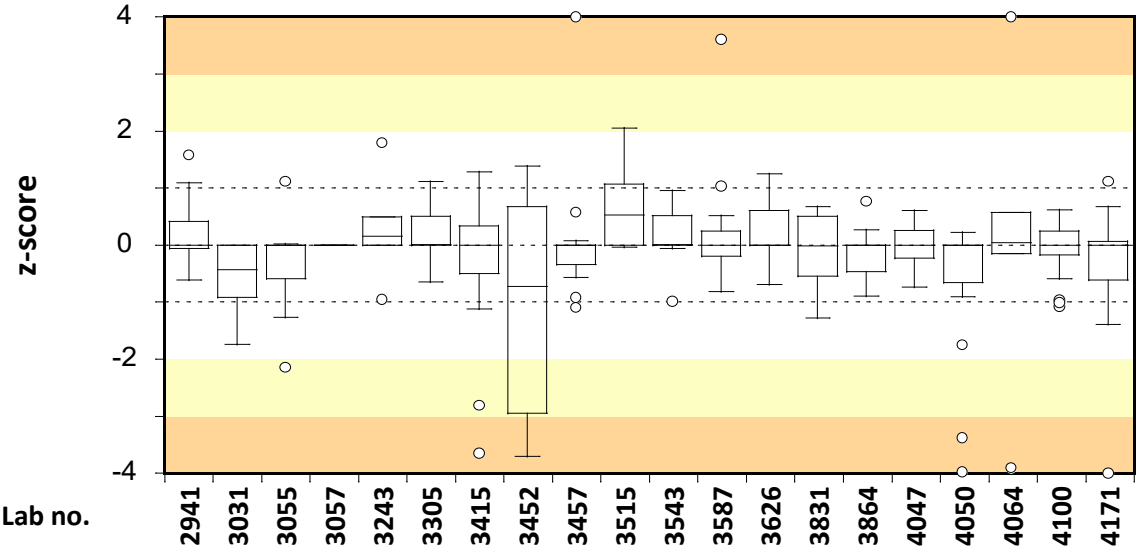
Z-scores >+4 and <−4 are positioned at +4 and −4, respectively, in the plot. The background is divided by lines and shaded fields to simplify identifying the range in which the results are located.

* < [lowest value in the box −1,5 × (highest value in the box − lowest value in the box)] or

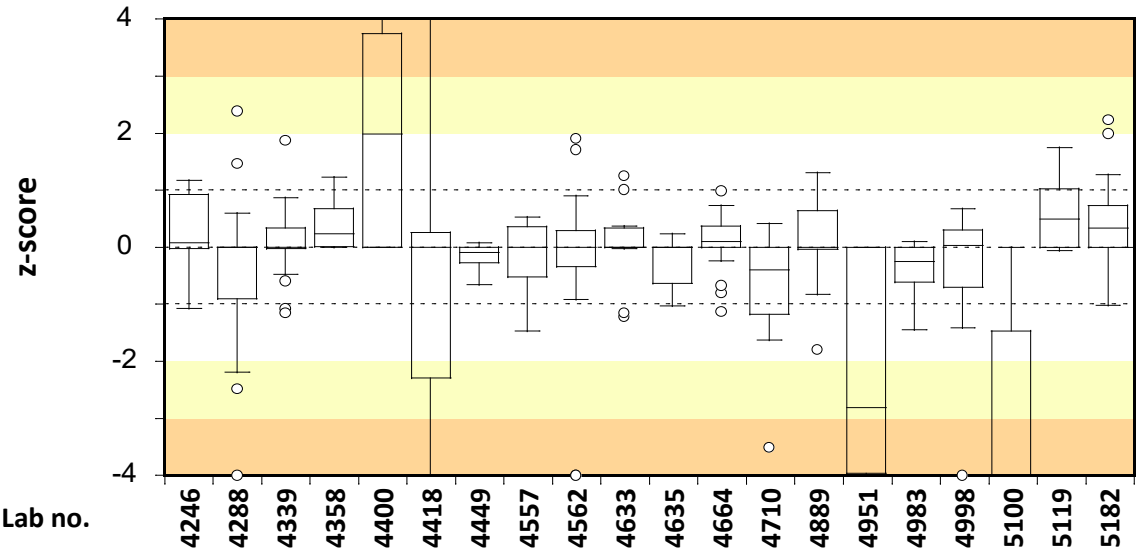
> [highest value in the box + 1,5 × (highest value in the box − lowest value in the box)].



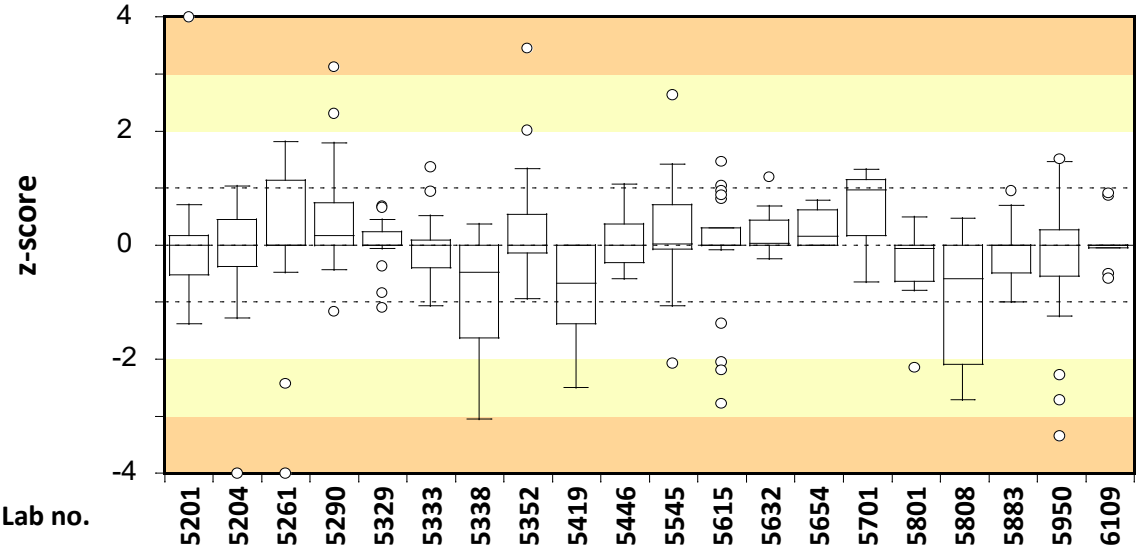
Lab no.	1149	1545	1970	2035	2058	2064	2109	2221	2317	2324	2386	2402	2459	2637	2659	2720	2745	2757	2794	2915
No. of results	15	24	30	3	9	9	6	27	24	21	21	12	18	18	12	9	18	12	0	21
False positive	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
False negative	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
Low outliers	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
High outliers	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	1



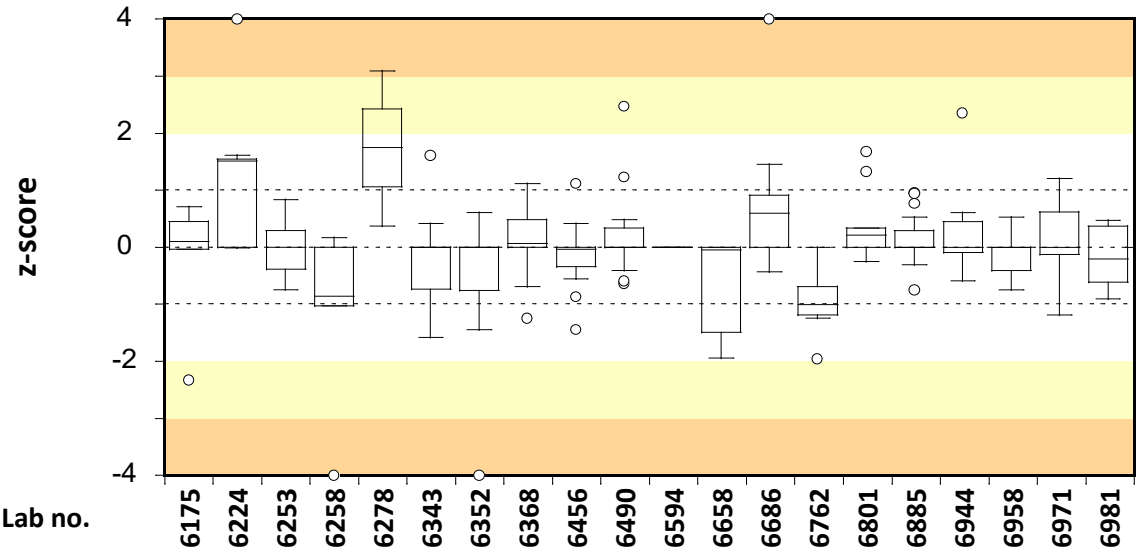
Lab no.	2941	3031	3055	3057	3243	3305	3415	3452	3457	3515	3543	3587	3626	3831	3864	4047	4050	4064	4100	4171
No. of results	18	9	12	0	6	18	21	6	21	15	15	18	27	12	9	10	15	6	24	14
False positive	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
False negative	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Low outliers	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	1	0	2
High outliers	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	0



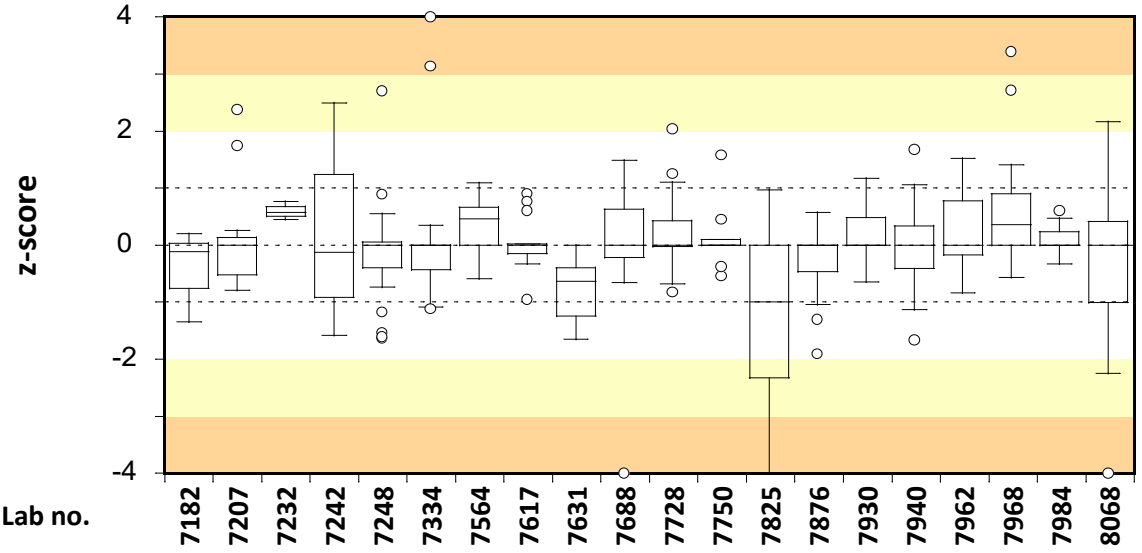
	4246	4288	4339	4358	4400	4418	4449	4557	4562	4633	4635	4664	4710	4889	4951	4983	4998	5100	5119	5182
No. of results	12	24	30	6	12	36	9	15	21	15	15	21	33	24	9	9	9	9	12	15
False positive	0	0	0	0	0	3	0	0	0	1	0	0	0	1	0	0	1	0	0	0
False negative	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	2	0	0
Low outliers	0	1	0	0	0	7	0	0	3	0	0	0	1	0	4	0	1	4	0	0
High outliers	0	0	0	0	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0



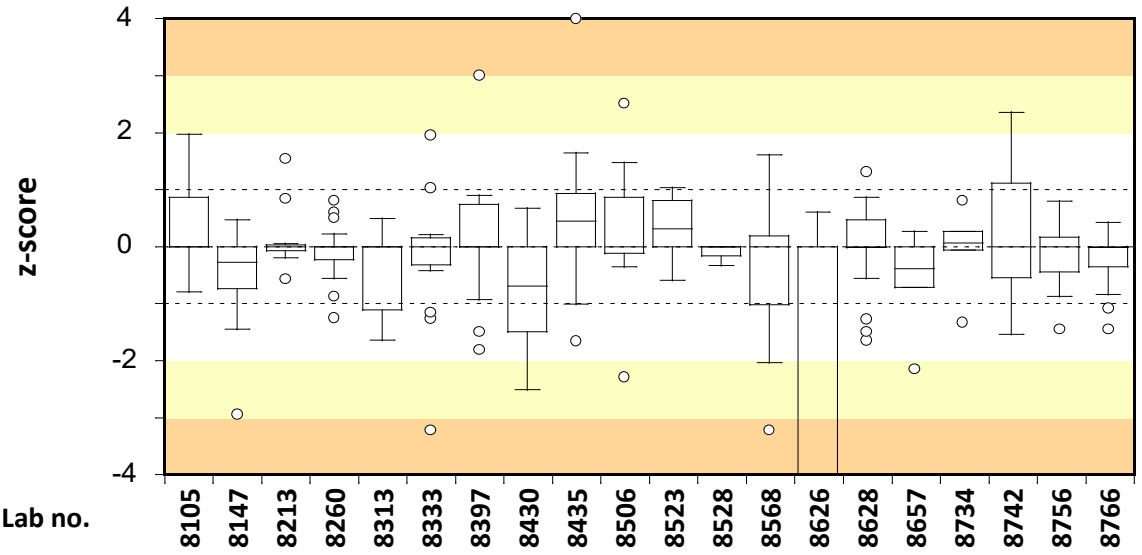
	5201	5204	5261	5290	5329	5333	5338	5352	5419	5446	5545	5615	5632	5654	5701	5801	5808	5883	5950	6109
No. of results	15	30	15	21	18	27	6	24	21	15	18	21	12	9	3	9	12	15	36	9
False positive	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
False negative	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
Low outliers	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0
High outliers	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0



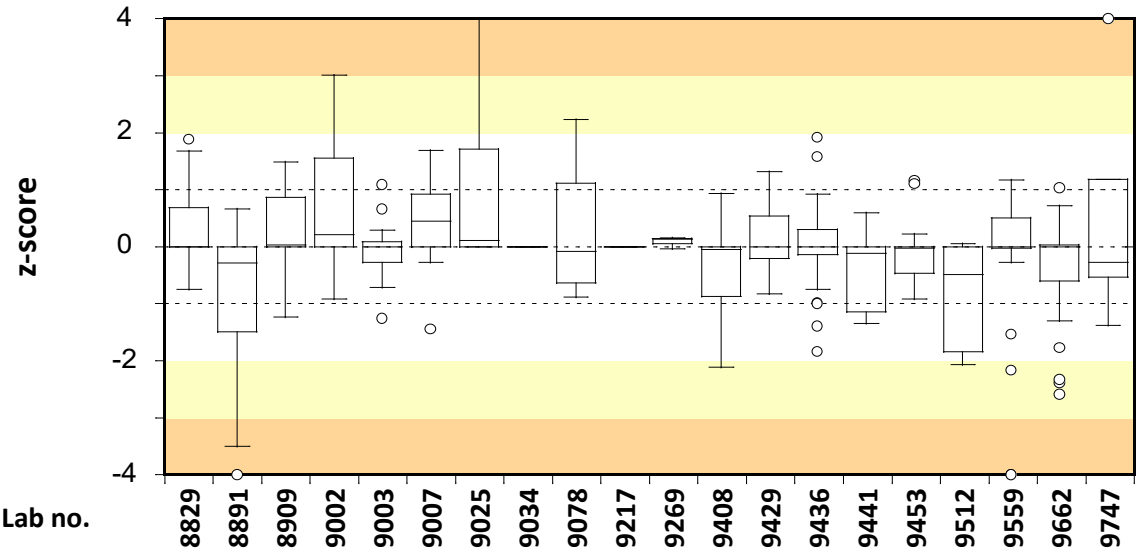
Lab no.	6175	6224	6253	6258	6278	6343	6352	6368	6456	6490	6594	6658	6686	6762	6801	6885	6944	6958	6971	6981
No. of results	6	9	12	6	3	14	21	27	15	18	0	12	21	9	9	20	12	9	9	6
False positive	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
False negative	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Low outliers	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
High outliers	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0



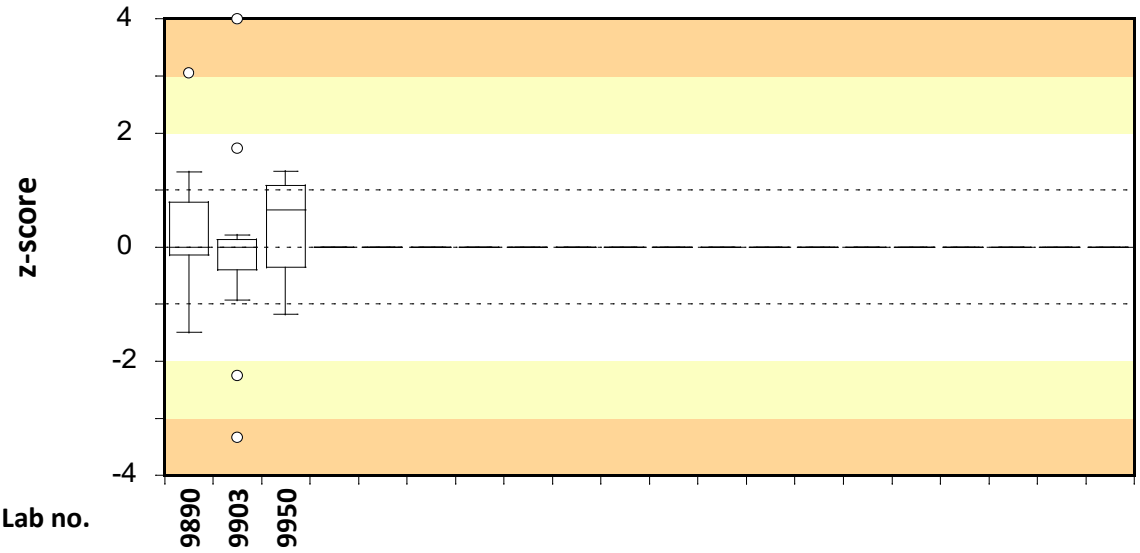
Lab no.	7182	7207	7232	7242	7248	7334	7564	7617	7631	7688	7728	7750	7825	7876	7930	7940	7962	7968	7984	8068
No. of results	12	12	3	4	33	13	15	15	9	27	24	9	18	18	21	9	27	27	12	29
False positive	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3
False negative	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1
Low outliers	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0	0	0	1
High outliers	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0



	8105	8147	8213	8260	8313	8333	8397	8430	8435	8506	8523	8528	8568	8626	8628	8657	8734	8742	8756	8766
No. of results	15	12	12	17	15	15	18	15	30	12	12	3	15	15	30	6	6	15	18	18
False positive	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
False negative	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Low outliers	0	0	0	0	0	1	0	0	0	0	0	0	1	8	0	0	0	0	0	0
High outliers	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0



	8829	8891	8909	9002	9003	9007	9025	9034	9078	9217	9269	9408	9429	9436	9441	9453	9512	9559	9662	9747
No. of results	9	21	18	15	18	15	12	0	6	0	3	21	18	27	18	18	9	24	27	6
False positive	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
False negative	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Low outliers	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
High outliers	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1



No. of results	21	18	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
False positive	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
False negative	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Low outliers	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
High outliers	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Test material and quality control

Test material

Each participant received three samples with freeze-dried microorganisms, designated A–C. The test material was freeze-dried in 0.5 ml portions in glass vials, as described by Peterz and Steneryd [3]. Before analysing the samples, the contents of each vial should be reconstituted in 254 ml of sterile diluent. The microorganism content of the samples and the concentrations determined at the Swedish Food Agency are listed in the table below.

Table 14. Microorganisms and approximate concentrations in the samples.

Sample	Microorganism	Strain			
		SLV no.[1]	Origin	Reference[2]	$\log_{10}$ cfu ml^{-1}
A	*Escherichia coli*	SLV-477	Cheese	CCUG 43601	4.20
	Serratia marcescens	SLV-040	-	ATCC 13 880	3.80
	Staphylococcus aureus	SLV-280	Egg	-	4.60
B	*Enterococcus faecium*	SLV-459	-	CCUG 35172	4.80
	Escherichia coli	SLV-085	Water	-	4.90
	Staphylococcus aureus	SLV-280	Egg	-	4.90
	Staphylococcus saprophyticus	SLV-013	-	CCUG 45100	4.50
C	*Bacillus cereus*	SLV-518	Couscous	CCUG 44741	4.20
	Enterococcus durans	SLV-078	Fresh meat	CCUG 44816	4.60
	Staphylococcus xylosus	SLV-283	Cheese	-	5.10

[1] Internal strain identification no. at the Swedish Food Agency

[2] Culture collection. ATCC: American Type Culture Collection, CBS: Centraalbureau voor Schimmelcultures (Westerdijk Institute), CCUG: Culture Collection University of Gothenburg, Sweden; Fohm: Public Health Agency of Sweden.

Quality control of the samples

In order to allow comparison of the freeze-dried samples, it is essential to have aliquots of homogeneous test material and equal volume in all vials. Quality control is performed on 10 randomly chosen vials in conjunction with manufacturing of the samples or on 5 vials if an "old" sample mixture was used and the last quality control was performed more than 6 months ago. Homogeneity of a test material is approved if, for each analysis, the values obtained for the test for "Index of dispersion" between vials (I_2) and the test for reproducibility (T) do not simultaneously exceed 2.0 and 2.6, respectively. (For definitions of I_2, and T, see references [4] and [5] respectively.)

Table 15. Concentration mean (m), I_2 and T values from the quality control of the sample mixtures; m is expressed in $\log_{10}$ cfu (colony forming units) per ml of sample.

Analysis and method	A[1]			B[1]			C[2]		
	m	I_2	T	m	I_2	T	m	I_2	T
Aerobic microorganisms, 30 ˚C NMKL method no. 86:2013	4.77	1.86	1.43	5.45	1.82	1.64	5.18	0.62	1.20
Aerobic microorganisms, 20 ˚C NMKL method no. 86:2013	4.75	1.51	1.40	5.45	1.08	1.47	5.18	1.07	1.26
Contaminating microorganisms ISO method no. 13559:2002 IDF method no. 153:2002	4.77	1.23	1.34	5.53	0.98	1.39	5.14	1.06	1.28
Enterobacteriaceae NMKL method no. 144:2005	4.27	0.24	1.11	4.67	**2.78**	1.70	-	-	-
Coliform bacteria, 30 ˚C NMKL method no. 44:2004	4.27	1.08	1.24	4.64	**3.09**	1.69	-	-	-
Coliform bacteria, 37 ˚C NMKL method no. 44:2004	4.27	**2.01**	1.34	4.60	**3.30**	1.77	-	-	-
Thermotolerant coliform bacteria NMKL method no. 125:2005	4.22	0.49	1.16	4.88	**2.70**	1.44	-	-	-
Escherichia coli NMKL method no. 125:2005	4.22	0.49	1.16	4.88	**2.70**	1.44	-	-	-
Presumptive Bacillus cereus NMKL method no. 67:2021	-	-	-	-	-	-	4.20	**2.87**	1.32
Coagulase-positive staphylococci NMKL method no. 66:2009	4.57	0.38	1.23	4.91	0.84	1.34	*5.09*[3]	*0.81*[3]	*1.25*[3]
Enterococci NMKL method no. 68:2011	-	-	-	4.77	0.62	1.23	4.57	**2.09**	1.96
Gram-negative bacteria in milk and cream NMKL method no. 192:2011	Pos.	-	-	Pos.	-	-	Neg.	-	-

– No target organism or no value

[1] n = 5 vials analysed in duplicate

[2] n = 10 vials analysed in duplicate

[3] False positive,

References

1. ISO 13528:2022 Statistical methods for use in proficiency testing by interlaboratory comparison.
2. Ilbäck J and Blom L. 2022. Protocol – Microbiological Proficiency Testing, Swedish Food Agency.
3. Peterz M and Steneryd AC. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. *Journal of Applied Bacteriology*. 74:143–148.
4. Heisterkamp SH, Hoekstra JA, van Strijp-Lockefeer NGWM, Havelaar AH, Mooijman KA, in't Veld PH, Notermans SHW, Maier EA and Griepink B. 1993. Statistical analysis of certification trials for microbiological reference materials. Luxembourg: Commission of the European Communities, Report EUR 15008 EN.
5. Mooijman KM, During M and Nagelkerke NJD 2003. MICROCRM: Preparation and control of batches of microbiological materials consisting of capsules. RIVM report 250935001/2003. RIVM, Bilthoven, Holland.

Annex 1. Results of the participating laboratories

Lab no.	Aerobic micro-organisms, 30 °C			Aerobic micro-organisms, 20 °C			Contaminating microorganisms			Enterobacteriaceae			Coliform bacteria, 30 °C			Coliform bacteria, 37 °C			Thermotolerant coliform bacteria			*Escherichia coli*			Presumptive *Bacillus cereus*			Coagulase-positive staphylococci			Enterococci			Gram-negative bacteria in dairy products		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
1149	4.65	5.58	5.15	-	-	-	-	-	-	4.48	4.9	0	-	-	-	4.18	4.85	0	-	-	-	4.18	4.85	0	0	0	4.2	-	-	-	-	-	-	-	-	-
1545	4.77	5.61	5.33	4.89	5.56	5.35	-	-	-	**4.63**	4.82	<1	-	-	-	-	-	-	4.26	4.82	<1	4.26	4.82	<1	<1	<1	4.52	4.46	4.85	<1	<1	4.82	4.85	-	-	-
1970	4.61	5.41	5.2	4.76	5.46	5.11	-	-	-	4.3	4.7	0	4.32	4.91	0	4.51	5.04	0	4.28	4.94	0	4.28	4.94	0	0	0	4.48	4.57	5.18	0	0	4.84	4.71	-	-	-
2035	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.2	4.9	<1	-	-	-	-	-	-	-	-	-	-	-	-
2058	4.73	5.41	5.03	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.35	4.59	0	0	0	3.71	-	-	-	-	-	-	-	-	-
2064	4.71	5.56	4.96	-	-	-	-	-	-	3.95	4.29	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.3	-	-	-	-	-	-	-	-	-
2109	4.71	5.51	5.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.04	4.74	0	-	-	-	-	-	-	-	-	-	-	-	-
2221	4.71	5.59	5.16	-	-	-	4.33	5.23	3.93	4.27	4.66	<1	4.32	4.65	<1	4.3	4.69	<1	-	-	-	4.1	**3.78**	<1	<1	<1	4.29	4.54	4.9	<1	<1	**<1**	4.51	-	-	-
2317	4.56	5.4	5.05	-	-	-	-	-	-	4.14	4.69	0	4.14	4.85	0	4.11	4.9	0	-	-	-	4.04	4.84	0	0	0	3.78	4.21	4.82	0	**1.15**	4.75	4.34	-	-	-
2324	4.69	5.53	5.18	-	-	-	4.7	5.54	5.3	4.19	4.68	<1	-	-	-	-	-	-	-	-	-	4.2	4.69	<1	<1	<1	**5.12**	4.26	4.63	<1	<1	4.73	4.52	-	-	-
2386	4.78	5.54	5.48	-	-	-	-	-	-	4.26	4.81	<1	-	-	-	4.17	4.9	<1	4.28	4.87	<1	4.26	4.89	<1	<1	<1	3.9	4.68	4.92	<1	-	-	-	-	-	-
2402	4.74	5.65	5.2	-	-	-	-	-	-	4.15	4.59	0	-	-	-	4.32	4.45	0	-	-	-	4.32	4.45	0	-	-	-	-	-	-	-	-	-	-	-	-
2459	4.75	5.63	5.12	-	-	-	-	-	-	4.07	4.58	0	-	-	-	**3.28**	**0**	0	-	-	-	4.13	4.57	0	0	0	4.2	4.45	4.61	**4.82**	-	-	-	-	-	-
2637	4.62	5.49	5.11	-	-	-	4.63	5.54	5.04	4.08	4.45	<1	-	-	-	-	-	-	-	-	-	4.18	4.76	<1	<1	<1	3.95	4.49	4.82	<2	-	-	-	-	-	-
2659	4.76	5.73	5.09	-	-	-	-	-	-	4.1	4.7	<1	-	-	-	4.41	4.79	<1	-	-	-	4.06	4.75	<1	-	-	-	-	-	-	-	-	-	-	-	-
2720	4.73	5.58	5.14	-	-	-	-	-	-	4.37	4.67	<1	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	3.96	-	-	-	-	-	-	-	-	-
2745	4.64	5.4	5	-	-	-	-	-	-	4.25	4.86	0	-	-	-	-	-	-	4.14	4.75	0	4.14	4.75	0	0	0	4.4	4.57	4.96	0	-	-	-	-	-	-
2757	4.83	5.63	5	4.69	5.48	5.04	-	-	-	4.34	4.84	0	**5.15**	4.84	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2794	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2915	**5.18**	5.32	5.34	4.83	5.4	5.04	-	-	-	4.15	5.04	<1	-	-	-	3.92	4.96	<1	-	-	-	4.38	4.96	<1	<2	<2	4.11	4.57	4.69	<1	-	-	-	-	-	-
2941	4.85	5.61	5.04	-	-	-	-	-	-	4.18	4.73	0	4.2	4.52	0	-	-	-	-	-	-	4.25	4.79	0	0	0	4.11	4.47	4.75	0	-	-	-	-	-	-
3031	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.05	4.51	<1	4.05	4.51	<1	-	-	-	-	-	-	-	-	-	<1	4.66	4.41	-	-	-
3055	4.48	5.35	5.04	-	-	-	-	-	-	4.19	4.54	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.45	-	-	-	-	-	-	Pos	Pos	Neg
3057	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3243	4.71	5.39	5.2	-	-	-	-	-	-	4.4	4.69	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3305	4.69	5.63	5.15	-	-	-	-	-	-	4.2	4.66	<1	-	-	-	-	-	-	4.08	4.86	<1	4.08	4.86	<1	<1	<1	4.45	4.48	4.91	<1	-	-	-	-	-	-
3415	4.62	5.46	5.11	-	-	-	3.85	4.88	4.67	4.34	4.9	<1	-	-	-	4.04	4.86	<1	-	-	-	4.04	4.86	<1	<2	<2	4.25	4.36	4.85	<2	-	-	-	-	-	-
3452	4.76	5.69	4.92	-	-	-	-	-	-	-	-	-	3.54	**3.46**	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3457	4.66	5.47	5.14	-	-	-	-	-	-	4.15	4.78	0	-	-	-	4.1	4.82	0	4.05	4.74	0	4.06	4.6	0	-	-	-	**5.47**	4.8	0	0	4.72	4.29	-	-	-
3515	4.69	5.58	5.32	-	-	-	-	-	-	4.3	4.8	0	-	-	-	-	-	-	-	-	-	4.37	5.1	0	0	0	4.47	4.49	4.84	0	-	-	-	-	-	-
3543	4.71	5.59	5.13	-	-	-	-	-	-	4.18	4.82	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.91	4.53	4.93	0	0	4.82	4.52	-	-	-
3587	4.67	5.47	5.1	-	-	-	-	-	-	4.31	4.71	0	-	-	-	-	-	-	-	-	-	4.11	4.73	0	0	0	4.06	4.48	4.87	0	0	**5.18**	4.34	-	-	-
3626	4.7	5.5	5.1	-	-	-	-	-	-	4.2	4.8	<1	4.1	4.5	<1	4.2	4.5	<1	4.2	5	<1	4.2	5	<1	<1	<1	4.2	4.5	4.9	<1	<1	4.8	4.6	-	-	-
3831	4.75	5.47	5.02	4.69	5.55	5.14	-	-	-	-	-	-	-	-	-	4.22	4.44	0	-	-	-	4.17	4.44	0	-	-	-	-	-	-	-	-	-	-	-	-
3864	4.72	5.61	5	-	-	-	-	-	-	4.09	4.56	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Pos	Pos	Neg
4047	4.62	-	5.17	-	-	-	-	-	-	4.16	-	<1	-	-	-	-	-	-	-	-	-	4.06	-	<1	<1	-	4.32	4.45	-	<1	-	-	-	-	-	-
4050	4.68	5.46	5.16	-	-	-	-	-	-	4.08	**3.81**	0	3.77	**3.56**	0	-	-	-	-	-	-	-	-	-	0	0	4.13	-	-	-	-	-	-	Pos	Pos	Neg
4064	4.75	**5.01**	5.14	-	-	-	-	-	-	4.17	**5.89**	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4100	4.69	5.54	5.15	-	-	-	4.7	5.51	5.18	4.22	4.79	<1	-	-	-	4.04	4.43	<1	-	-	-	3.98	4.5	<1	<1	<1	4.13	4.35	4.79	<1	<1	4.75	4.59	-	-	-
4171	4.7	5.6	5.04	-	-	-	-	-	-	4.32	4.36	<1	-	-	-	**2.2**	**2.71**	<0,60	-	-	-	**>1,00**	**>1,00**	<1	<1	<1	4.2	**>1,00**	**>1,00**	<1	-	-	-	-	-	-
4246	4.81	5.58	5.25	-	-	-	-	-	-	4.18	4.69	0	-	-	-	-	-	-	-	-	-	3.98	4.63	0	-	-	-	4.54	4.94	0	-	-	-	-	-	-
4288	4.62	**4.38**	5.14	-	-	-	-	-	-	4.07	4.53	0	-	-	-	3.93	4.74	0	3.88	4.69	0	3.84	4.58	0	0	0	4.78	4.3	5	0	0	4.84	4.34	-	-	-
4339	4.88	5.46	5.08	-	-	-	4.58	5.49	5.18	4.2	4.8	<1	4.18	4.83	<1	4.23	4.74	<1	4.18	4.81	<1	4.04	4.75	<1	<1	<1	4.04	4.41	4.65	<1	<1	4.87	4.28	-	-	-
4358	4.76	5.67	5.13	-	-	-	-	-	-	4.22	4.7	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4400	**5.96**	**6.07**	5.48	-	-	-	-	-	-	4.23	5.15	<1	-	-	-	-	-	-	-	-	-	**4.74**	**5.53**	<1	<1	<1	4.59	-	-	-	-	-	-	-	-	-
4418	**4.08**	**4.65**	**5.72**	4.38	5.51	**6.03**	4.51	5.36	6.15	4.38	4.87	0	**4.8**	4.79	0	4.04	4.81	0	4.04	**4.08**	0	3.94	**3.79**	0	**3.11**	**3.84**	3.81	**3.72**	**4.32**	**3.76**	0	**4.23**	4.08	Pos	Pos	Neg
4449	4.67	5.5	5.14	-	-	-	-	-	-	4.11	4.6	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.08	-	-	-	-	-	-	-	-	-
4557	4.74	5.58	5.2	-	-	-	-	-	-	4.2	4.74	0	3.95	4.68	0	-	-	-	-	-	-	3.93	4.68	0	-	-	-	4.3	4.65	0	-	-	-	-	-	-
4562	**4.15**	5.43	5.08	-	-	-	-	-	-	4.39	4.85	0	-	-	-	4.41	**2.86**	0	-	-	-	4	4.75	0	0	0	4.24	4.52	**4.24**	0	0	4.81	4.46	-	-	-
4633	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.19	4.85	<1	4.24	4.78	<1	<1	<1	3.85	4.57	4.64	<1	**4.51**	4.77	4.51	-	-	-
4635	4.6	5.38	5.16	-	-	-	-	-	-	4.12	4.66	<1	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	4	4.34	4.83	<1	<1	4.76	4.37	-	-	-
4664	4.67	5.6	5.27	4.76	5.41	5.16	-	-	-	4.18	4.79	<1	-	-	-	4.14	4.86	<1	4.16	4.61	<1	-	-	-	-	-	-	4.34	4.85	<1	<1	4.85	4.51	-	-	-
4710	4.6	5.34	4.98	4.62	5.37	5.02	-	-	-	4.14	4.32	<1	4.04	4.23	<1	4.11	4.28	<1	4.13	**4.22**	<1	4.02	4.36	<1	<1	<1	4.27	4.26	4.67	<1	<1	4.64	4.23	Pos	Pos	Neg
4889	4.81	5.68	5.15	-	-	-	-	-	-	4.2	4.77	0	-	-	-	4.26	4.88	0	4.11	4.9	0	4.11	4.9	0	0	0	3.7	4.34	4.79	0	**4.45**	4.68	**0**	-	-	-
4951	-	-	-	-	-	-	-	-	-	**3.72**	**3.58**	<1	-	-	-	**3.29**	**<1**	<1	-	-	-	**3.68**	4.24	<1	-	-	-	-	-	-	-	-	-	-	-	-
4983	4.64	5.48	5.04	-	-	-	-	-	-	4.11	4.68	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.79	-	-	-	-	-	-	-	-	-
4998	4.7	5.6	5.2	-	-	-	-	-	-	4.2	**3.8**	<1	-	-	-	-	-	-	-	-	-	-	-	-	**1.7**	<1	3.8	-	-	-	-	-	-	-	-	-

Annex 1. Results of the participating laboratories

Lab no.	Aerobic micro-organisms, 30 °C			Aerobic micro-organisms, 20 °C			Contaminating microorganisms			Enterobacteriaceae			Coliform bacteria, 30 °C			Coliform bacteria, 37 °C			Thermotolerant coliform bacteria			*Escherichia coli*			Presumptive *Bacillus cereus*			Coagulase-positive staphylococci			Enterococci			Gram-negative bacteria in dairy products		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
5100	3.62	4.1	3.78	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	-	-	-	3.6	4.06	0	-	-	-	-	-	-	-	-	-	-	-	-
5119	4.7	5.54	5.12	-	-	-	-	-	-	4.28	5.03	<1	4.36	4.91	<1	-	-	-	-	-	-	4.22	4.95	<1	-	-	-	-	-	-	-	-	-	-	-	-
5182	4.82	5.8	5.24	-	-	-	-	-	-	4.27	4.44	<1	-	-	-	4.18	5.18	<1	-	-	-	4.17	4.6	<1	<1	<1	4.25	-	-	-	-	-	-	-	-	-
5201	4.62	6.6	4.93	-	-	-	-	-	-	4.2	4.81	<	-	-	-	-	-	-	-	-	-	4.15	4.66	<	<	<	3.83	4.33	4.83	<	-	-	-	-	-	-
5204	4.63	5.52	5.07	-	-	-	4.74	5.41	5.11	4.15	4.88	<1	3.98	4.52	<1	3.92	4.58	<1	4.22	4.92	<1	4.17	4.92	<1	<1	<1	4.36	3.38	4.66	<1	<1	4.64	4.58	-	-	-
5261	4.7	5.2	5.06	-	-	-	-	-	-	4.38	4.9	0	-	-	-	3.48	0	0	-	-	-	4.34	5	0	0	0	4.18	-	-	-	-	-	-	-	-	-
5290	4.84	5.54	5.46	-	-	-	-	-	-	4.4	4.72	0	4.18	4.45	0	4.6	4.38	0	-	-	-	4.28	4.9	0	0	0	4.2	4.44	4.9	0	-	-	-	-	-	-
5329	4.7	5.53	5.12	-	-	-	-	-	-	4.2	4.48	<1	-	-	-	-	-	-	-	-	-	4.17	4.48	<1	<1	<1	4.07	4.47	4.83	<1	<1	4.85	4.6	-	-	-
5333	4.83	5.54	5.12	-	-	-	4.57	5.46	4.81	4.1	4.86	0	4.17	4.49	0	4.02	4.79	0	-	-	-	4.11	4.85	0	0	0	3.89	4.36	4.78	0	0	4.69	4.32	-	-	-
5338	4.73	5.12	5.12	-	-	-	-	-	-	4.08	4.31	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5352	4.77	5.49	5.16	-	-	-	-	-	-	4.16	4.61	0	-	-	-	4.1	4.86	0	4.08	4.87	0	4.08	4.87	0	0	0	4.51	4.46	4.67	0	0	5	5.09	-	-	-
5419	4.51	5.21	4.95	-	-	-	4.27	5.39	4.59	4.14	<1	<1	-	-	-	-	-	-	-	-	-	3.94	4.16	<1	<1	<1	4	4.27	4.64	<1	<1	4.72	4.36	-	-	-
5446	4.76	5.65	5.05	-	-	-	-	-	-	4.14	4.8	<1	-	-	-	4.11	4.62	<1	-	-	-	4.04	4.62	<1	-	-	-	4.43	4.94	<1	-	-	-	-	-	-
5545	4.62	5.59	4.83	-	-	-	4.75	5.51	5.34	4.25	4.43	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.13	4.59	0	5.03	0	5.07	4.49	-	-	-
5615	4.72	5.7	5.28	-	-	-	-	-	-	4.3	4.83	<1	-	-	-	3.8	4.74	<1	-	-	-	3.84	4.8	<1	<1	<1	3.81	4.41	4.92	<1	<1	4.46	4.52	-	-	-
5632	4.7	5.6	5.3	-	-	-	-	-	-	4.2	4.7	<1	-	-	-	-	-	-	-	-	-	4.2	4.7	<1	<2	<2	4.1	-	-	-	-	-	-	-	-	-
5654	4.76	5.53	5.15	-	-	-	-	-	-	4.28	4.79	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.29	-	-	-	-	-	-	-	-	-
5701	4.79	5.43	5.32	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5801	4.48	5.41	5.2	-	-	-	-	-	-	4.18	4.61	<1	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	4	-	-	-	-	-	-	-	-	-
5808	4.52	5.23	4.96	-	-	-	-	-	-	-	-	-	-	-	-	4.19	4.11	<1	-	-	-	4.13	4.11	<1	<1	<1	3.65	-	-	-	-	-	-	-	-	-
5883	4.6	5.51	5.03	-	-	-	-	-	-	4.3	4.62	<1	-	-	-	-	-	-	-	-	-	4.18	4.89	<1	<1	<1	3.97	4.3	4.76	<1	-	-	-	-	-	-
5950	4.57	5.49	5.16	4.72	5.56	5.07	4.89	4.9	5.28	4.13	4.77	<1	3.67	4.38	<1	3.6	4.43	<1	4.16	4.81	<1	4.16	4.81	<1	<2	<2	4.45	4.3	4.67	<2	<2	4.81	4.74	Pos	Pos	Neg
6109	4.78	5.51	5.26	-	-	-	-	-	-	-	-	-	-	-	-	4.04	4.53	<0,6	-	-	-	-	-	-	<1	<1	4.15	-	-	-	-	-	-	-	-	-
6175	4.69	5.57	5.23	-	-	-	-	-	-	4.21	4.16	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6224	5.4	5.71	5.36	-	-	-	-	-	-	4.37	4.98	<1	-	-	-	-	-	-	-	-	-	-	-	-	<2	<2	4.16	-	-	-	-	-	-	-	-	-
6253	-	-	-	-	-	-	-	-	-	4.23	4.72	<1	3.98	4.49	<1	-	-	-	-	-	-	4.15	4.56	<1	-	-	-	-	-	-	<1	4.72	4.63	-	-	-
6258	4.71	5.39	4.98	-	-	-	-	-	-	-	-	-	3.96	2.29	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6278	4.73	5.91	5.38	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6343	4.58	-	5.36	-	-	-	-	-	-	4	-	0	0	-	0	4.18	-	0	-	-	-	4.08	-	0	0	-	3.79	4.38	-	3.78	-	-	-	-	-	-
6352	4.67	5.59	4.92	-	-	-	-	-	-	4.11	4.52	<1	-	-	-	4	4.34	<1	-	-	-	4	3.15	<1	<1	<1	3.85	4.46	4.78	<1	<1	4.8	4.57	-	-	-
6368	4.76	5.56	5.16	4.68	5.59	5.11	-	-	-	4.04	4.51	<1	-	-	-	4.13	4.69	<1	4.2	4.87	<1	4.2	4.87	<1	<1	<1	4.45	4.51	4.86	<1	<1	4.83	4.48	-	-	-
6456	-	-	-	-	-	-	-	-	-	4.15	4.54	<1	3.94	4.57	<1	4.06	4.6	<1	-	-	-	4.08	4.4	<1	-	-	-	-	-	-	<1	4.82	4.68	-	-	-
6490	4.63	5.67	5.07	-	-	-	-	-	-	4.48	4.76	<	-	-	-	4.17	4.76	<	-	-	-	-	-	-	<	<	4.23	4.4	4.83	<	<	4.81	4.38	-	-	-
6594	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6658	4.5	5.5	4.9	-	-	-	-	-	-	4	4.5	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.8	-	-	-	-	-	-	Pos	Pos	Neg
6686	4.65	5.67	5.2	5.59	5.57	5.26	-	-	-	4.36	4.83	<1	-	-	-	-	-	-	4.26	4.89	<1	4.11	4.94	<1	-	-	-	4.51	4.88	<1	<1	4.86	4.45	-	-	-
6762	4.58	5.36	5.01	-	-	-	-	-	-	4.04	4.51	<1	-	-	-	-	-	-	-	-	-	3.87	4.5	<1	-	-	-	-	-	-	-	-	-	-	-	-
6801	4.86	5.48	5.32	-	-	-	-	-	-	-	-	-	-	-	-	4.15	4.76	<1	-	-	-	4.15	4.76	<1	-	-	-	-	-	-	-	-	-	-	-	-
6885	4.68	>6,48	5.02	-	-	-	-	-	-	4.3	4.86	0	-	-	-	-	-	-	-	-	-	4.18	4.83	0	0	0	4.36	4.43	4.82	0	0	4.77	4.43	Pos	Pos	Neg
6944	4.68	5.46	5.12	-	-	-	-	-	-	-	-	-	-	-	-	4.21	5.27	0	-	-	-	4.15	5.27	0	-	-	-	4.35	4.84	4.58	-	-	-	-	-	-
6958	4.74	5.46	5.03	-	-	-	-	-	-	4.25	4.62	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.97	-	-	-	-	-	-	-	-	-
6971	4.65	5.36	5.11	-	-	-	-	-	-	4.33	4.79	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.34	-	-	-	-	-	-	-	-	-
6981	4.74	5.56	5.04	-	-	-	-	-	-	4.08	4.57	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7182	4.56	5.52	5.02	-	-	-	-	-	-	4.12	4.7	<1	-	-	-	4	4.69	<1	-	-	-	4	4.68	<1	-	-	-	-	-	-	-	-	-	-	-	-	-
7207	4.93	5.41	5.38	-	-	-	-	-	-	4.11	4.56	<1	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	4.23	-	-	-	<1	4.74	4.38	-	-	-
7232	4.77	5.57	5.21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7242	-	5.48	4.9	-	-	-	-	-	-	-	5.19	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7248	4.62	5.52	5.09	4.49	5.34	5	4.56	5.95	5.23	4.15	4.54	<1	4.15	4.85	<1	4.18	4.76	<1	4.15	4.73	<1	4.18	4.85	<1	<1	<1	4	4.36	4.79	<1	<1	4.76	4.2	-	-	-
7334	4.65	6.05	5.01	-	-	-	-	-	-	-	-	-	-	-	-	4.17	4.39	<1	-	-	-	>1	>1	<1	<1	<1	4.12	4.29	5.23	<1	-	-	-	-	-	-
7564	-	-	-	4.78	5.45	5.12	-	-	-	-	-	-	4.26	4.91	0	-	-	-	4.2	4.9	0	4.2	4.9	0	-	-	-	-	-	-	<1	4.83	4.38	-	-	-
7617	4.69	5.39	5.11	-	-	-	-	-	-	4.19	4.85	<1	-	-	-	4.09	4.87	<1	-	-	-	4.09	4.87	<1	-	-	-	4.38	4.8	<1	-	-	-	-	-	-
7631	4.63	5.3	4.94	-	-	-	-	-	-	4.04	4.54	0	3.93	4.46	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7688	4.63	5.5	5.15	-	-	-	-	-	-	4.26	4.65	<1	4.28	4.38	<1	4.04	3.15	<1	4.3	4.9	<1	4.3	4.9	<1	<1	<1	4.04	4.38	4.98	<1	<1	4.94	4.4	-	-	-
7728	4.72	5.49	5.16	4.72	5.59	5.06	-	-	-	4.28	4.53	0	-	-	-	4.18	4.66	0	4.18	4.66	0	4.18	4.66	0	0	0	4.28	4.57	5.08	0	-	-	-	-	-	-
7750	4.7	5.57	5.05	-	-	-	-	-	-	-	-	-	-	-	-	4.36	4.58	0	-	-	-	-	-	-	0	0	4.19	-	-	-	-	-	-	-	-	-
7825	4.79	5.53	5.11	-	-	-	-	-	-	3.89	4.2	<1	-	-	-	-	-	-	3.25	4.03	<1	<1	3.37	<1	-	-	-	4.29	4.52	4.78	<1	4.67	4.24	-	-	-
7876	4.75	5.55	5.15	-	-	-	-	-	-	3.96	4.38	<1	-	-	-	-	-	-	-	-	-	4.06	4.83	<1	<1	<1	4.08	4.4	4.72	<1	<1	4.72	4.3	-	-	-

Annex 1. Results of the participating laboratories

Lab no.	Aerobic micro-organisms, 30 °C			Aerobic micro-organisms, 20 °C			Contaminating microorganisms			Enterobacteriaceae			Coliform bacteria, 30 °C			Coliform bacteria, 37 °C			Thermotolerant coliform bacteria			*Escherichia coli*			Presumptive *Bacillus cereus*			Coagulase-positive staphylococci			Enterococci			Gram-negative bacteria in dairy products		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
7930	4.78	5.43	5.06	-	-	-	-	-	-	4.16	4.69	0	-	-	-	-	-	-	4.26	4.91	0	4.26	4.91	0	0	0	4.23	4.41	4.83	0	0	4.8	**0**	-	-	-
7940	4.86	5.46	4.89	-	-	-	-	-	-	4.15	4.73	0	3.89	4.9	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7962	4.67	5.59	5.24	-	-	-	-	-	-	4.28	4.56	0	4.01	4.79	0	4.3	4.9	0	4.1	4.97	0	4.1	4.97	0	0	0	3.95	4.32	4.69	0	0	4.91	4.75	-	-	-
7968	4.77	5.61	5.52	-	-	-	-	-	-	4.23	4.66	0	4.22	4.77	0	4.28	4.73	0	4.29	4.89	0	4.29	4.89	0	0	0	4.43	4.42	4.72	0	0	4.9	**5.08**	-	-	-
7984	4.74	5.48	5.18	-	-	-	-	-	-	4.26	4.68	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.08	-	-	-	-	-	-	Pos	Pos	Neg
8068	4.47	5.34	4.97	4.45	5.39	4.92	-	-	-	4.14	5.12	0	4.26	4.72	0	4.18	4.66	0	4.15	4.86	0	**0**	4.86	0	**4.34**	0	**>5,18**	**3.91**	4.91	**1.78**	**1.85**	4.86	4.4	-	-	-
8105	4.89	5.65	5.06	-	-	-	-	-	-	-	-	-	-	-	-	4.18	4.95	0	-	-	-	4.08	5.06	0	0	0	3.96	4.5	4.85	0	-	-	-	-	-	-
8147	4.62	5.46	4.92	-	-	-	-	-	-	4.1	4.63	<1	4.2	4.68	<1	-	-	-	-	-	-	**<1**	4.06	**4.4**	-	-	-	-	-	-	-	-	-	-	-	-
8213	4.68	5.44	5.1	-	-	-	-	-	-	4.37	4.67	<1	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	4.38	-	-	-	-	-	-	Pos	Pos	Neg
8260	4.67	5.4	4.95	-	-	-	-	-	-	4.16	4.61	0	-	-	0	4.21	4.73	0	-	-	-	-	-	0	0	0	4.02	4.48	4.91	0	-	-	-	-	-	-
8313	4.53	5.36	4.95	-	-	-	-	-	-	4.1	4.43	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.11	4.45	4.64	0	0	4.79	4.57	-	-	-
8333	4.71	5.53	5.41	-	-	-	-	-	-	4.16	4.39	<1	-	-	-	4.15	4.57	<0,6	-	-	-	-	-	-	<1	<1	4.43	-	-	-	<1	**4.41**	4.28	-	-	-
8397	4.7	5.28	5.2	-	-	-	-	-	-	4.01	4.85	0	-	-	-	-	-	-	-	-	-	4.18	4.9	0	0	0	4.94	4.52	4.91	0	0	4.7	4.32	-	-	-
8430	4.45	5.44	4.99	-	-	-	-	-	-	3.89	4.34	<1	3.95	4.24	<1	-	-	-	-	-	-	3.88	4.64	<1	-	-	-	4.5	4.81	**4.81**	-	-	-	-	-	-
8435	4.74	5.56	5.34	4.84	5.53	5.28	-	-	-	4.32	4.66	<1	4.1	4.08	<1	4.08	4.79	<1	4.32	4.89	<1	4.32	4.89	<1	<1	**2**	4.38	4.58	4.88	<1	<1	4.66	**5.22**	-	-	-
8506	4.84	5.59	5.49	-	-	-	-	-	-	-	-	-	-	-	-	4.29	4.62	0	-	-	-	4.07	4.21	0	0	0	4.18	-	-	-	-	-	-	-	-	-
8523	4.74	5.61	5.2	-	-	-	-	-	-	4.31	4.88	<1	-	-	-	-	-	-	-	-	-	4.04	4.93	<1	-	-	-	4.41	4.82	<1	-	-	-	-	-	-
8528	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	4.08	-	-	-	-	-	-	-	-	-
8568	4.8	5.72	5.14	-	-	-	-	-	-	4.09	4.26	0	-	-	-	3.93	4.16	0	-	-	-	-	-	-	0	0	4.24	-	-	-	0	**4.41**	4.55	-	-	-
8626	4.67	**4.34**	**4.34**	-	-	-	-	-	-	4.26	4.28	0	-	-	-	**3.04**	**3.38**	0	**3.04**	**3.38**	0	**3.04**	**3.38**	0	-	-	-	-	-	-	-	-	-	-	-	-
8628	4.53	5.32	5.19	4.54	5.53	5.15	-	-	-	4.13	4.69	0	4	4.8	0	4.04	4.85	0	4.15	4.88	0	4.15	4.88	0	0	0	4.16	4.48	4.98	0	0	4.87	4.43	-	-	-
8657	4.72	5.42	5.1	-	-	-	-	-	-	4.12	4.2	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8734	4.72	5.53	5.12	-	-	-	-	-	-	4.03	4.83	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8742	4.54	5.57	5.04	-	-	-	-	-	-	-	-	-	-	-	-	4.04	5.18	<1	4.04	5.18	<1	4.04	5.18	<1	-	-	-	4.6	4.9	<1	-	-	-	-	-	-
8756	4.73	5.4	5.2	4.78	5.44	5.24	-	-	-	**<1**	4.61	<1	-	-	-	-	-	-	-	-	-	4.02	4.63	<1	<1	<1	4.1	4.44	4.6	<1	-	-	-	-	-	-
8766	4.72	5.46	5.19	-	-	-	-	-	-	4.2	4.48	0	-	-	-	-	-	-	-	-	-	3.98	4.66	0	0	0	4.08	4.41	4.75	0	0	4.61	4.48	-	-	-
8829	4.86	5.59	5.4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.2	4.56	<1	<1	<1	4.05	-	-	-	-	-	-	-	-	-
8891	4.4	5.48	4.96	-	-	-	4.72	5.3	4.96	**3.61**	4.58	<1	3.76	4.23	<1	-	-	-	-	-	-	3.82	4.76	<1	<1	<1	4.08	**4**	4.78	**4.83**	-	-	-	-	-	-
8909	4.73	5.52	5.2	-	-	-	-	-	-	4.29	4.41	<1	4.3	4.35	<1	-	-	-	-	-	-	4.13	4.45	<1	<1	<1	4.53	-	-	-	<1	4.94	4.65	-	-	-
9002	4.86	5.9	5.42	-	-	-	-	-	-	4.11	5.08	0	-	-	-	4.15	5.04	<1	-	-	-	4	5	<1	< 0,70	< 0,70	4.24	-	-	-	-	-	-	-	-	-
9003	4.63	5.46	5.14	-	-	-	-	-	-	4.19	4.8	<1	4.15	4.91	<1	4.09	4.75	<1	-	-	-	4.08	4.75	<1	-	-	-	4.27	4.7	<1	-	-	-	-	-	-
9007	4.76	5.73	5.34	-	-	-	-	-	-	4.3	4.85	0	-	-	-	4.15	4.79	0	-	-	-	4.08	4.86	0	-	-	-	4.6	4.6	0	-	-	-	-	-	-
9025	**5.2**	5.8	5.3	-	-	-	-	-	-	4.2	4.7	<1	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	4.9	-	-	-	-	-	-	Pos	Pos	**Pos**
9034	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9078	4.63	5.49	5.45	-	-	-	-	-	-	4.32	4.47	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9217	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9269	4.69	5.53	5.15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9408	4.58	5.4	4.95	-	-	-	-	-	-	4.17	4.77	0	-	-	-	4.06	4.63	0	3.92	4.53	0	4.23	4.72	0	0	0	4.32	4.17	4.76	0	-	-	-	-	-	-
9429	-	-	-	-	-	-	-	-	-	4.3	4.8	<1	4.15	4.79	<1	4.32	4.81	<1	4.08	4.66	<1	4.04	4.7	<1	-	-	-	-	-	-	<1	4.75	4.34	-	-	-
9436	4.51	5.48	5.02	-	-	-	-	-	-	4.07	4.36	<1	4.2	4.86	<1	4.26	4.71	<1	4.15	4.81	<1	4.11	4.84	<1	<1	<1	4.57	4.3	4.76	<1	<1	4.83	4.82	-	-	-
9441	4.58	5.34	4.95	-	-	-	-	-	-	4.08	4.38	<1	-	-	-	4.08	4.56	<1	-	-	-	3.97	4.52	<1	<1	<1	4.2	-	-	-	<1	4.84	4.49	-	-	-
9453	4.64	5.45	5.16	-	-	-	4.54	5.65	4.89	4.18	4.64	<1	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	3.95	4.41	4.95	<1	<1	4.67	4.51	-	-	-
9512	4.51	5.45	4.83	-	-	-	-	-	-	4.13	4.67	<2	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	3.65	-	-	-	-	-	-	-	-	-
9559	4.75	5.57	5.15	4.81	5.56	5.18	-	-	-	3.93	**3.2**	<1	-	-	-	3.88	**3.18**	<1	-	-	-	4.08	4.72	<1	<1	<1	4.39	4.52	4.96	<1	-	-	-	Pos	Pos	Neg
9662	4.65	5.18	5.15	4.7	5.26	5.15	-	-	-	4.15	4.28	0	4.18	4.28	0	4.2	4.48	0	-	-	-	4.14	4.2	0	0	0	4.11	4.38	4.62	0	0	4.89	4.61	-	-	-
9747	4.64	5.49	4.93	-	-	-	-	-	-	**4.92**	4.91	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.07	-	-	-	-	-	-	-	-	-
9890	4.68	5.67	5.23	4.7	5.56	5.26	-	-	-	4.01	4.94	0	-	-	-	3.98	4.9	0	-	-	-	3.98	4.9	0	0	0	**4.95**	4.4	4.6	0	-	-	-	-	-	-
9903	4.71	**6.55**	5.11	-	-	-	-	-	-	4.14	4.46	0	-	-	-	-	-	-	-	-	-	4.11	4.76	0	0	0	4.61	4.37	**4.34**	0	0	4.52	4.52	-	-	-
9950	4.74	5.62	5.32	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4.3**	4.64	**0**	-	-	-

Annex 1. Results of the participating laboratories

Lab no.	Aerobic micro-organisms, 30 °C			Aerobic micro-organisms, 20 °C			Contaminating microorganisms			Enterobacteriaceae			Coliform bacteria, 30 °C			Coliform bacteria, 37 °C			Thermotolerant coliform bacteria			*Escherichia coli*			Presumptive *Bacillus cereus*			Coagulase-positive staphylococci			Enterococci			Gram-negative bacteria in dairy products		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
N	148	146	149	21	21	21	15	15	15	131	130	131	39	38	40	72	71	72	36	36	36	102	100	105	104	102	104	82	80	83	60	60	60	12	12	12
n	141	135	146	20	21	20	15	15	15	126	124	131	36	35	40	64	62	72	34	32	36	95	94	104	101	100	102	77	75	74	55	55	54	12	12	11
Min	3.62	4.10	3.78	4.38	5.26	4.92	3.85	4.88	3.93	0	0	0	0	2.29	0	0	0	0	3.04	3.38	0	0	3.15	0	0	0	3.65	3.38	0	0	0	0	0	-	-	-
Max	5.96	6.60	5.72	5.59	5.59	6.03	4.89	5.95	6.15	4.92	5.89	0	5.15	4.91	0	4.60	5.27	0	4.32	5.18	0	4.74	5.53	4.40	4.34	3.84	5.12	5.47	5.23	5.03	4.51	5.18	5.22	-	-	-
Med	4.70	5.52	5.14	4.71	5.51	5.13	4.58	5.46	5.11	4.18	4.69	0	4.15	4.68	0	4.15	4.74	0	4.16	4.87	0	4.11	4.76	0	0	0	4.14	4.43	4.82	0	0	4.80	4.48	-	-	-
m_{PT}	**4.693**	**5.512**	**5.128**	**4.712**	**5.486**	**5.143**	**4.586**	**5.425**	**5.045**	**4.187**	**4.658**	**-**	**4.108**	**4.580**	**-**	**4.117**	**4.675**	**-**	**4.150**	**4.794**	**-**	**4.114**	**4.731**	**-**	**-**	**-**	**4.163**	**4.420**	**4.798**	**-**	**-**	**4.773**	**4.483**	**Pos**	**Pos**	**Neg**
s_{PT}	**0.099**	**0.129**	**0.144**	**0.137**	**0.095**	**0.122**	**0.202**	**0.194**	**0.334**	**0.119**	**0.214**	**-**	**0.193**	**0.302**	**-**	**0.155**	**0.253**	**-**	**0.109**	**0.164**	**-**	**0.125**	**0.229**	**-**	**-**	**-**	**0.258**	**0.120**	**0.138**	**-**	**-**	**0.113**	**0.176**	**-**	**-**	**-**
u_{PT}	0.010	0.013	0.015	0.037	0.026	0.033	0.065	0.063	0.108	0.013	0.023	-	0.039	0.061	-	0.023	0.039	-	0.023	0.034	-	0.016	0.029	-	-	-	0.032	0.017	0.019	-	-	0.018	0.029	-	-	-
F+	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	2	0	0	0	9	5	0	0	0	0	1
F-	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	1	4	0	0	0	0	3	0	0	0	0	0	0	1	0	0	1	3	0	0	0
<	3	6	2	0	0	0	0	0	0	2	4	0	0	3	0	6	5	0	2	4	0	3	5	0	0	0	0	4	3	0	0	3	0	-	-	-
>	4	5	1	1	0	1	0	0	0	2	1	0	2	0	0	1	0	0	0	0	0	1	1	0	0	0	2	1	1	0	0	1	3	-	-	-
Lower	**4.39**	**5.13**	**4.70**	**4.30**	**5.20**	**4.78**	**3.85**	**4.84**	**3.93**	**3.83**	**4.02**	**0**	**3.53**	**3.67**	**0**	**3.65**	**3.92**	**0**	**3.82**	**4.30**	**0**	**3.74**	**4.04**	**0**	**0**	**0**	**3.39**	**4.06**	**4.39**	**0**	**0**	**4.43**	**3.95**	**-**	**-**	**-**
Upper	**4.99**	**5.90**	**5.56**	**5.12**	**5.77**	**5.51**	**5.19**	**6.01**	**6.15**	**4.54**	**5.30**	**0**	**4.69**	**5.49**	**0**	**4.58**	**5.43**	**0**	**4.48**	**5.29**	**0**	**4.49**	**5.42**	**0**	**0**	**0**	**4.94**	**4.78**	**5.21**	**0**	**0**	**5.11**	**5.01**	**-**	**-**	**-**

N = number of reported results
n = results without annotation
Min = lowest reported result
Max = highest reported result
Med = median value
m_{PT} = assigned value
s_{PT} = standard deviation
u_{PT} = measurement uncertainty
F+ = false positive
F- = false negative
< = low outlier
> = high outlier
Lower = lowest accepted value
Upper = highest accepted value

False positive or false negative
Outside the acceptance limits
Results "larger than" are not evalutated
The parameter is not evaluated
The result not evaluated
u_{PT} > 0,3 s_{PT} and/or > 20 % outliers

Annex 2. Z-scores of all participants

Lab no.	Aerobic micro-organisms, 30 °C			Aerobic micro-organisms, 20 °C			Contaminating microorganisms			Enterobacteriaceae			Coliform bacteria, 30 °C			Coliform bacteria, 37 °C			Thermotolerant coliform bacteria			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive staphylococci			Enterococci			Gram-negative bacteria in dairy products		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
1149	-0.436	0.527	0.151							2.469	1.135	0				0.411	0.694	0				0.530	0.523	0	0	0	0.143									
1545	0.771	0.760	1.402	1.303	0.785	1.695				3.734	0.760	0							1.016	0.156	0	1.172	0.391	0	0	0	1.386	0.336	0.375	0	0	0.419	2.086			
1970	-0.838	-0.795	0.499	0.351	-0.270	-0.271				0.952	0.198	0	1.096	1.093	0	2.546	1.445	0	1.200	0.889	0	1.332	0.916	0	0	0	1.230	1.254	2.773	0	0	0.596	1.291			
2035																						0.691	0.741	0												
2058	0.368	-0.795	-0.683																			1.893	-0.615	0	0	0	-1.760									
2064	0.167	0.371	-1.169							-1.999	-1.722	0													0	0	0.531									
2109	0.167	-0.017	-0.196																			-0.592	0.041	0												
2221	0.167	0.604	0.221				-1.267	-1.006	-3.338	0.699	0.011	0	1.096	0.233	0	1.187	0.061	0				-0.111	-4.000	0	0	0	0.493	1.004	0.738	0	0		0.154			
2317	-1.341	-0.872	-0.544							-0.397	0.151	0	0.164	0.894	0	-0.042	0.891	0				-0.592	0.479	0	0	0	-1.488	-1.751	0.157	0		-0.203	-0.812			
2324	-0.034	0.138	0.360				0.566	0.593	0.765	0.025	0.104	0										0.691	-0.177	0	0	0	3.715	-1.333	-1.224	0	0	-0.381	0.211			
2386	0.871	0.216	2.445							0.615	0.713	0				0.346	0.891	0	1.200	0.461	0	1.172	0.697	0	0	0	-1.022	2.172	0.883	0						
2402	0.469	1.071	0.499							-0.313	-0.317	0				1.317	-0.889	0				1.653	-1.227	0												
2459	0.569	0.915	-0.057							-0.987	-0.364	0				-4.000		0				0.129	-0.702	0	0	0	0.143	0.253	-1.369							
2637	-0.738	-0.173	-0.127				0.219	0.593	-0.014	-0.903	-0.973	0										0.530	0.129	0	0	0	-0.828	0.587	0.157	0						
2659	0.670	1.692	-0.266							-0.734	0.198	0				1.899	0.456	0				-0.432	0.085	0												
2720	0.368	0.527	0.082							1.542	0.057	0													0	0	-0.789									
2745	-0.537	-0.872	-0.891							0.530	0.947	0							-0.089	-0.272	0	0.210	0.085	0	0	0	0.920	1.254	1.174	0						
2757	1.374	0.915	-0.891	-0.162	-0.059	-0.845				1.289	0.854	0	4.000	0.861	0																					
2794																																				
2915	4.000	-1.494	1.472	0.864	-0.903	-0.845				-0.313	1.790	0				-1.272	1.129	0				2.134	1.004	0	0	0	-0.206	1.254	-0.788	0						
2941	1.575	0.760	-0.613							-0.060	0.338	0	0.474	-0.198	0							1.091	0.260	0	0	0	-0.206	0.420	-0.352	0						
3031																-0.431	-0.651	0	-0.918	-1.739	0										0	-1.002	-0.414			
3055	-2.145	-1.261	-0.613							0.025	-0.551	0													0	0	1.114							0	0	0
3057																																				
3243	0.167	-0.950	0.499							1.795	0.151	0																								
3305	-0.034	0.915	0.151							0.109	0.011	0							-0.642	0.400	0	-0.272	0.566	0	0	0	1.114	0.503	0.811	0						
3415	-0.738	-0.406	-0.127				-3.645	-2.812	-1.122	1.289	1.135	0				-0.495	0.733	0				-0.592	0.566	0	0	0	0.337	-0.499	0.375	0						
3452	0.670	1.382	-1.447										-2.943	-3.705	0																					
3457	-0.335	-0.328	0.082							-0.313	0.573	0				-0.107	0.575	0	-0.918	-0.333	0	-0.432	-0.571	0				4.000	0.011	0	0	-0.469	-1.096			
3515	-0.034	0.527	1.333							0.952	0.666	0										2.054	1.616	0	0	0	1.191	0.587	0.302	0						
3543	0.167	0.604	0.012							-0.060	0.760	0													0	0	-0.983	0.920	0.956	0	0	0.419	0.211			
3587	-0.235	-0.328	-0.196							1.036	0.245	0										-0.031	-0.002	0	0	0	-0.401	0.503	0.520	0	0	3.615	-0.812			
3626	0.067	-0.095	-0.196							0.109	0.666	0	-0.043	-0.264	0	0.540	-0.691	0	0.464	1.256	0	0.691	1.179	0	0	0	0.143	0.670	0.738	0	0	0.241	0.666			
3831	0.569	-0.328	-0.752	-0.162	0.680	-0.025										0.670	-0.928	0				0.450	-1.271	0												
3864	0.268	0.760	-0.891							-0.819	-0.458	0																						0	0	0
4047	-0.738		0.290							-0.228		0										-0.432		0	0		0.609	0.253		0						
4050	-0.134	-0.406	0.221							-0.903	-3.970	0	-1.752	-3.374	0										0	0	-0.129							0	0	0
4064	0.569	-3.904	0.082							-0.144	4.000	0																								
4100	-0.034	0.216	0.151				0.566	0.439	0.405	0.277	0.619	0				-0.495	-0.968	0				-1.073	-1.008	0	0	0	-0.129	-0.582	-0.061	0	0	-0.203	0.609			
4171	0.067	0.682	-0.613							1.121	-1.394	0				-4.000	-4.000	0							0	0	0.143			0						
4246	1.173	0.527	0.846							-0.060	0.151	0										-1.073	-0.440	0				1.004	1.029	0						
4288	-0.738	-4.000	0.082							-0.987	-0.598	0				-1.207	0.258	0	-2.483	-0.639	0	-2.196	-0.658	0	0	0	2.395	-0.999	1.465	0	0	0.596	-0.812			
4339	1.876	-0.406	-0.335				-0.028	0.335	0.405	0.109	0.666	0	0.371	0.828	0	0.734	0.258	0	0.279	0.095	0	-0.592	0.085	0	0	0	-0.478	-0.081	-1.079	0	0	0.862	-1.153			
4358	0.670	1.226	0.012							0.277	0.198	0																								
4400	4.000	4.000	2.445							0.362	2.305	0										4.000	3.497	0	0	0	1.657									
4418	-4.000	-4.000	4.000	-2.433	0.258	4.000	-0.375	-0.335	3.311	1.626	0.994	0	3.581	0.696	0	-0.495	0.535	0	-1.010	-4.000	0	-1.394	-4.000	0			-1.371	-4.000	-3.477		0	-4.000	-2.289	0	0	0
4449	-0.235	-0.095	0.082							-0.650	-0.270	0													0	0	-0.323									
4557	0.469	0.527	0.499							0.109	0.385	0	-0.820	0.332	0							-1.474	-0.221	0				-0.999	-1.079	0						
4562	-4.000	-0.639	-0.335							1.711	0.900	0				1.899	-4.000	0				-0.913	0.085	0	0	0	0.298	0.837	-4.000	0	0	0.330	-0.130			
4633																			0.371	0.339	0	1.011	0.216	0	0	0	-1.216	1.254	-1.151	0		-0.025	0.154			
4635	-0.939	-1.028	0.221							-0.566	0.011	0													0	0	-0.634	-0.666	0.229	0	0	-0.114	-0.641			
4664	-0.235	0.682	0.985	0.351	-0.797	0.139				-0.060	0.619	0				0.152	0.733	0	0.095	-1.128	0							-0.666	0.375	0	0	0.685	0.154			
4710	-0.939	-1.339	-1.030	-0.675	-1.220	-1.008				-0.397	-1.582	0	-0.354	-1.157	0	-0.042	-1.561	0	-0.181	-3.511	0	-0.753	-1.621	0	0	0	0.415	-1.333	-0.933	0	0	-1.180	-1.437	0	0	0
4889	1.173	1.304	0.151							0.109	0.526	0				0.928	0.812	0	-0.365	0.645	0	-0.031	0.741	0	0	0	-1.798	-0.666	-0.061	0		-0.825			
4951										-3.938	-4.000	0				-4.000		0				-3.479	-2.145	0												
4983	-0.537	-0.251	-0.613							-0.650	0.104	0													0	0	-1.449									
4998	0.067	0.682	0.499							0.109	-4.000	0														0	-1.410									

Annex 2. Z-scores of all participants

Lab no.	Aerobic micro-organisms, 30 °C			Aerobic micro-organisms, 20 °C			Contaminating microorganisms			Enterobacteriaceae			Coliform bacteria, 30 °C			Coliform bacteria, 37 °C			Thermotolerant coliform bacteria			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive staphylococci			Enterococci			Gram-negative bacteria in dairy products		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
5100	-4.000	-4.000	-4.000															0				-4.000	-2.933	0												
5119	0.067	0.216	-0.057							0.783	1.743	0	1.303	1.093	0							0.851	0.960	0												
5182	1.273	2.237	0.777							0.699	-1.020	0				0.411	1.999	0				0.450	-0.571	0	0	0	0.337									
5201	-0.738	4.000	-1.378							0.109	0.713	0										0.290	-0.308	0	0	0	-1.294	-0.749	0.229	0						
5204	-0.637	0.060	-0.405				0.764	-0.077	0.196	-0.313	1.041	0	-0.665	-0.198	0	-1.272	-0.374	0	0.648	0.767	0	0.450	0.829	0	0	0	0.764	-4.000	-1.006	0	0	-1.180	0.552			
5261	0.067	-2.427	-0.474							1.626	1.135	0				-4.000		0				1.813	1.179	0	0	0	0.065									
5290	1.474	0.216	2.306							1.795	0.292	0	0.371	-0.429	0	3.129	-1.166	0				1.332	0.741	0	0	0	0.143	0.169	0.738	0						
5329	0.067	0.138	-0.057							0.109	-0.832	0										0.450	-1.096	0	0	0	-0.362	0.420	0.229	0	0	0.685	0.666			
5333	1.374	0.216	-0.057				-0.078	0.181	-0.703	-0.734	0.947	0	0.319	-0.297	0	-0.625	0.456	0				-0.031	0.523	0	0	0	-1.061	-0.499	-0.134	0	0	-0.736	-0.926			
5338	0.368	-3.049	-0.057							-0.903	-1.629	0																								
5352	0.771	-0.173	0.221							-0.228	-0.224	0				-0.107	0.733	0	-0.642	0.461	0	-0.272	0.610	0	0	0	1.347	0.336	-0.933	0	0	2.017	3.450			
5419	-1.844	-2.349	-1.239				-1.564	-0.181	-1.362	-0.397		0										-1.394	-2.495	0	0	0	-0.634	-1.250	-1.151	0	0	-0.469	-0.698			
5446	0.670	1.071	-0.544							-0.397	0.666	0				-0.042	-0.216	0				-0.592	-0.483	0				0.086	1.029	0						
5545	-0.738	0.604	-2.073				0.814	0.439	0.885	0.530	-1.067	0													0	0	-0.129	1.421			0	2.638	0.040			
5615	0.268	1.459	1.055							0.952	0.807	0				-2.048	0.258	0				-2.196	0.304	0	0	0	-1.371	-0.081	0.883	0	0	-2.778	0.211			
5632	0.067	0.682	1.194							0.109	0.198	0										0.691	-0.134	0	0	0	-0.245									
5654	0.670	0.138	0.151							0.783	0.619	0													0	0	0.493									
5701	0.972	-0.639	1.333																																	
5801	-2.145	-0.795	0.499							-0.060	-0.224	0													0	0	-0.634									
5808	-1.743	-2.194	-1.169													0.475	-2.233	0				0.129	-2.714	0	0	0	-1.993									
5883	-0.939	-0.017	-0.683							0.952	-0.177	0										0.530	0.697	0	0	0	-0.750	-0.999	-0.279	0						
5950	-1.240	-0.173	0.221	0.058	0.785	-0.599	1.507	-2.708	0.705	-0.481	0.526	0	-2.270	-0.661	0	-3.343	-0.968	0	0.095	0.095	0	0.370	0.348	0	0	0	1.114	-0.999	-0.933	0	0	0.330	1.461	0	0	0
6109	0.871	-0.017	0.916													-0.495	-0.572	0							0	0	-0.051									
6175	-0.034	0.449	0.707							0.193	-2.331	0																								
6224	4.000	1.537	1.611							1.542	1.509	0													0	0	-0.012									
6253										0.362	0.292	0	-0.665	-0.297	0							0.290	-0.746	0							0	-0.469	0.836			
6258	0.167	-0.950	-1.030										-0.768	-4.000	0																					
6278	0.368	3.092	1.750																																	
6343	-1.140		1.611							-1.577		0			0	0.411		0				-0.272		0	0		-1.449	-0.332								
6352	-0.235	0.604	-1.447							-0.650	-0.645	0				-0.754	-1.324	0				-0.913	-4.000	0	0	0	-1.216	0.336	-0.134	0	0	0.241	0.495			
6368	0.670	0.371	0.221	-0.235	1.102	-0.271				-1.240	-0.692	0				0.087	0.061	0	0.464	0.461	0	0.691	0.610	0	0	0	1.114	0.753	0.447	0	0	0.507	-0.016			
6456										-0.313	-0.551	0	-0.872	-0.032	0	-0.366	-0.295	0				-0.272	-1.446	0							0	0.419	1.120			
6490	-0.637	1.226	-0.405							2.469	0.479	0				0.346	0.338	0							0	0	0.260	-0.165	0.229	0	0	0.330	-0.585			
6594																																				
6658	-1.944	-0.095	-1.586							-1.577	-0.739	0													0	0	-1.410							0	0	0
6686	-0.436	1.226	0.499	4.000	0.891	0.958				1.458	0.807	0							1.016	0.584	0	-0.031	0.916	0				0.753	0.593	0	0	0.774	-0.187			
6762	-1.140	-1.183	-0.822							-1.240	-0.692	0										-1.955	-1.008	0												
6801	1.675	-0.251	1.333													0.217	0.338	0				0.290	0.129	0												
6885	-0.134		-0.752							0.952	0.947	0										0.530	0.435	0	0	0	0.764	0.086	0.157	0	0	-0.025	-0.300	0	0	0
6944	-0.134	-0.406	-0.057													0.605	2.355	0				0.290	2.359	0				-0.582	0.302							
6958	0.469	-0.406	-0.683							0.530	-0.177	0													0	0	-0.750									
6971	-0.436	-1.183	-0.127							1.205	0.619	0													0	0	0.687									
6981	0.469	0.371	-0.613							-0.903	-0.411	0																								
7182	-1.341	0.060	-0.752							-0.566	0.198	0				-0.754	0.061	0				-0.913	-0.221	0												
7207	2.379	-0.795	1.750							-0.650	-0.458	0													0	0	0.260				0	-0.292	-0.585			
7232	0.771	0.449	0.568																																	
7242		-0.251	-1.586								2.493	0																								
7248	-0.738	0.060	-0.266	-1.627	-1.536	-1.172	-0.128	2.709	0.555	-0.313	-0.551	0	0.215	0.894	0	0.411	0.338	0	0.003	-0.394	0	0.530	0.523	0	0	0	-0.634	-0.499	-0.061	0	0	-0.114	-1.607			
7334	-0.436	4.000	-0.822													0.346	-1.126	0						0	0	0	-0.168	-1.083	3.136	0						
7564				0.497	-0.375	-0.189							0.785	1.093	0				0.464	0.645	0	0.691	0.741	0							0	0.507	-0.585			
7617	-0.034	-0.950	-0.127							0.025	0.900	0				-0.172	0.773	0				-0.191	0.610	0				-0.332	0.011	0						
7631	-0.637	-1.650	-1.308							-1.240	-0.551	0	-0.924	-0.396	0																					
7688	-0.637	-0.095	0.151							0.615	-0.036	0	0.889	-0.661	0	-0.495	-4.000	0	1.384	0.645	0	1.492	0.741	0	0	0	-0.478	-0.332	1.319	0	0	1.484	-0.471			
7728	0.268	-0.173	0.221	0.058	1.102	-0.681				0.783	-0.598	0				0.411	-0.058	0	0.279	-0.822	0	0.530	-0.308	0	0	0	0.454	1.254	2.046	0						
7750	0.067	0.449	-0.544													1.576	-0.374	0							0	0	0.104									
7825	0.972	0.138	-0.127							-2.505	-2.144	0							-4.000	-4.000	0		-4.000	0				-1.083	-2.023		0	-0.913	-1.380			
7876	0.569	0.293	0.151							-1.915	-1.301	0										-0.432	0.435	0	0	0	-0.323	-0.165	-0.570	0	0	-0.469	-1.039			

Annex 2. Z-scores of all participants

Lab no.	Aerobic micro-organisms, 30 °C			Aerobic micro-organisms, 20 °C			Contaminating microorganisms			Enterobacteriaceae			Coliform bacteria, 30 °C			Coliform bacteria, 37 °C			Thermotolerant coliform bacteria			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive staphylococci			Enterococci			Gram-negative bacteria in dairy products		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
7930	0.871	-0.639	-0.474							-0.228	0.151	0							1.016	0.706	0	1.172	0.785	0	0	0	0.260	-0.081	0.229	0	0	0.241				
7940	1.675	-0.406	-1.656							-0.313	0.338	0	-1.131	1.060	0																				
7962	-0.235	0.604	0.777							0.783	-0.458	0	-0.509	0.696	0	1.187	0.891	0	-0.457	1.073	0	-0.111	1.047	0	0	0	-0.828	-0.832	-0.788	0	0	1.218	1.518			
7968	0.771	0.760	**2.723**							0.362	0.011	0	0.578	0.630	0	1.058	0.219	0	1.292	0.584	0	1.412	0.697	0	0	0	1.036	0.002	-0.570	0	0	1.129	**3.393**			
7984	0.469	-0.251	0.360							0.615	0.104	0													0	0	-0.323							0	0	0
8068	**-2.246**	-1.339	-1.100	-1.920	-1.008	-1.828				-0.397	**2.165**	0	0.785	0.464	0	0.411	-0.058	0	0.003	0.400	0		0.566	0		0		**-4.000**	0.811			0.774	-0.471			
8105	1.977	1.071	-0.474													0.411	1.089	0				-0.272	1.441	0	0	0	-0.789	0.670	0.375	0						
8147	-0.738	-0.406	-1.447							-0.734	-0.130	0	0.474	0.332	0								**-2.933**													
8213	-0.134	-0.562	-0.196							1.542	0.057	0													0	0	0.842							0	0	0
8260	-0.235	-0.872	-1.239							-0.228	-0.224	0			0	0.605	0.219	0						0	0	0	-0.556	0.503	0.811	0						
8313	-1.642	-1.183	-1.239							-0.734	-1.067	0													0	0	-0.206	0.253	-1.151	0	0	0.152	0.495			
8333	0.167	0.138	1.959							-0.228	-1.254	0				0.217	-0.414	0							0	0	1.036				0	**-3.222**	-1.153			
8397	0.067	-1.805	0.499							-1.493	0.900	0										0.530	0.741	0	0	0	**3.016**	0.837	0.811	0	0	-0.647	-0.926			
8430	**-2.447**	-0.562	-0.961							**-2.505**	-1.488	0	-0.820	-1.124	0							-1.875	-0.396	0				0.670	0.084							
8435	0.469	0.371	1.472	0.937	0.469	1.122				1.121	0.011	0	-0.043	-1.654	0	-0.236	0.456	0	1.569	0.584	0	1.653	0.697	0	0		0.842	1.338	0.593	0	0	-1.002	**4.000**			
8506	1.474	0.604	**2.515**													1.123	-0.216	0				-0.352	**-2.277**	0	0	0	0.065								
8523	0.469	0.760	0.499							1.036	1.041	0										-0.592	0.872	0				-0.081	0.157	0						
8528																									0	0	-0.323									
8568	1.072	1.615	0.082							-0.819	-1.863	0				-1.207	**-2.036**	0							0	0	0.298				0	**-3.222**	0.381			
8626	-0.235	**-4.000**	**-4.000**							0.615	-1.769	0				**-4.000**	**-4.000**	0	**-4.000**	**-4.000**	0	**-4.000**	**-4.000**	0												
8628	-1.642	-1.494	0.429	-1.261	0.469	0.057				-0.481	0.151	0	-0.561	0.729	0	-0.495	0.694	0	0.003	0.523	0	0.290	0.654	0	0	0	-0.012	0.503	1.319	0	0	0.862	-0.300			
8657	0.268	-0.717	-0.196							-0.566	**-2.144**	0																								
8734	0.268	0.138	-0.057							-1.324	0.807	0																								
8742	-1.542	0.449	-0.613													-0.495	1.999	0	-1.010	**2.356**	0	-0.592	1.966	0				1.505	0.738	0						
8756	0.368	-0.872	0.499	0.497	-0.481	0.794					-0.224	0										-0.753	-0.440	0	0	0	-0.245	0.169	-1.442	0						
8766	0.268	-0.406	0.429							0.109	-0.832	0										-1.073	-0.308	0	0	0	-0.323	-0.081	-0.352	0	0	-1.446	-0.016			
8829	1.675	0.604	1.889																			0.691	-0.746	0	0	0	-0.439									
8891	**-2.949**	-0.251	-1.169				0.665	-0.645	-0.253	**-4.000**	-0.364	0	-1.804	-1.157	0							**-2.356**	0.129	0	0	0	-0.323	**-3.504**	-0.134							
8909	0.368	0.060	0.499							0.868	-1.160	0	0.992	-0.760	0							0.129	-1.227	0	0	0	1.424				0	1.484	0.950			
9002	1.675	**3.014**	**2.028**							-0.650	1.978	0				0.217	1.445	0				-0.913	1.179	0	0	0	0.298									
9003	-0.637	-0.406	0.082							0.025	0.666	0	0.215	1.093	0	-0.172	0.298	0				-0.272	0.085	0				-1.250	-0.715	0						
9007	0.670	1.692	1.472							0.952	0.900	0				0.217	0.456	0				-0.272	0.566	0				1.505	-1.442	0						
9025	**4.000**	**2.237**	1.194							0.109	0.198	0													0	0	**2.861**							0	0	
9034																																				
9078	-0.637	-0.173	**2.237**							1.121	-0.879	0																								
9217																																				
9269	-0.034	0.138	0.151																																	
9408	-1.140	-0.872	-1.239							-0.144	0.526	0				-0.366	-0.177	0	**-2.115**	-1.617	0	0.931	-0.046	0	0	0	0.609	**-2.085**	-0.279	0						
9429										0.952	0.666	0	0.215	0.696	0	1.317	0.535	0	-0.642	-0.822	0	-0.592	-0.134	0							0	-0.203	-0.812			
9436	-1.844	-0.251	-0.752							-0.987	-1.394	0	0.474	0.928	0	0.928	0.140	0	0.003	0.095	0	-0.031	0.479	0	0	0	1.580	-0.999	-0.279	0	0	0.507	1.916			
9441	-1.140	-1.339	-1.239							-0.903	-1.301	0				-0.236	-0.454	0				-1.153	-0.921	0	0	0	0.143				0	0.596	0.040			
9453	-0.537	-0.484	0.221				-0.227	1.161	-0.463	-0.060	-0.083	0													0	0	-0.828	-0.081	1.101	0	0	-0.913	0.154			
9512	-1.844	-0.484	**-2.073**							-0.481	0.057	0													0	0	-1.993									
9559	0.569	0.449	0.151	0.717	0.785	0.302				**-2.168**	**-4.000**	0				-1.531	**-4.000**	0				-0.272	-0.046	0	0	0	0.881	0.837	1.174	0				0	0	0
9662	-0.436	**-2.582**	0.151	-0.089	**-2.380**	0.057				-0.313	-1.769	0	0.371	-0.992	0	0.540	-0.770	0				0.210	**-2.320**	0	0	0	-0.206	-0.332	-1.297	0	0	1.040	0.722			
9747	-0.537	-0.173	-1.378							**4.000**	1.181																-0.362									
9890	-0.134	1.226	0.707	-0.089	0.785	0.958				-1.493	1.322	0				-0.884	0.891	0				-1.073	0.741	0	0	0	**3.055**	-0.165	-1.442	0						
9903	0.167	**4.000**	-0.127							-0.397	-0.926	0										-0.031	0.129	0	0	0	1.735	-0.415	**-3.331**	0	0	**-2.245**	0.211			
9950	0.469	0.837	1.333																													-1.180				

|z| ≥ 3,0 ("Unacceptable" or "Action")
2,0 < |z| < 3,0 ("Warning")
The parameter is not evaluated
The result is not evaluated

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 participants carry out some form of internal quality assurance, but the analytical work also needs 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 PT, identical test material is analysed by a number of participants. After reporting of results by the participants, the organiser evaluates the results and compiles them in a report.

The Swedish Food Agency's PT program offers

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

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

The Swedish Food Agency's reference material

As a complement to the proficiency testing, but without specific accreditation, the Swedish Food Agency also manufactures a number of reference materials (RM) for internal quality control of food and drinking water microbiological analyses, including pathogens.

For more information, visit our website: www.livsmedelsverket.se/en/RM-micro

Livsmedelsverket
Swedish Food Agency