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Proficiency Testing

Microbiology – Food

October 2018

Accred. no. 1457
Proficiency testing
ISO/IEC 17043

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

Qualitative analyses

- Gram-negative bacteria in pasteurized dairy products

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Abbreviations

Media

BA	Blood agar
BEA	Bile esculin agar
BcsA	*Bacillus cereus* selective agar
BGLB	Brilliant green lactose bile broth
BHI	Brain heart infusion broth
BP	Baird-Parker agar
CBC	Oxoid Brilliance™ *Bacillus cereus* agar
COMPASS	COMPASS *Enterococcus* agar
EC	*E. coli* broth
ENT	Slanetz & Bartley *Enterococcus* agar
IA	Iron agar
KEAA	Kanamycin esculin azide agar
LSB	Lauryl sulphate broth
LTLSB	Lactose tryptone lauryl sulphate broth
MPCA	Milk plate count agar
MYP	Mannitol egg yolk polymyxin agar
MSA	Mannitol salt agar
PCA	Plate count agar
PEMBA	Polymyxin pyruvate egg yolk mannitol bromothymol blue agar
RPFA	Rabbit plasma fibrinogen agar
SFA	Sugar-free agar
TBX	Tryptone bile X-glucuronide agar
TGE	Tryptone glucose extract agar
TSA	Tryptone soya agar
VRB	Violet red bile agar
VRBG	Violet red bile glucose agar

Organisations

AFNOR	French National Standardization Association
AOAC	AOAC INTERNATIONAL
ISO	International Organization for Standardization
NMKL	Nordic Committee for Food Analyses
SLV/NFA	Livsmedelsverket/National Food Agency, Sweden

Contents

General information on results evaluation

Statistical evaluation of the results

Highly deviating values that did not belong to a strictly normal distribution after $\log_{10}$ transformation were identified as statistical outliers (Grubbs' test modified by Kelly [1]). In some cases, subjective adjustments were made to set limits based on knowledge of the samples contents. Outliers and false results were not included in the calculations of means and standard deviations. Results reported as "> value" were excluded from the evaluation. Results reported as "< value" were interpreted as being zero (negative result). All reported results are presented in Annex 1.

According to EN ISO/IEC 17043, for which the proficiency testing programme is accredited, it is mandatory for the participating laboratories to report method information for all their analyses. Method information is sometimes difficult to interpret, since many laboratories report a medium that is not included in the standard method they refer to. Results from laboratories that report contradictory data on methods/media have normally either been excluded from the method analysis, or been added to the group of "Others", together with results from methods and media that are only used by 1-2 laboratories.

Mean values and standard deviations are normally provided for the different analyses. When the total number of reported results for an analysis is fewer than 20, the median is provided instead of the mean value. For method groups with fewer than 5 results, only the number of false results and outliers are provided.

Uncertainty of measurement for the assigned values

The measurement uncertainty for an assigned value is calculated as the standard deviation divided by the square root of the number of correct results ("standard error"). The assigned value of an evaluated parameter is the mean value of the participants' results.

Table and figure legends

Tables

N	number of laboratories that reported results for the analysis
n	number of laboratories with satisfactory result
m	mean value in $\log_{10}$ cfu/ml (false results and outliers excluded)
s	standard deviation
F	number of false positive or false negative results
<	number of low outliers
>	number of high outliers
	global results for the analysis
	values discussed in the text

Figures

Histograms of the results for each sample and parameter are presented. The mean value of the analysis results is indicated in each histogram.

	values within the interval of acceptance (Annex 1)
	outliers
	false negative results
*	values outside of the x-axis scale

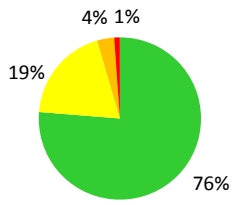
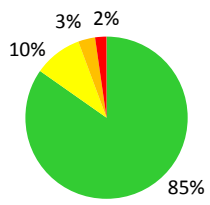
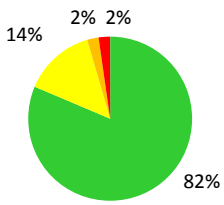
Results of the PT round October 2018

General outcome

Samples were sent to 183 laboratories, 47 in Sweden, 115 in other European countries, and 21 outside Europe. Of the 177 laboratories that reported results, 71 (40 %) provided at least one result that received an annotation. In the previous round with similar analyses (October 2017), the proportion was 39 %.

Individual results for each analysis in the PT round are listed in Annex 1 and are also available on the website after logging in: https://www2.slv.se/absint.

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

		Sample A				Sample B				Sample C			
% participants with 0 annotation 1 annotation 2 annotations >2 annotations													
Microorganisms		*Bacillus cereus* *Pediococcus acidilactici* *Staphylococcus xylosus*				*Enterococcus hirae* *Kocuria rhizophila* *Klebsiella pneumoniae*				*Enterococcus durans* *Escherichia coli* *Serratia marcescens* *Staphylococcus aureus*			
Analysis		**Target organism**	**N**	**F%**	**X%**	**Target organism**	**N**	**F%**	**X%**	**Target organism**	**N**	**F%**	**X%**
Aerobic micro-organisms	30˚C	All	166	0	5	All	166	0	8	All	165	0	4
	20˚C	All	29	0	0	All	29	0	0	All	29	0	0
Contaminating microorganisms		*S. xylosus* *B. cereus*	18	0	6	All	18	0	6	All	18	0	11
Enterobacteriaceae		-	137	0	0	*K. pneumoniae*	140	1	4	*E. coli* *S. marcescens*	140	0	5
Coliform bacteria	30˚C	-	57	2	0	*K. pneumoniae*	57	0	7	*E. coli*	57	0	4
	37˚C	-	94	1	0	*K. pneumoniae*	93	3	2	*E. coli*	92	2	1
Thermotolerant coliform bacteria		-	48	0	0	*K. pneumoniae*	46	0	2	*E. coli*	48	2	2
E. coli		-	119	0	0	-	119	3	0	*E. coli*	115	2	3
Presumptive *B. cereus*		*B. cereus*	109	1	5	-	109	1	0	*(S. aureus)* *(S. marcescens)*	109	2	0
Coagulase-positive staphylococci		*(S. xylosus)*	105	12	0	-	105	3	0	*S. aureus*	105	4	5
Enterococci		*(P. acidilactici)**	66	32	0	*E. hirae*	66	0	5	*E. durans*	67	1	7
Gram-negative bacteria in dairy prod.		-	11	0	0	*K. pneumoniae*	11	0	0	*E. coli* *S. marcescens*	11	0	0

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

Positive results are also considered correct for this analysis

Aerobic microorganisms, 30 °C and 20 °C

Sample A
All strains in the sample were target organisms. The strain of *S. xylosus* was present in a somewhat higher concentration than *B. cereus* and *P. acidilactici*. Five low and three high outliers were reported for the analysis at 30 °C. No outliers or false negative results were reported for the analysis at 20 °C.

Sample B
All strains in the sample were target organisms. *K. rhizophila*, *K. pneumoniae* and *E. hirae* were present in similar concentrations. Five low and nine high outliers were reported for the analysis at 30 °C. No outliers or false negative results were reported for the analysis at 20 °C.

Sample C
All strains in the sample were target organisms. *S. marcescens* and *S. aureus* were present in somewhat higher concentrations than *E. coli* and *E. durans*. Five low and two high outliers were reported for the analysis at 30 °C. No outliers or false negative results were reported for the analysis at 20 °C.

General remarks
As a whole, the analyses were without problem for the laboratories. No differences in the results attributed to the use of a specific method or medium could be identified, neither at 30 °C nor at 20 °C.

A relatively high number of outliers were reported at 30 °C, but no outliers were reported at 20 °C. In total, 17 laboratories reported at least one outlier at 30 °C. Of these, eight reported at least two outliers at 30 °C, and six of these further reported false results or outliers for other analyses in this proficiency testing round.

Similar methods and media were used at both temperatures. At 30 °C the most common methods were NMKL 86:2013 (25 %), 3M Petrifilm (22 %) and ISO 4833-1:2013 (20 %). The older methods NMKL 86:2006 and ISO 4833:2003 were still used by 9 % and 5 % of the laboratories respectively. The different methods are however very similar. All are also based on incubation on plate count agar (PCA) or milk plate count agar (MPCA). Laboratories that use Petrifilm AC may however use different times/temperatures, depending on which method is followed. For example, AOAC® 990.12 prescribes incubation at 35 °C for 48 h while AFNOR 3M 01/1-09/89 prescribes 30 °C for 72 h.

As in previous proficiency testing rounds, MPCA was mainly used by laboratories in the dairy industry. Incubation on tryptone soya agar (TSA) was mainly attributed to the use of a company-specific method. The results for both media were similar to PCA and Petrifilm AC.

At 30 °C, a smaller number of laboratories used TEMPO® AC (bioMérieux® SA, Marcy l`Etoile, France), which is based on MPN (Most Probable Number). With this method, the sample is incubated in a card that contains wells with different volumes. A substrate in the wells emits fluorescence when hydrolysed by the microorganisms. The concentration is determined by the number and size of the fluorescent wells.

At 20 °C, three laboratories followed NMKL 184, which is a method for enumeration of aerobic microorganisms and specific spoilage organisms in fish and fish products. With this method, incubation is done on iron agar (IA).

Results from analysis of aerobic microorganisms, 30 °C

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	166	158	5.262	0.156	0	5	3	152	4.207	0.107	0	5	9	158	4.963	0.116	0	5	2
PCA	79	76	5.243	0.173	0	2	1	73	4.207	0.103	0	3	3	76	4.943	0.121	0	2	0
Petrifilm AC	40	37	5.277	0.108	0	2	1	36	4.200	0.101	0	1	3	38	5.011	0.107	0	1	1
MPCA	21	21	5.245	0.113	0	0	0	21	4.190	0.077	0	0	0	20	4.916	0.073	0	1	0
TSA	11	11	5.279	0.157	0	0	0	10	4.257	0.116	0	0	1	11	4.966	0.085	0	0	0
TGE	5	5	5.274	0.155	0	0	0	5	4.192	0.107	0	0	0	5	4.970	0.104	0	0	0
TEMPO AC	4	4	-	-	0	0	0	3	-	-	0	0	1	4	-	-	0	0	0
Compact Dry TC	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	0	0	0
Blood agar	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	0	0	0
Other	4	2	-	-	0	1	1	2	-	-	0	1	1	2	-	-	0	1	1

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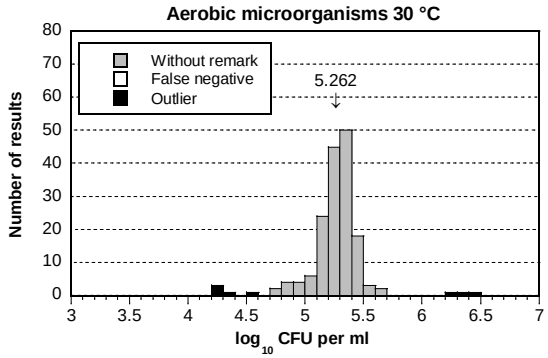

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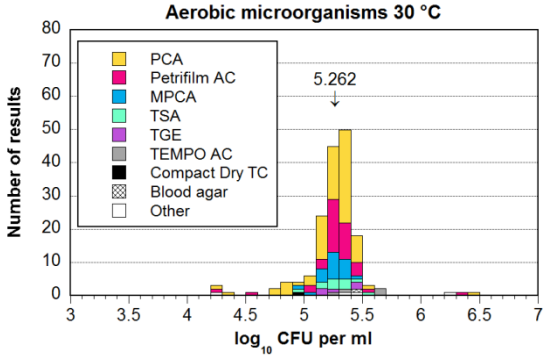

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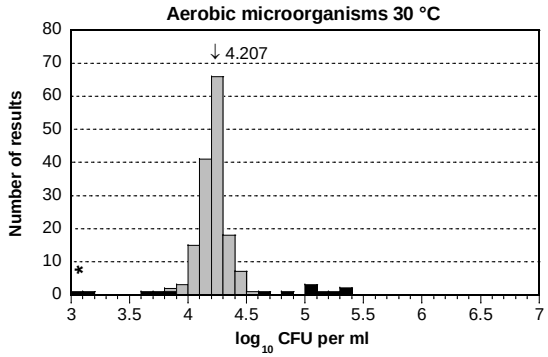

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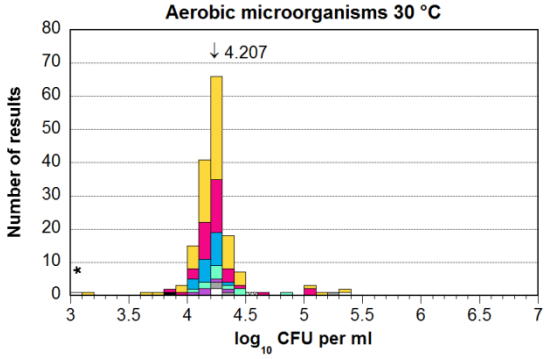

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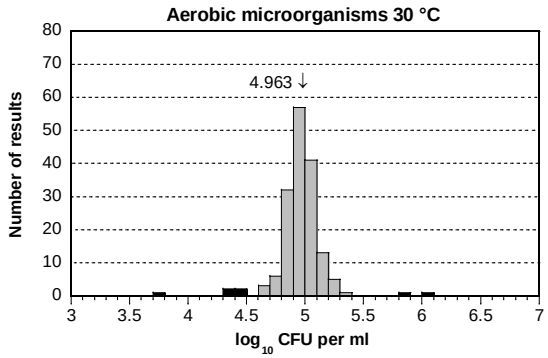

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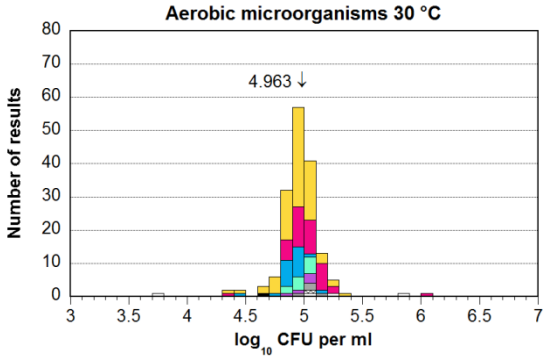

Results from analysis of aerobic microorganisms, 20 °C

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	29	29	5.262	0.140	0	0	0	29	4.121	0.127	0	0	0	29	4.929	0.105	0	0	0
PCA	20	20	5.289	0.147	0	0	0	20	4.141	0.100	0	0	0	20	4.951	0.097	0	0	0
Petrifilm AC	3	3	-	-	0	0	0	3	-	-	0	0	0	3	-	-	0	0	0
IA	3	3	-	-	0	0	0	3	-	-	0	0	0	3	-	-	0	0	0
MPCA	2	2	-	-	0	0	0	2	-	-	0	0	0	2	-	-	0	0	0
Yeast extract agar	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	0	0	0

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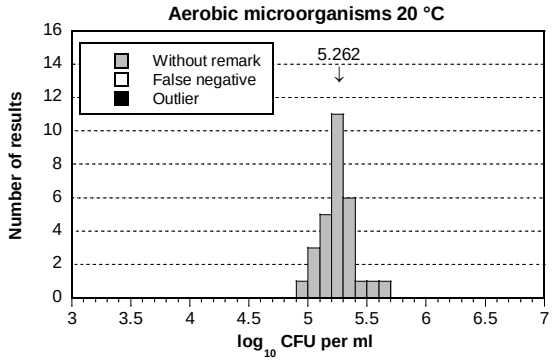

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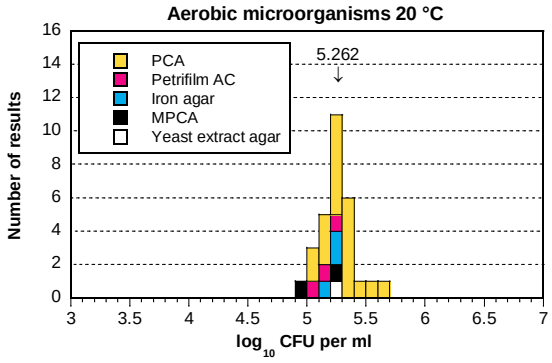

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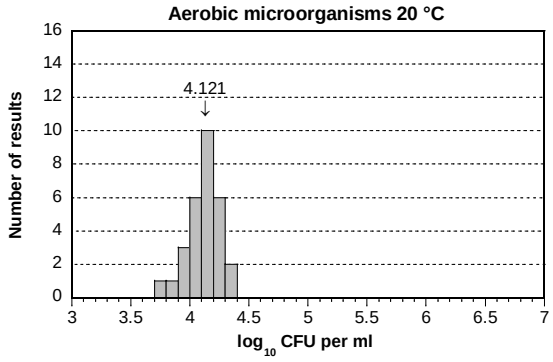

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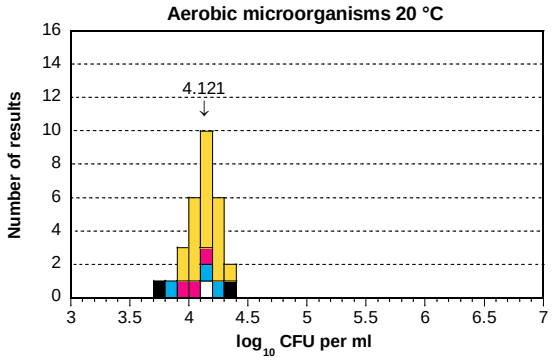

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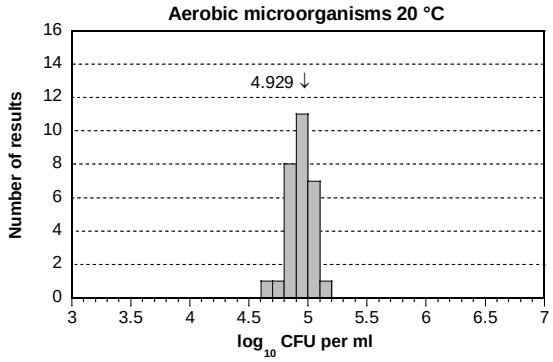

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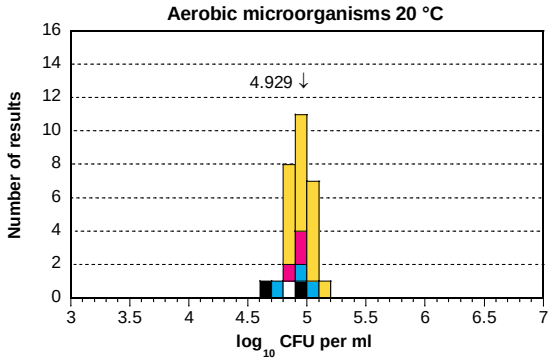

Contaminating microorganisms in dairy products

Sample A
All microorganisms in the sample can form colonies on sugar-free agar (SFA). The strain of *S. xylosus* was however present in a higher concentration than *B. cereus* and *P. acidilactici*. The strain of *P. acidilactici* has in previous proficiency testing rounds (October 2013) formed very small (pin-point) colonies on SFA. According to ISO 13559:2002 / IDF 153:2002, such colonies shall be excluded in the enumeration of colonies. One of the results deviated clearly from the median, and was considered as a low outlier.

Sample B
All microorganisms in the sample can form colonies on SFA. *K. rhizophila, K. pneumoniae* and *E. hirae* were also present in similar concentrations. *E. hirae* is catalase negative, and may therefore have been excluded if a confirmation test was performed. Despite this, no low results were reported. One of the results was however clearly higher than the median, and was considered as a high outlier.

Sample C
All microorganisms in the sample can form colonies on SFA. The strain of *E. durans* is catalase negative and formed small white colonies at the National Food Agency. It may therefore have been excluded during confirmation. At the same time, *E. durans* was present in a low concentration in the sample, and exclusion of this strain should only have had a marginal effect on the result. The two results that were clearly lower than the median were therefore considered as low outliers.

General remarks
Only 18 laboratories performed the analysis, and the results were therefore difficult to evaluate statistically. Deciding which results that are outliers has therefore been done by a manual inspection. This included consideration of the species and concentrations present in the sample (Table 3), the median of the laboratories' results, as well as the distribution of results that is normally seen in this analysis.

Ten of the 18 laboratories (56 %) followed ISO 13559:2002 / IDF 153:2002. One laboratory stated the older IDF 153:1999. The remaining laboratories followed either internal methods, or did not specify further what method they used. All laboratories incubated on SFA.

The goal of the analysis is to identify potential contaminating microorganisms in dairy products. According to ISO 13559:2002 / IDF 153:2002, lactic acid bacteria are in this sense not classified as contaminating microorganisms. Lactic acid bacteria are catalase negative, and several laboratories therefore perform a catalase test as confirmation. Such a test is however not included in ISO 13559:2002 / IDF 153:2002, which only specifies the enumeration of colonies that are "characteristic contaminating microorganisms". In total, nine of the laboratories (50 %) reported performing a confirmation test, in most cases a catalase test. No obvious difference could be seen between results from laboratories that performed a confirmation and those that did not.

Results from analysis of contaminating microorganisms

Method	N	Sample A						Sample B						Sample C					
		n	Med*	s	F	<	>	n	Med*	s	F	<	>	n	Med*	s	F	<	>
All results	18	17	5.190	0.261	0	1	0	17	4.060	0.223	0	0	1	16	4.900	0.206	0	2	0
Confirmation**	9	8	5.245	0.367	0	1	0	8	3.965	0.279	0	0	1	7	4.880	0.179	0	2	0
No confirmation	9	9	5.190	0.134	0	0	0	9	4.090	0.162	0	0	0	9	4.910	0.217	0	0	0

* Med: median.

** ”Confirmation” includes three laboratories for which the method of confirmation is not clearly specified.

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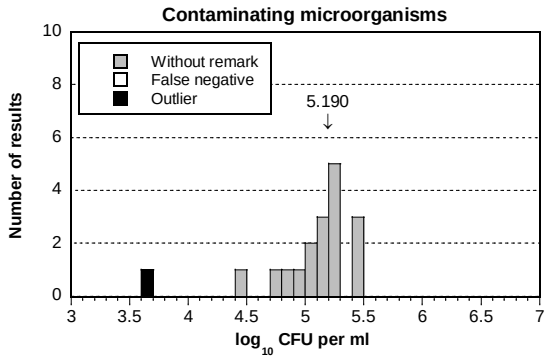

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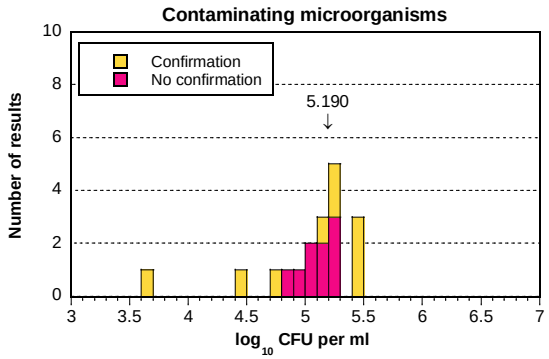

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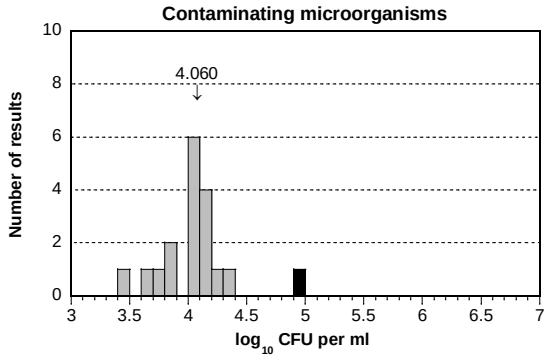

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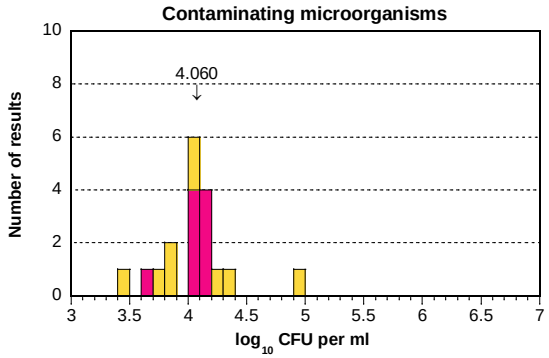

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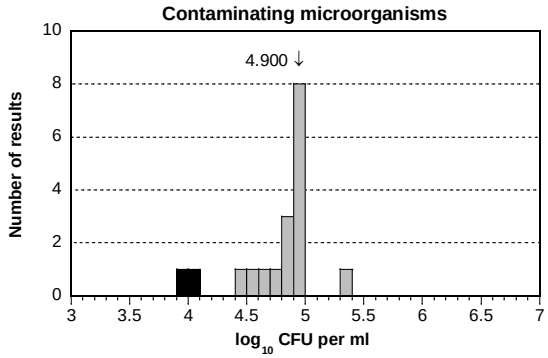

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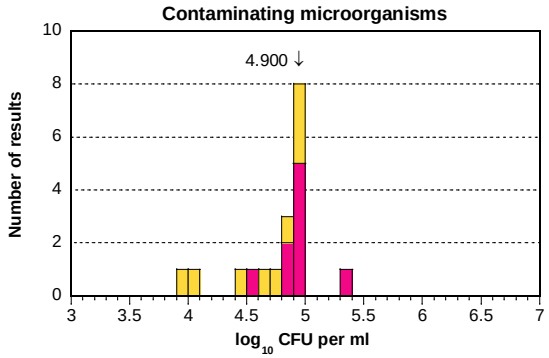


Enterobacteriaceae

Sample A
No target organism was present in the sample. No false positive results were reported.

Sample B
The strain of *K. pneumoniae* was target organism. Four low and two high outliers were reported, as well as one false negative result.

Sample C
The strains of *E. coli* and *S. marcescens* were target organisms. At the National Food Agency, two types of colonies were observed on violet red bile glucose agar (VRBG). Both were red, and surrounded by typical precipitation zones. They were also oxidase negative upon confirmation. The results were distributed around a distinct peak, but with a tail of low values. Six low and one high outlier were reported.

General remarks
Similar to previous proficiency testing rounds, most laboratories followed NMKL 144:2005 (48 %), or used Petrifilm EB (22 %). The different ISO methods (various editions) were in total used by 20 % of the laboratories. Comparable numbers of laboratories used the new ISO 21528-2:2017 and the older ISO 21528-2:2004 (7 % and 8 % respectively). The new ISO 21528-1:2017 was however only used by two laboratories (1 %). ISO 21528-2:2017 is based on colony-count, whereas ISO 21528-1:2017 is based on MPN (Most Probable Number). The MPN method is recommended when the expected concentration of Enterobacteriaceae is lower than 100 cfu g^{-1}. The mean values for the different ISO methods were however very similar, for all three samples.

As in the analysis of aerobic microorganisms, a smaller number of laboratories used a method based on detection of fluorescence (TEMPO® Enterobacteriaceae).With this method, there was a tendency towards higher results, mainly in sample C, but also in sample B. No outliers were however reported by users of this method. Such somewhat higher results – but within the acceptance limits – have been seen in several previous proficiency testing rounds. The number of users of this method is however small, which makes it difficult to evaluate this observation further.

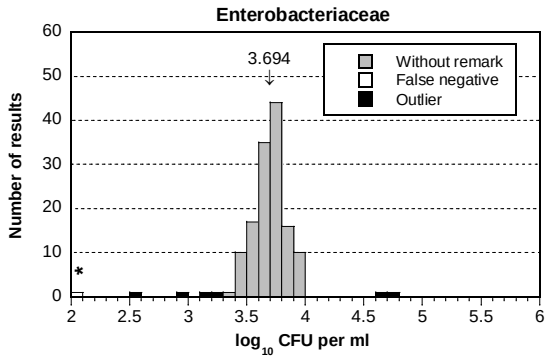
Enterobacteriaceae are Gram-negative and oxidase negative bacteria, that ferment glucose with the production of acid by-products. With both NMKL 144 and ISO 21528-2, they are enumerated on VRBG. On this medium, Enterobacteriaceae form pink/red colonies, with or without a bile precipitation zone. The 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.

According to NMKL 144:2005, presumptive colonies on VRBG shall be confirmed with an oxidase test. With ISO 21528 2:2017, confirmation is done with both an oxidase test and a test for glucose fermentation. Oxidase-negative bacteria that also ferment glucose in glucose oxidation/fermentation (OF) medium are considered as Enterobacteriaceae. In total, 66 % of the laboratories reported performing some kind of confirmation test. The most common was an oxidase test, but the use of a glucose fermentation test was also fairly frequent. Other methods used for confirmation included API 20 E and Maldi-Tof. Performing or not performing a confirmation test does not appear to have had an effect on the overall performance of the laboratories.

Results from analysis of Enterobacteriaceae

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	137	137	-	-	0	-	-	133	3.694	0.132	1	4	2	133	4.541	0.172	0	6	1
VRBG	91	91	-	-	0	-	-	90	3.692	0.129	0	3	0	89	4.561	0.154	0	4	0
Petrifilm EB	30	30	-	-	0	-	-	27	3.690	0.168	1	1	2	28	4.485	0.188	0	2	1
TSA/VRBG	7	7	-	-	0	-	-	7	3.657	0.076	0	0	0	7	4.426	0.256	0	0	0
TEMPO EB	7	7	-	-	0	-	-	7	3.757	0.063	0	0	0	7	4.680	0.075	0	0	0
Other	2	2	-	-	0	-	-	2	-	-	0	0	0	2	-	-	0	0	0

B



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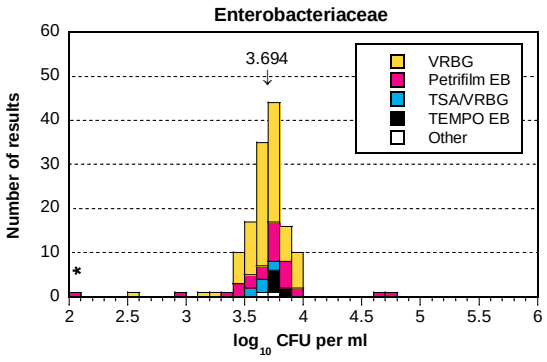

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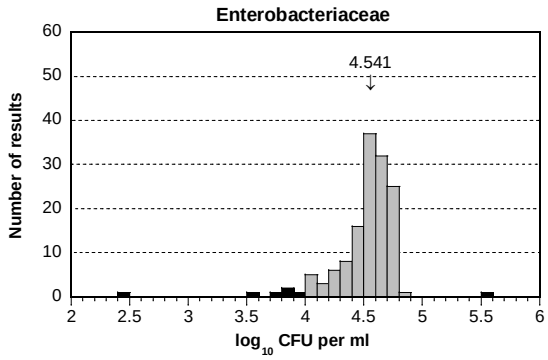

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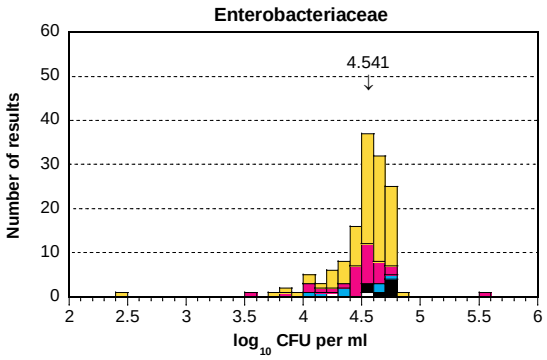

Coliform bacteria, 30 °C and 37 °C

Sample A

No target organism was present in the sample. One false positive result was reported at both 30 °C and at 37 °C.

Sample B

The strain of *K. pneumoniae* was target organism. It forms typical red colonies on violet red bile agar (VRB) and produces gas in brilliant green lactose bile broth (BGLB). At the National Food Agency, the production of gas was observed to be lesser at 30 °C than at 37 °C.

At 30 °C, two low and two high outliers were reported. At 37 °C, one low and one high outlier were reported, as well as three false negative results.

Sample C

The strain of *E. coli* was target organism. At the National Food Agency, two types of colonies were observed on VRB. Large red colonies with a precipitation zone, and a smaller number of colonies with a less prominent zone. Both colony types were oxidase negative, but only the larger colonies produced gas in BGLB. In addition to *E. coli*, the sample contained *S. aureus*, *E. durans* and *S. marcescens. S. aureus* and *E. durans* are Gram-positive and should normally not form colonies on VRB, as they are inhibited by the presence of bile salts and crystal violet in VRB. The smaller colonies can therefore be assumed to be *S. marcescens*, which is a weak fermenter of lactose and thus capable of forming small colonies on VRB.

The results at both 30 °C and 37 °C were distributed with two overlapping peaks, one at approximately $\log_{10}$ 4.0 and one at $\log_{10}$ 4.5 cfu ml^{-1}. The two peaks could not be separated statistically, but the low and high peaks correspond very well to the concentrations of *E. coli* and *E. coli* + *S. marcescens* in the sample respectively.

It is difficult to attribute the low and high results to the use of a specific method or medium, partly since several methods/media were used by a smaller number of laboratories. Performing a confirmation test was also reported in by comparable numbers of laboratories in both peaks. Possibly, users of Petrifilm appear to have reported relatively more results in the lower peak compared to users of other media. Users of TSA/VRB also appear to have somewhat more results reported in the higher peak. Different results can also have been obtained due to variations in the definition of coliform bacteria by the different methods.

At 30 °C, one low and one high outlier were reported. At 37 °C, one high outlier was reported, as well as two false negative results.

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. They are normally surrounded by a red/pink zone of precipitation, which is formed due to the precipitation of bile salts when the pH decreases.

The most commonly used methods at both temperatures were NMKL 44:2004, ISO 4832:2006 and 3M™ Petrifilm™. Both NMKL 44:2004 and ISO 4832:2006 prescribe incubation on VRB, but the confirmation steps differ somewhat. NMKL 44:2004 states that all presumptive colonies on VRB shall be confirmed in BGLB, whereas ISO 4832:2006 states that only atypical colonies require further confirmation. Such differences between the methods may (at least partially) explain why *S. marcescens* was counted as a coliform bacterium by some laboratories. Further, if the sample is suspected to contain stressed coliform bacteria, NMKL 44:2004 recommends pre-incubation on tryptone soya agar (TSA). Such a pre-incubation could also contribute to higher results. Petrifilm CC and Petrifilm EC/CC are also based on VRB, and have a plastic film that facilitates detection of gas production.

Lauryl sulphate broth (LSB) in combination with BGLB was used by laboratories that followed ISO 4831 and NMKL 96 (various editions). ISO 4831:2006 is based on MPN (Most Probable Number) and is adapted for use when the expected concentration of coliform bacteria is lower than or equal to 100 cfu g^{-1}. NMKL 96 is also based on

MPN, and is adapted for the analysis of coliform bacteria in fish and seafood. It is recommended when the expected concentration of microorganisms is lower than or equal to 300 cfu g^{-1}. In some previous proficiency testing rounds, users of these methods have had problems with correctly determining higher concentrations – such as those in samples B and C. However in the current proficiency testing round, all results were without remark.

For the analysis at 37 °C, four laboratories used RAPID'E. coli 2 agar, which is a chromogenic medium that detects β-glucuronidase and β-galactosidase activity. On this medium, coliform bacteria (Gal+/Gluc-) form blue/green colonies, while *E. coli* (Gal+/Gluc+) form pink/purple colonies.

Results from analysis of coliform bacteria, 30 °C

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	57	56	-	-	1	-	-	53	3.693	0.161	0	2	2	55	4.209	0.331	0	1	1
VRB	39	38	-	-	1	-	-	37	3.687	0.122	0	2	0	38	4.228	0.303	0	0	1
Petrifilm CC	6	6	-	-	0	-	-	4	3.713	0.189	0	0	2	5	3.968	0.390	0	1	0
TSA/VRB	5	5	-	-	0	-	-	5	3.788	0.095	0	0	0	5	4.440	0.220	0	0	0
LSB/BGLB	4	4	-	-	0	-	-	4	-	-	0	0	0	4	-	-	0	0	0
Petrifilm EC/CC	2	2	-	-	0	-	-	2	-	-	0	0	0	2	-	-	0	0	0
TEMPO CC	1	1	-	-	0	-	-	1	-	-	0	0	0	1	-	-	0	0	0

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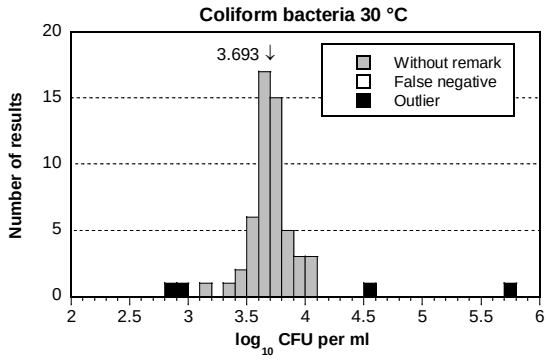

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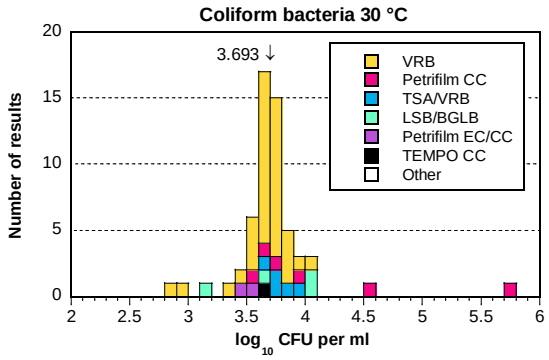

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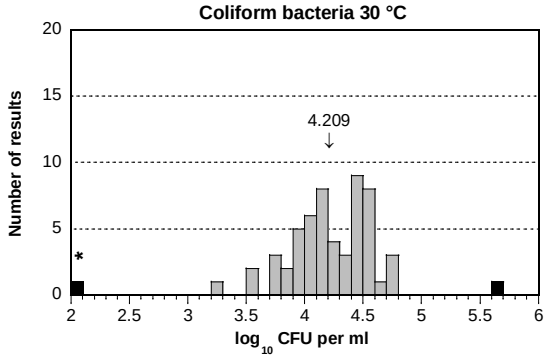

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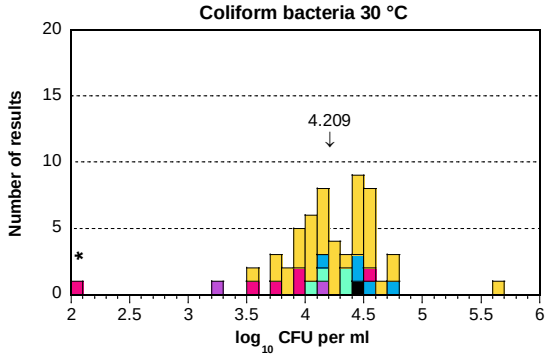

Results from analysis of coliform bacteria, 37 °C

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	94	93	-	-	1	-	-	88	3.703	0.191	3	1	1	89	4.232	0.305	2	0	1
VRB	44	44	-	-	0	-	-	44	3.663	0.164	0	0	0	43	4.269	0.315	0	0	0
Petrifilm EC/CC	17	16	-	-	1	-	-	15	3.710	0.187	1	1	0	16	4.115	0.208	1	0	0
Petrifilm CC	10	10	-	-	0	-	-	9	3.768	0.175	1	0	0	9	4.012	0.373	0	0	1
TSA/VRB	6	6	-	-	0	-	-	6	3.707	0.241	0	0	0	6	4.347	0.229	0	0	0
LSB/BGLB	9	9	-	-	0	-	-	8	3.894	0.202	0	0	0	8	4.238	0.286	0	0	0
Rapid'E.coli2	4	4	-	-	0	-	-	4	-	-	0	0	0	3	-	-	1	0	0
TEMPO CC	1	1	-	-	0	-	-	1	-	-	0	0	0	1	-	-	0	0	0
Brilliance EC/CC	1	1	-	-	0	-	-	0	-	-	0	0	1	1	-	-	0	0	0
Other	2	2	-	-	0	-	-	1	-	-	1	0	0	2	-	-	0	0	0

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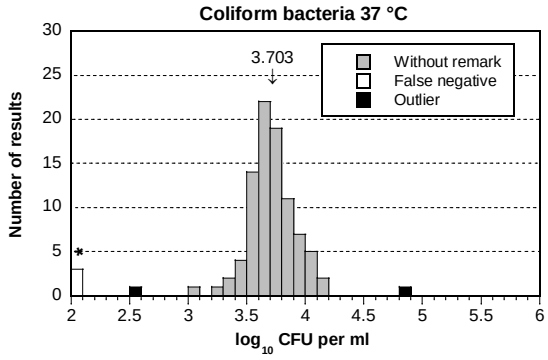

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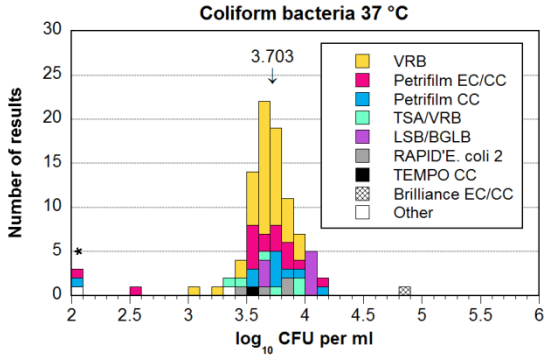

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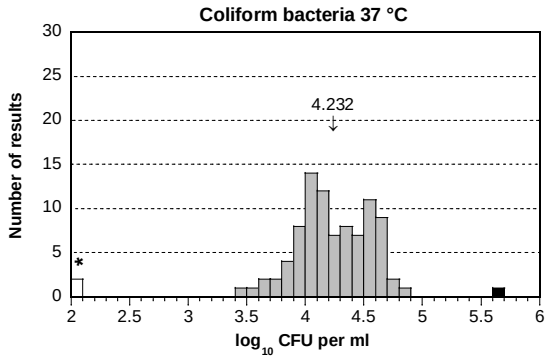

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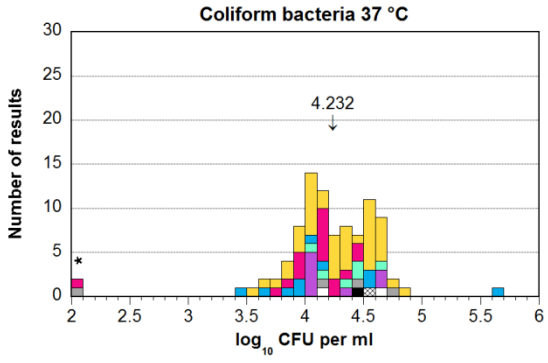

Thermotolerant coliform bacteria and *Escherichia coli*

Sample A
No target organism was present in the sample. No false results were reported, neither for thermotolerant coliform bacteria nor for *E. coli*.

Sample B
The strain of *K. pneumoniae* was target organism for the analysis of thermotolerant coliform bacteria, but not for *E. coli*. The strain produces gas but not indole in lactose tryptone lauryl sulphate broth (LTLSB).

One low outlier was reported for thermotolerant coliform bacteria. Four false positive results were reported for *E. coli*.

Sample C
The strain of *E. coli* was target organism for both analyses. At the National Food Agency, it produced both gas and indole in LTLSB. It was also positive for β-glucuronidase.

One low outlier was reported for thermotolerant coliform bacteria, as well as one false negative result. Three low and one high outlier were reported for *E. coli*, as well as two false negative results.

General remarks
As a whole, the analyses were without problem for the laboratories. No obvious differences in the results from the methods and media that were used could be identified. However similar to previous proficiency testing rounds (October 2016, 2017), the group "Other" was fairly large for the analysis of *E. coli*. This was mainly due to unclear/ambiguous method information from some laboratories.

NMKL 125:2005 was the most commonly used method for the analysis of thermotolerant coliform bacteria. It describes the analysis of both thermotolerant coliform bacteria and of *E. coli*. Thermotolerant coliform bacteria are in the method defined as those that form typical dark red colonies surrounded by a zone of precipitation on VRB after 24 h at 44 °C. The colonies are confirmed by inoculation either in *E. coli* broth (EC) or in LTLSB. In both of these media, thermotolerant coliform bacteria produce gas as a consequence of lactose fermentation. Thermotolerant coliform bacteria that also produce indole either in LTLSB or in tryptone broth are considered as *E. coli*.

For the analysis of *E. coli*, most laboratories used methods based on 3M™ Petrifilm™ (either Petrifilm EC/CC or Petrifilm SEC), followed by NMKL 125:2005 and ISO 16649-2:2001. Both Petrifilm EC/CC and Petrifilm SEC include substrates that facilitate detection of β-glucuronidase, and thus *E. coli* form blue-green colonies on these media. The plastic film in Petrifilm EC/CC and Petrifilm SEC also facilitates detection of gas production due to lactose fermentation. ISO 16649-2:2001 is also based on detection of β-glucuronidase activity. The method uses tryptone bile X-glucuronide agar (TBX), on which *E. coli* form typical blue colonies after 18-24 h at 44 °C. No further confirmation of β-glucuronidase positive colonies is required according to ISO 16649-2:2001.

Confirmation of some kind was performed by 81 % of the laboratories in the analysis of thermotolerant coliform bacteria and by 63 % in the analysis of *E. coli*. Confirmation of *E. coli* was less often reported by laboratories that used Petrifilm or that followed

ISO 16649-2:2001, which is reasonable since confirmation is not required by those methods. No obvious difference in the results could however be seen between laboratories that performed a confirmation and those that did not. It should here be mentioned that NMKL 125 is currently being revised, and the new version will likely be more similar to ISO 16649-2. Among other things, changing the confirmation by replacing the use of Kovac's reagent is considered.

Among the less frequently used methods were ISO 7251 and NMKL 96 (different editions). ISO 7251 is an MPN-based method for the detection of *E. coli*. 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. A few laboratories also used methods based on the detection of fluorescence (TEMPO® E. coli).

As in previous proficiency testing rounds the results for *E. coli* were somewhat lower for TBX, and higher for TSA/VRB, compared to other media. A possible explanation could be if a pre-incubation has been performed or not. For samples that are suspected to contain stressed microorganisms, ISO 16649-2:2001 prescribes a pre-incubation at 37 °C for 4 h, prior to the final incubation at 44 °C. In comparison, with NMKL 125:2005 a similar pre-incubation is routinely carried out (1-2 h on TSA at 20-25 °C). As in previous proficiency testing rounds, the differences were however small.

Results from analysis of thermotolerant coliform bacteria

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	48	48	-	-	0	-	-	45	3.751	0.163	0	1	0	46	4.168	0.187	1	1	0
TSA/VRB	24	24	-	-	0	-	-	22	3.754	0.159	0	1	0	22	4.168	0.116	1	1	0
VRB	8	8	-	-	0	-	-	8	3.682	0.089	0	0	0	8	4.135	0.165	0	0	0
EC*	6	6	-	-	0	-	-	6	3.845	0.214	0	0	0	6	4.303	0.306	0	0	0
Petrifilm EC/CC	4	4	-	-	0	-	-	3	-	-	0	0	0	4	-	-	0	0	0
Petrifilm SEC	1	1	-	-	0	-	-	1	-	-	0	0	0	1	-	-	0	0	0
Rapid'E.coli	1	1	-	-	0	-	-	1	-	-	0	0	0	1	-	-	0	0	0
Other	4	4	-	-	0	-	-	4	-	-	0	0	0	4	-	-	0	0	0

* *E. coli* broth (EC) was mostly reported by laboratories that used MPN-based methods, where EC is normally used after a first enrichment in LSB.

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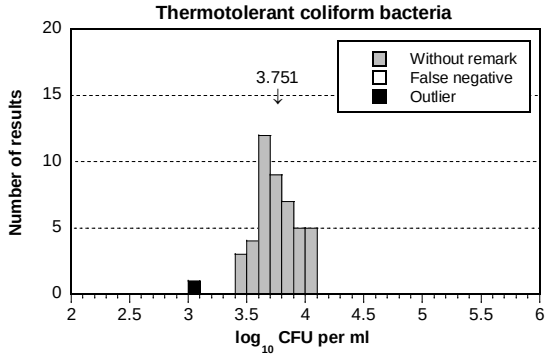

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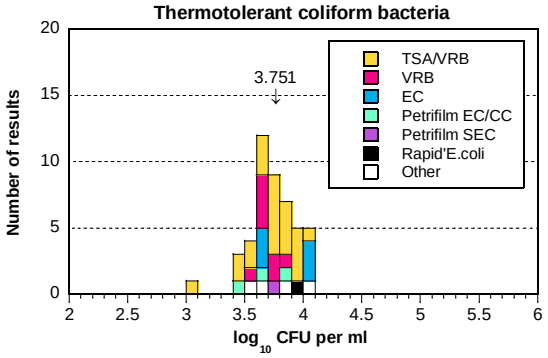

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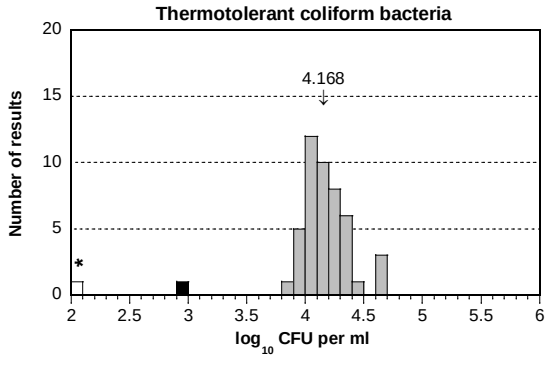

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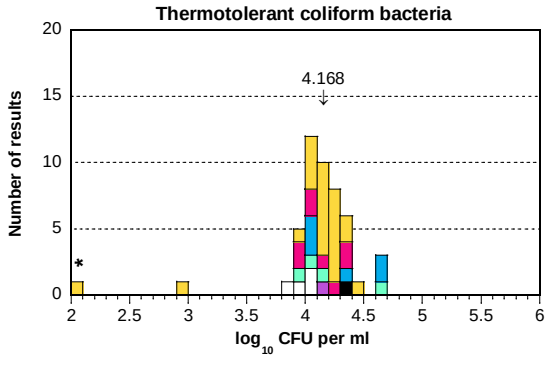

Results from analysis of Escherichia coli

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	119	119	-	-	0	-	-	115	-	-	4	-	-	109	4.065	0.221	2	3	1
Petrifilm EC/CC	27	27	-	-	0	-	-	26	-	-	1	-	-	26	4.082	0.190	1	0	0
TSA/VRB	26	26	-	-	0	-	-	26	-	-	0	-	-	26	4.095	0.176	0	0	0
Petrifilm SEC	22	22	-	-	0	-	-	21	-	-	1	-	-	19	4.036	0.157	1	1	1
TBX	12	12	-	-	0	-	-	12	-	-	0	-	-	11	3.879	0.227	0	0	0
VRB	10	10	-	-	0	-	-	9	-	-	1	-	-	9	4.001	0.300	0	1	0
TEMPO EC	4	4	-	-	0	-	-	4	-	-	0	-	-	4	-	-	0	0	0
Brilliance EC/CC	3	3	-	-	0	-	-	3	-	-	0	-	-	2	-	-	0	0	0
Compact Dry EC	1	1	-	-	0	-	-	1	-	-	0	-	-	1	-	-	0	0	0
Rapid'E.coli 2	1	1	-	-	0	-	-	1	-	-	0	-	-	1	-	-	0	0	0
Other	13	13	-	-	0	-	-	12	-	-	1	-	-	10	4.168	0.309	0	1	0

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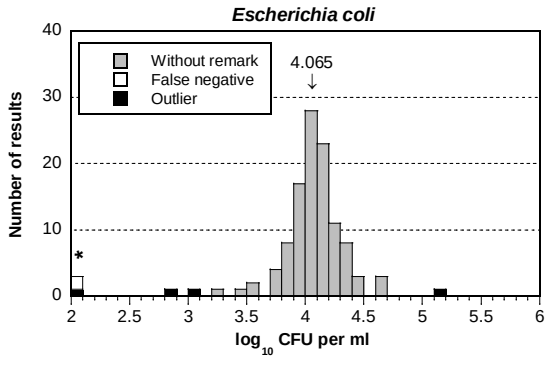

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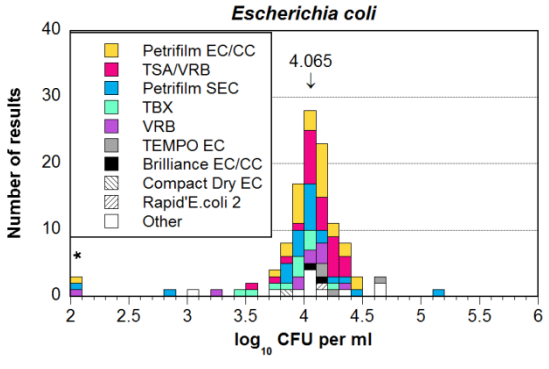


Presumptive *Bacillus cereus*

Sample A
The strain of *B. cereus* was target organism. In the homogeneity analysis at the National Food Agency, the strain formed typical grey colonies surrounded by a zone of haemolysis on blood agar (BA). On the same medium, two other types of colonies were observed. Both were atypical shiny colonies, without a zone of haemolysis. Further, only the colonies of *B. cereus* formed typical blue colonies with a zone of precipitation upon confirmation on *Bacillus cereus* selective agar (BcsA).

Three low and two high outliers were reported, as well as one false negative result.

Sample B
No target organism was present in the sample. One false positive result was reported.

Sample C
No target organism was present in the sample. Two false positive results were reported. Possibly, these may be due to detection of *S. marcescens* or *S. aureus*, which may sometimes grow on BcsA. At the National Food Agency, small atypical colonies were observed on BA. Upon confirmation, they formed atypical colonies without blue colour on BcsA.

General remarks
As in previous proficiency testing rounds most laboratories followed either NMKL 67:2010 (57 %) or ISO 7932:2004 (20 %). NMKL 67:2010 is based on incubation on BA. On this medium *B. cereus* forms large irregular grey colonies, surrounded by a distinct zone of haemolysis. Colonies are confirmed either on BcsA or on Cereus-Ident agar (a chromogenic medium). On BcsA presumptive *B. cereus* form bluish colonies that are surrounded by a zone of precipitation, due to lecithinase activity on egg yolk present in the medium. On Cereus-Ident agar, presumptive *B. cereus* are blue/turqoise and possibly surrounded by a blue ring. The colour is a result of *B. cereus* phosphatidylinositol phospholipase C (PI-PLC) cleavage of the chromogenic substrate X-myoinositol-1-phosphate present in Cereus-Ident agar. In comparison, ISO 7932:2004 prescribes plating onto mannitol egg yolk polymyxin agar (MYP), followed by confirmation on BA. 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. The ISO method uses haemolysis on BA as the method for confirmation.

In addition to BA, BcsA and MYP, Oxoid Brilliance™ Bacillus cereus agar (CBC) was used by a group of eight laboratories. CBC is a chromogenic medium, and cleavage of X-Gluc present in CBC by *B. cereus* β-glucuronidase results in white colonies with a blue/green centre. Two laboratories reported using BACARA®, which is another chromogenic medium used for detecting *B. cereus*. Another two laboratories used the fluorescence-based TEMPO® Bacillus cereus (TEMPO BC).

As in previous proficiency testing rounds the reporting of method data was in several cases unclear. For example, several laboratories reported that the same medium was used in both steps in the analysis. Other laboratories reported combinations of method and media that were incompatible. As a general rule, the tables and figures below are based on the methods/media stated by the laboratories, regardless if these are compatible or not. Laboratories that have only stated “chromogenic medium” are

included in the group “Other”. Despite these uncertainties the results and mean values for the different methods and media are very similar.

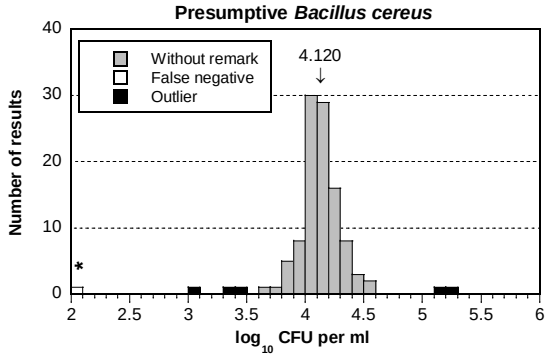
Confirmation was carried out by 59 % of the laboratories. No obvious difference in the results could be seen between laboratories that confirmed and those that did not.

Results from analysis of presumptive B. cereus

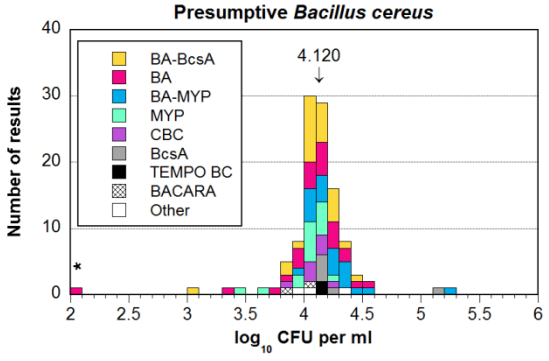
Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	109	103	4.120	0.156	1	3	2	108	-	-	1	-	-	107	-	-	2	-	-
BA-BcsA*	27	26	4.122	0.139	0	1	0	27	-	-	0	-	-	27	-	-	0	-	-
BA	24	22	4.125	0.183	1	1	0	23	-	-	0	-	-	22	-	-	1	-	-
BA-MYP	21	20	4.190	0.169	0	0	1	19	-	-	1	-	-	19	-	-	1	-	-
MYP	16	15	4.047	0.145	0	1	0	16	-	-	0	-	-	16	-	-	0	-	-
CBC	8	8	4.069	0.111	0	0	0	8	-	-	0	-	-	8	-	-	0	-	-
BcsA	6	5	4.165	0.073	0	0	1	7	-	-	0	-	-	7	-	-	0	-	-
TEMPO BC	2	2	-	-	0	0	0	2	-	-	0	-	-	2	-	-	0	-	-
BACARA	2	2	-	-	0	0	0	2	-	-	0	-	-	2	-	-	0	-	-
Other	3	3	-	-	0	0	0	4	-	-	0	-	-	4	-	-	0	-	-

* Use of PEMBA has been interpreted as BcsA and is therefore included in this group.

A



A



Coagulase-positive staphylococci

Sample A
No target organism was present in the sample. Thirteen false positive results were reported, most likely due to the detection of *S. xylosus* that was present in the sample. The strain can form colonies on for example Baird-Parker agar (BP) with characteristic grey, but coagulase-negative, colonies.

Sample B
No target organism was present. Three false positive results were reported.

Sample C
The strain of *S. aureus* was target organism. At the National Food Agency, this formed typical grey colonies with a precipitation zone on BP with rabbit plasma fibrinogen (RPFA). Two low and three high outliers were reported, as well as four false negative results.

General remarks
Similar to previous proficiency testing rounds most laboratories (45 %) followed NMKL 66:2009. Other commonly used methods were ISO 6888-1:1999 (13 %), ISO 6888-2:1999 (11 %) and 3M™ Petrifilm™ Staph Express (14 %). Both ISO 6888-1:1999 (based on BP) and ISO 6888-2:1999 (based on RPFA) were last reviewed by ISO in 2015 and remain current. An alternative confirmation by stab-culture in RPFA has however been added for ISO 6888-1 (ISO 6888-1:1999/Amd 2:2018).

NMKL 66:2009 prescribes incubation on BP and/or RPFA. On BP, *S. aureus* forms characteristic convex, shiny colonies that have a grey/black colour due to reduction of tellurite in the medium. Proteolysis of egg yolk in the medium (due to lecithinase activity) normally causes a clear zone around the colonies. An opaque halo may also form near the colony, due to precipitation caused by lipase activity. The colonies are confirmed by a positive result in a coagulase test. When using RPFA, the coagulase activity is instead tested directly in the medium, and no further confirmation is required. In comparison, ISO 6888-1:1999 stipulates surface spreading on BP followed by confirmation with a coagulase test, whereas 6888-2:1999 stipulates the use of RPFA. 3M™ Petrifilm™ Staph Express (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.

As a whole, the results were very similar for the most commonly used media BP, RPFA and Petrifilm Staph, in all of the samples. At the same time, the reported concentrations were somewhat lower for Petrifilm Staph in all three samples. Similar lower results have however been seen for Petrifilm Staph in several previous proficiency testing rounds (latest April 2018), and could in that sense be regarded as normal.

Several media were used only by a small number of laboratories, which makes them difficult to evaluate. As an example, both laboratories that used Compact Dry X-SA failed the analysis of sample A. The method is validated for enumeration of *S. aureus* against the reference method ISO 6888-1:1999 (NordVal 042).

Traditionally, coagulase-positive staphylococci are confirmed by detection of extracellular or bound coagulase (tube coagulase test and slide coagulase test respectively). Another common confirmation is a latex agglutination test. This is based

on latex particles coated either with fibrinogen or with IgG that binds to protein A on the bacterial cell surface. Antibodies targeted against polysaccharides on the bacterial cell surface are also used in variations of this test. With Petrifilm Staph, confirmation is instead often carried out with 3M™ Petrifilm™ Staph Express Disk (Petrifilm Disk). This test detects 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.

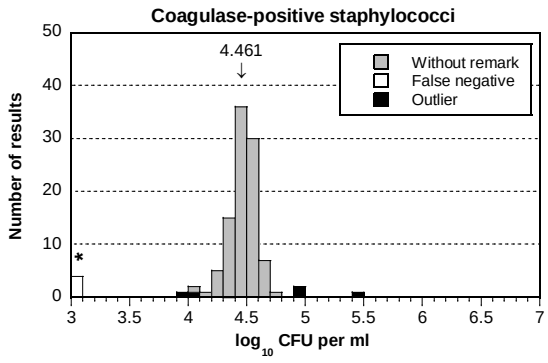
Confirmation of some kind was carried out by 73 % of the laboratories as a whole, and by 95 % of the laboratories that incubated on BP. The most common method for the confirmation was a tube coagulase test, followed by latex agglutination test and Petrifilm Disk. No clear difference could however be seen between laboratories that confirmed and those that did not.

Results from analysis of coagulase-positive staphylococci

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	105	92	-	-	13	-	-	102	-	-	3	-	-	96	4.461	0.114	4	2	3
BP	56	49	-	-	7	-	-	54	-	-	2	-	-	50	4.467	0.109	2	2	2
RPFA	20	20	-	-	0	-	-	20	-	-	0	-	-	20	4.467	0.074	0	0	0
Petrifilm Staph	17	14	-	-	3	-	-	16	-	-	1	-	-	15	4.381	0.129	1	0	1
Brilliance Staph 24	2	2	-	-	0	-	-	2	-	-	0	-	-	2	-	-	0	0	0
EASY Staph	2	2	-	-	0	-	-	2	-	-	0	-	-	2	-	-	0	0	0
MSA*	2	2	-	-	0	-	-	2	-	-	0	-	-	1	-	-	1	0	0
Compact Dry X-SA	2	0	-	-	2	-	-	2	-	-	0	-	-	2	-	-	0	0	0
TEMPO STA	2	1	-	-	1	-	-	2	-	-	0	-	-	2	-	-	0	0	0
RAPID'Staph**	1	1	-	-	0	-	-	1	-	-	0	-	-	1	-	-	0	0	0
Other	1	1	-	-	0	-	-	1	-	-	0	-	-	1	-	-	0	0	0

* MSA: Mannitol salt agar
** RAPID'Staph (BIO-RAD)

C



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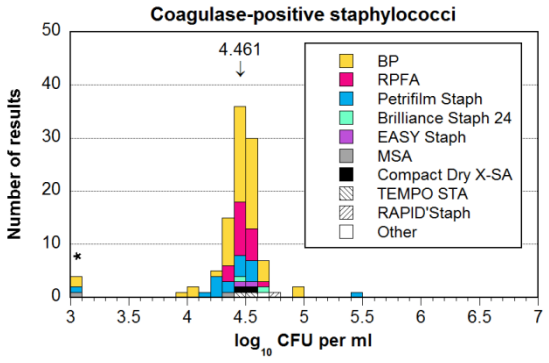


Enterococci

Sample A
No target organism was present in the sample. Twenty-one false positive results were reported, likely due to detection of *P. acidilactici* in the sample. The strain forms atypical, faint pink colonies on Slanetz & Bartley *Enterococcus*-agar (ENT). In subsequent confirmation on bile esculin agar (BEA) these normally do not cause any blackening of the medium after 2 hours, but a faint blackening may be seen after 24 hours. Since the various methods have different incubation times on BEA, and since the interpretation of blackening can differ, positive results are also considered correct. The analysis is therefore not evaluated and no z-scores have been calculated. The results are also not included in the tables under the box plots.

In a previous proficiency testing round (October 2003), the same strain of *P. acidilactici* was distinguished since, in contrast to *Enterococcus*, it does not grow in brain heart infusion broth (BHI) with 6.5 % salt or in BHI with pH 9.6. Confirmation with growth in BHI is included in the older NMKL 68:2004.

Sample B
The strain of *E. hirae* was target organism. One low and two high outliers were reported.

Sample C
The strain of *E. durans* was target organisms. Three low and two high outliers were reported, as well as one false negative result.

General remarks
A clear majority of the laboratories (70 %) reported following NMKL 68:2011. Less frequently used methods were IDF 149A:1997 (6 %), the older NMKL 68:2004 (3 %) and the water method ISO 7899-2:2000 (3 %). Most of the remaining laboratories used company-specific methods. It should be mentioned that according to ISO, IDF 149A:1997 has been replaced by ISO 27205:2010/IDF 149:2010.

With NMKL 68:2011, enterococci are defined as Gram-positive, coagulase negative and oval cocci that hydrolyse esculin at 44 °C. Incubation is done on Slanetz & Bartley Enterococcus-agar (ENT) at 44 °C. On ENT, enterococci 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. When stressed enterococci are suspected (e.g. in frozen foods) a pre-incubation in TSA for 2 hours at 37 °C is recommended, followed by overlay with ENT. Dark red colonies with typical morphology are counted as enterococci without further confirmation. Non-typical colonies are confirmed by sub-culturing on bile esculin agar (BEA). On BEA the substrate esculin is hydrolysed by β-glucosidase present in enterococci, which results in the formation of esculetin and glucose. Esculetin together with iron ions present in the medium then form a black precipitate. Colonies that cause a blackening of the medium after 2-24 hours are counted as enterococci. The drinking water method ISO 7899-2:2000 is based on membrane filtration followed by incubation on ENT at 37 °C. Confirmation is, as in the NMKL method, by sub-culture on BEA (possibly with the addition of azide), but incubation is only for 2 hours. With the older NMKL 68:2004 confirmation is not done with BEA, but with a catalase test, as well as tests for the growth in BHI with 6.5 % salt and in BHI with pH 9.6. Despite this, both laboratories that analysed according to NMKL 68:2004 reported false positive results for sample A.

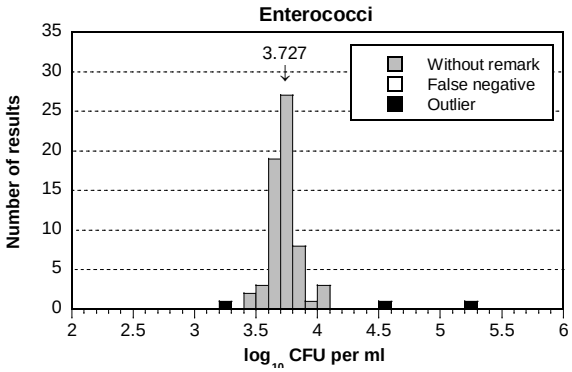
In total, 86 % of the laboratories incubated either on ENT or on TSA/ENT. In addition to these media, a smaller number of laboratories used kanamycin esculin azide agar (KEAA) or COMPASS® Enterococcus Agar (COMPASS). Another laboratory used Compact Dry ETC. KEAA was used by laboratories that followed IDF 149A:1997. With KEAA, the esculin hydrolysis is tested directly in the medium. Similar to BEA, COMPASS detects β-glucosidase activity, but is instead based on the substrate X-Gluc. Enterococci therefore form blue colonies on this medium. No clear difference in the results could be seen between the different media that were used.

Confirmation of some kind was performed by 76 % of the laboratories. Performing or not performing a confirmation does not appear to have had an effect on the outcome as a whole. Of the 21 laboratories that reported a false positive result for sample A, 14 stated that they performed a confirmation test.

Results from analysis of enterococci.

Medium	N	Sample A						Sample B						Sample C					
		n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
All results	66	45	-	-	21	-	-	63	3.727	0.116	0	1	2	61	4.065	0.096	1	3	2
ENT	48	31	-	-	17	-	-	46	3.729	0.123	0	0	1	44	4.073	0.107	0	2	2
TSA/ENT	9	5	-	-	4	-	-	9	3.691	0.041	0	0	0	9	4.021	0.064	0	0	0
KEAA	3	3	-	-	0	-	-	3	-	-	0	0	0	3	-	-	0	0	0
COMPASS	2	2	-	-	0	-	-	2	-	-	0	1	0	3	-	-	0	0	0
Compact Dry ETC	1	1	-	-	0	-	-	1	-	-	0	0	0	1	-	-	0	0	0
Other	3	3	-	-	0	-	-	2	-	-	0	0	1	1	-	-	1	1	0

B



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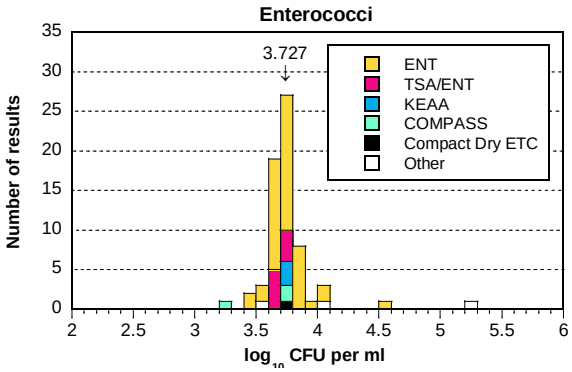

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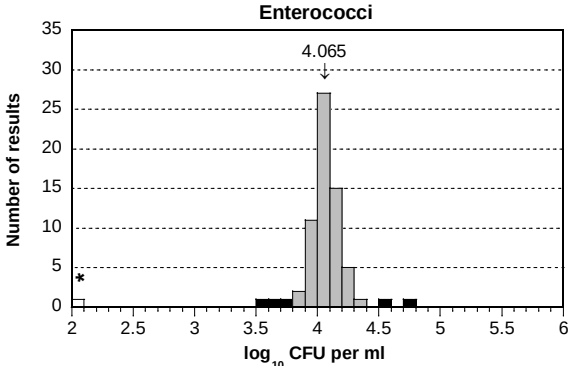
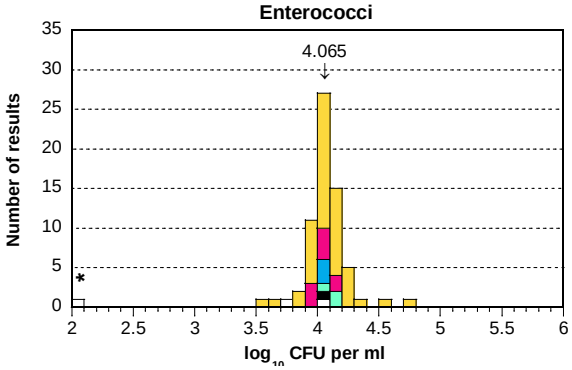


C



Gram-negative bacteria in pasteurized dairy products

Sample A
No Gram-negative bacteria were present in the sample. All laboratories reported a correct negative result.

Sample B
The strain of *K. pneumoniae* was target organism. All laboratories reported a correct positive result.

Sample C
The strains of *E. coli* and *S. marcescens* were target organisms. All laboratories reported a correct positive result.

General remarks
The analysis was without problem for the laboratories. All eleven laboratories stated the use of violet red bile glucose agar (VRBG). Nine laboratories followed NMKL 192:2011. The remaining two laboratories followed a company-specific method.

NMKL 192:2011 is a qualitative method for detecting recontamination of Gram-negative bacteria in pasteurised milk and cream. Gram-negative 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 which may limit the shelf-life of the product. With the method, the unopened package of milk/cream is incubated at 25 °C for 24 hours, followed by plating of 10 µl onto VRBG. As an alternative, 100 µl can be plated after incubation at room temperature for 28 hours. No matter which incubation that is used, presence of five or more colonies on VRBG is considered a positive result, regardless of colony morphology and colour. When needed, confirmation can be done with potassium hydroxide (KOH). Colonies that form a viscous string after 5-10 seconds of stirring in KOH are considered as Gram-negative.

Results from analysis of Gram-negative bacteria in dairy products

Method	N	Sample A		Sample B		Sample C	
		n	F	n	F	n	F
All results	11	11	0	11	0	11	0
NMKL 192:2011	9	9	0	9	0	9	0
Other	2	2	0	2	0	2	0

Outcome of the results of individual laboratory - assessment

Reporting and evaluation of results

The reported results of all participating laboratories are listed in Annex 1, together with the minimum and maximum accepted values for each analysis. Results that received a remark (false results and outliers) are highlighted in yellow, with bold font.

It is the responsibility of the participating laboratories to correctly report results according to the instructions. When laboratories incorrectly report their results, for example by stating “pos” or “neg” for quantitative analyses, the results cannot be correctly processed. Such incorrectly reported results are normally excluded. Inclusion and further processing of such results may still be done, after manual assessment in each individual case.

Z-scores (see below) for individual analyses are shown in Annex 2 and can be used as a tool by laboratories when following up on the results.

The laboratories are not grouped or ranked based on their results. The performance of a laboratory as a whole can only be evaluated from the number of false results and outliers that are listed in Annex 1 and below the box plots.

Information on the results processing and recommendations for follow-up work are given in the Scheme Protocol [2]. Samples for follow-up can be ordered, free of charge via our website: www.livsmedelsverket.se/en/PT-extra

Z-scores, box plots and deviating results

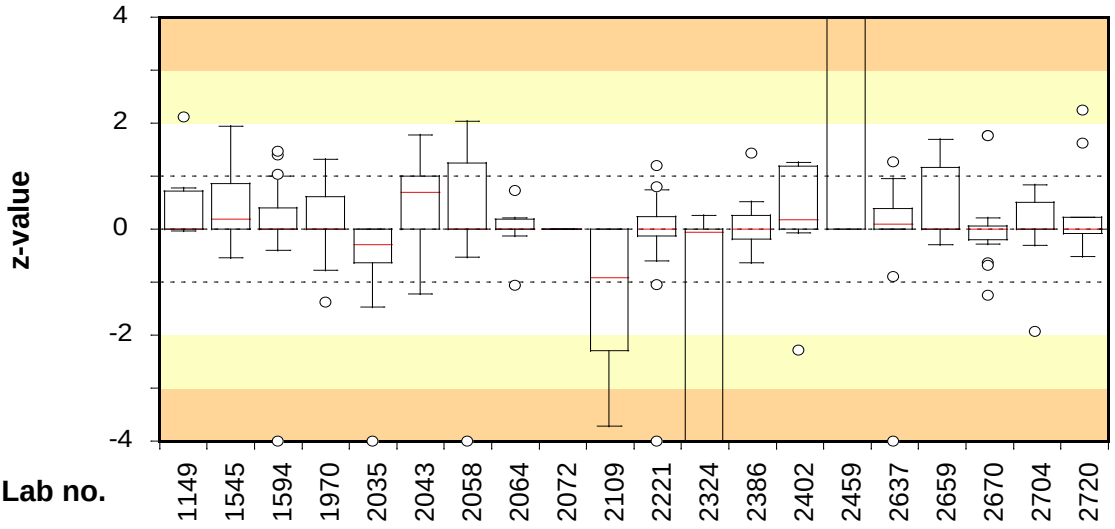
In order to allow comparison of the results from different analyses and samples, all results are transformed into standard values (z-scores). For quantitative analyses, a z-score is either positive or negative, depending on whether the individual result is higher or lower than the mean value calculated from all laboratory results for each analysis.

The box plots are based on the z-scores listed in Annex 2, and give a comprehensive view of the achievement of each laboratory. The range of z-scores is indicated by the size of the box and, for most laboratories, by lines and/or circles above and beneath the box. A small box, centred around zero, indicates the results of that individual laboratory, with false results excluded, are close to the general mean values calculated for all laboratory results. For each laboratory, the number of false results and outliers are also listed in the tables below the box plots.

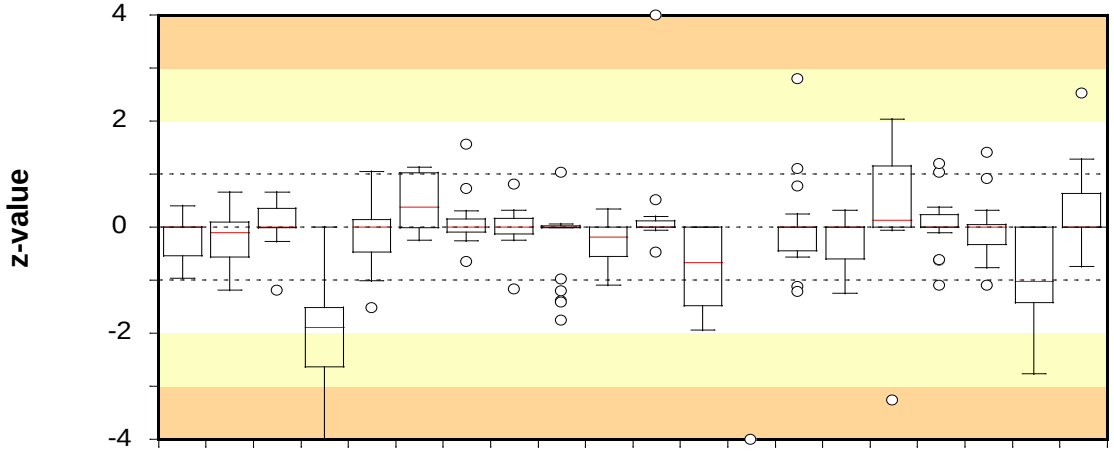
Box plots and numbers of deviating results for each laboratory

- *Z-scores are calculated according to the formula: z = (x-m)/s, where x is the result of the individual laboratory, m is the mean of the results of all participating laboratories, and s is the standard deviation of the participating laboratories, after removing outliers and false results.*
- *Outliers are included in the figures after being calculated to z-scores in the same way as for other results.*
- *False results do not generate any z-scores, and are not included in "No. of results".*
- *Correct results for qualitative analyses and correct negative results for quantitative analyses without target organism generate a z-score of 0.*
- *The laboratory median value is illustrated by a horizontal red line in the box.*
- *The box includes 50 % of a laboratory'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.*

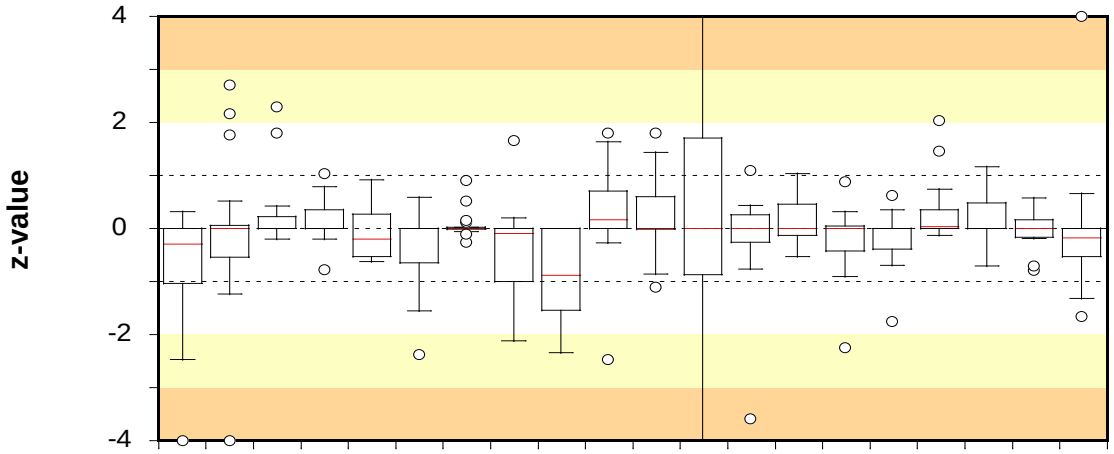
* *< [lowest value in the box −1,5 × (highest value in the box− lowest value in the box)]* or *> [highest value in the box + 1,5 × (highest value in the box − lowest value in the box)].*



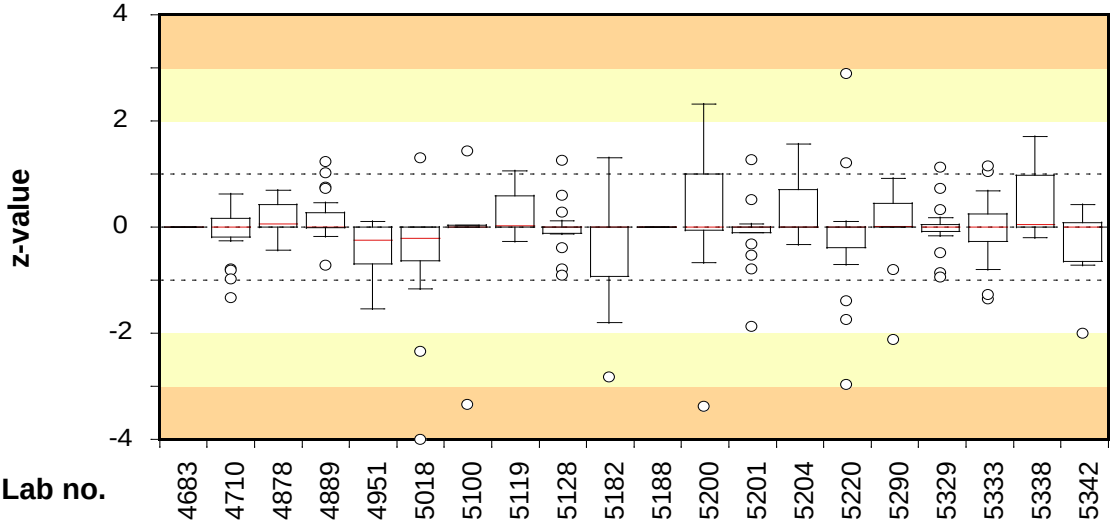
	1149	1545	1594	1970	2035	2043	2058	2064	2072	2109	2221	2324	2386	2402	2459	2637	2659	2670	2704	2720
No. of results	15	20	29	29	9	6	9	9	-	8	26	15	12	12	17	20	18	15	18	9
False positive	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	-	1	-	1	-	-	1	-	-	-	-	-
Low outliers	-	-	1	-	1	-	1	-	-	-	1	6	-	-	-	1	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9	-	-	-	-	-



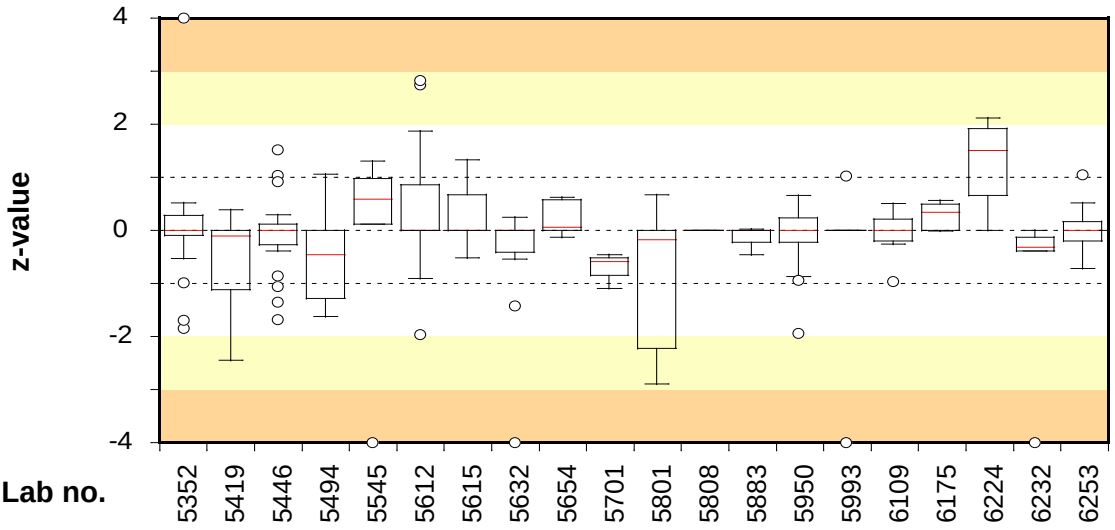
Lab no.	2745	2757	2764	2794	2941	3031	3055	3155	3159	3243	3305	3327	3452	3457	3533	3543	3587	3626	3831	3864
No. of results	18	12	14	6	20	8	12	8	21	6	18	12	5	20	15	14	23	26	9	9
False positive	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Low outliers	-	-	-	1	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	2	-	4	-	-	-	-	-	-	-



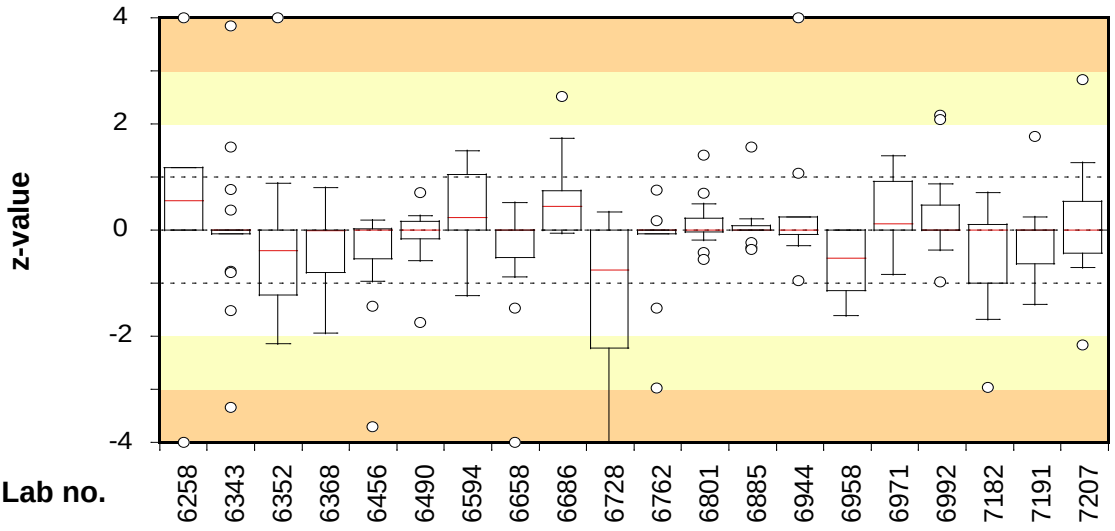
Lab no.	3878	3923	4047	4050	4064	4100	4171	4246	4278	4288	4339	4352	4400	4449	4557	4560	4562	4633	4635	4664
No. of results	12	27	15	15	6	20	18	18	8	23	29	24	11	9	16	9	20	19	14	16
False positive	-	2	-	-	-	-	-	-	-	-	-	2	1	-	-	-	-	1	-	-
False negative	-	-	-	-	-	-	-	-	1	-	-	3	-	-	-	-	-	-	-	1
Low outliers	1	1	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	1



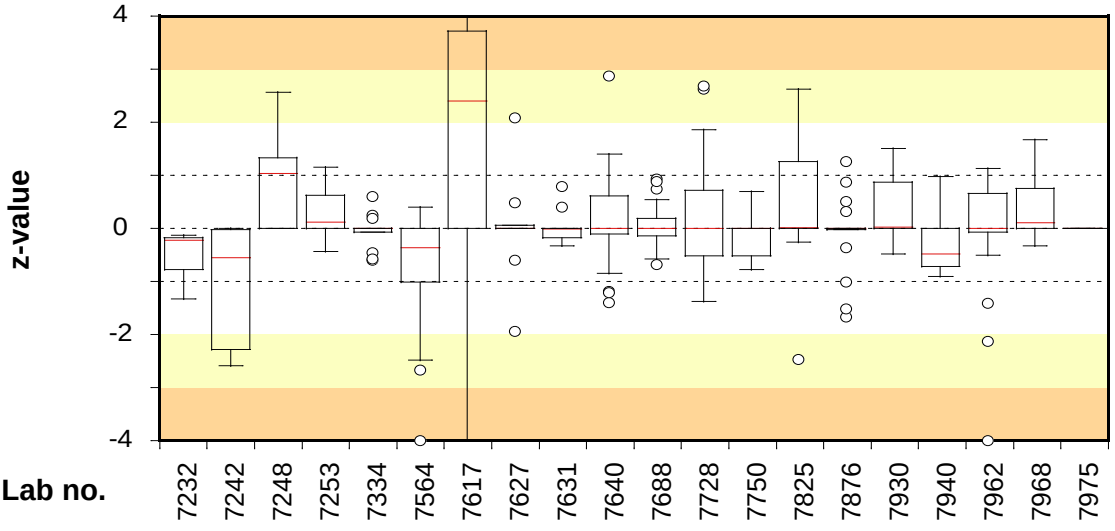
Lab no.	4683	4710	4878	4889	4951	5018	5100	5119	5128	5182	5188	5200	5201	5204	5220	5290	5329	5333	5338	5342
No. of results	-	21	9	23	11	26	6	12	18	11	-	24	17	26	15	20	17	26	6	11
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1
False negative	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
Low outliers	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



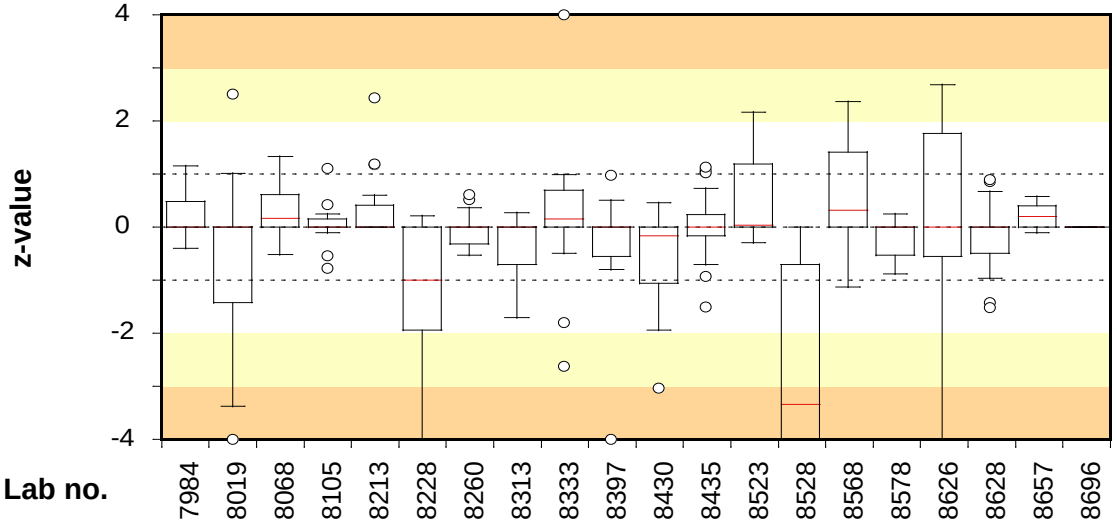
Lab no.	5352	5419	5446	5494	5545	5612	5615	5632	5654	5701	5801	5808	5883	5950	5993	6109	6175	6224	6232	6253
No. of results	23	20	21	9	6	21	18	12	9	3	12	-	15	35	5	9	6	8	6	20
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	-	-
False negative	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Low outliers	-	-	-	-	1	-	-	1	-	-	-	-	-	-	1	-	-	-	1	-
High outliers	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



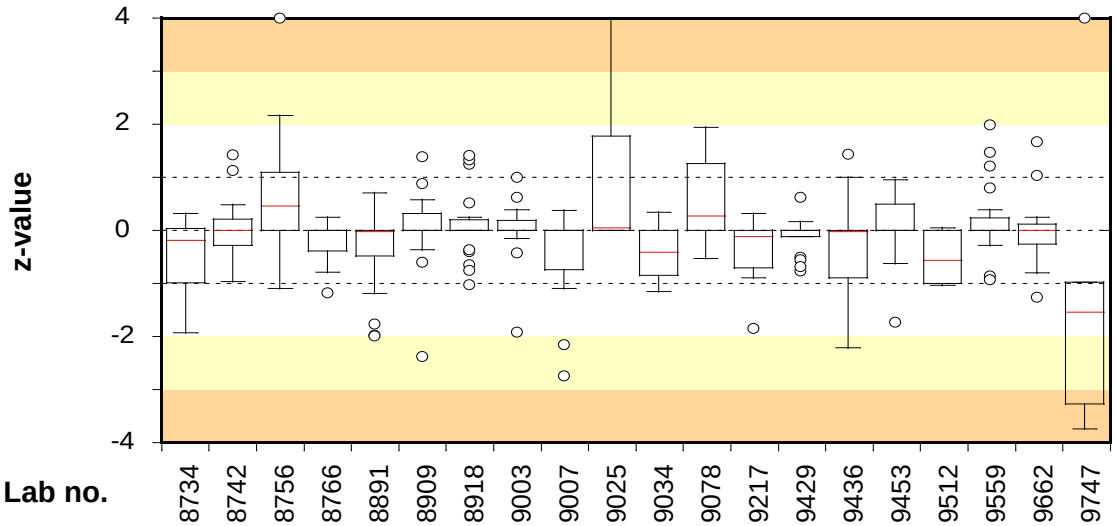
Lab no.	6258	6343	6352	6368	6456	6490	6594	6658	6686	6728	6762	6801	6885	6944	6958	6971	6992	7182	7191	7207
No. of results	6	18	18	26	23	14	12	12	18	13	9	14	20	9	9	9	15	21	14	11
False positive	-	-	2	-	-	-	-	-	1	1	-	1	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-
Low outliers	1	-	-	-	1	-	-	1	-	3	-	-	-	-	-	-	-	-	-	-
High outliers	1	1	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-



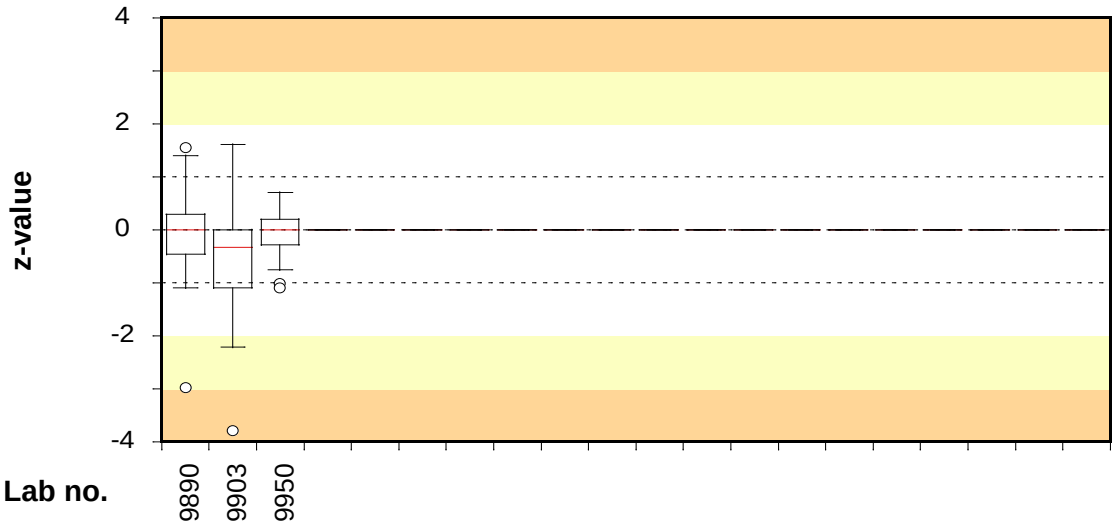
Lab no.	7232	7242	7248	7253	7334	7564	7617	7627	7631	7640	7688	7728	7750	7825	7876	7930	7940	7962	7968	7975
No. of results	3	6	29	18	14	23	9	9	9	32	26	24	9	16	17	26	6	26	26	-
False positive	-	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	-	-	-	-
False negative	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-
Low outliers	-	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	1	-	-
High outliers	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-



Lab no.	7984	8019	8068	8105	8213	8228	8260	8313	8333	8397	8430	8435	8523	8528	8568	8578	8626	8628	8657	8696
No. of results	12	30	29	15	15	14	25	20	14	17	14	29	12	6	14	6	18	29	6	-
False positive	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
Low outliers	-	5	-	-	-	1	-	-	-	1	-	-	-	3	-	-	1	-	-	-
High outliers	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-



Lab no.	8734	8742	8756	8766	8891	8909	8918	9003	9007	9025	9034	9078	9217	9429	9436	9453	9512	9559	9662	9747
No. of results	12	15	14	17	21	20	21	15	15	9	12	6	14	17	26	17	6	27	23	6
False positive	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
High outliers	-	-	2	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1



No. of results	21	17	15
False positive	-	-	-
False negative	-	-	-
Low outliers	-	1	-
High outliers	-	-	-

Test material and quality control

Test material

Each laboratory received three manufactured freeze-dried microbial samples, designated A-C. The test material was freeze-dried in portions of 0.5 ml in vials, as described by Peterz and Steneryd [3]. Before analysing the samples, the contents of each vial had to be dissolved in 254 ml of sterile diluent. The organisms present in the sample mixtures are listed in Table 2.

Table 2. *Microorganisms present in samples A-C.*

Sample[1]	Microorganism	Strain	
		SLV no.[2]	Reference[3]
A	*Bacillus cereus*	SLV-518	CCUG 44741
	Pediococcus acidilactici	SLV-213	CCUG 45146
	Staphylococcus xylosus	SLV-283	Cheese, 1989
B	*Enterococcus hirae*	SLV-536	CCUG 46536
	Kocuria rhizophila	SLV-055	CCUG 35073
	Klebsiella pneumoniae	SLV-186	CCUG 45102
C	*Enterococcus durans*	SLV-078	CCUG 44816
	Escherichia coli	SLV-477	CCUG 43601
	Serratia marcescens	SLV-040	ATCC 13 880
	Staphylococcus aureus	SLV-280	Egg, 1989

[1] The links between the samples and the randomised sample numbers are shown in Annex 1.
[2] Internal strain identification no. at the National Food Agency.
[3] Origin or culture collection (CCUG: Culture Collection University of Gothenburg, Sweden ; ATCC: American Type Culture Collection)

Quality control of the samples

In order to allow comparison of the freeze-dried samples, it is essential to have equal volumes of a homogeneous sample mixture in all vials. Quality control is therefore performed on 10 randomly chosen vials in conjunction with the manufacture, 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 sample mixture is approved if, for each analysis, the values obtained for the test of reproducibility (T) and the test "Index of dispersion" between vials (I_2) do not simultaneously exceed 2.6 and 2.0, respectively. (For definitions of T and I_2, see references [4] and [5] respectively.)

Table 3. *Concentration mean (m), T and I_2 values from the quality control of the samples; m is expressed in log_{10} cfu (colony forming units) per ml of sample.*

Analysis and method	A[1]			B[1]			C[2]		
	m	T	I_2	m	T	I_2	m	T	I_2
Aerobic microorganisms, 30 °C NMKL method no. 86:2013	5.382	1.37	2.803	4.186	1.16	0.896	4.998	1.32	1.821
Aerobic microorganisms, 20 °C NMKL method no. 86:2013	5.317	1.08	0.153	4.147	1.23	1.565	4.980	1.20	0.830
Contaminating microorganisms ISO method no. 13559:2002 IDF method no. 153:2002	5.363	1.41	3.599	4.279	1.52	0.825	5.011	1.20	0.842
Enterobacteriaceae NMKL method no. 144:2005	-	-	-	3.744	1.73	4.581	4.693	1.39	1.372
Coliform bacteria 30, °C NMKL method no. 44:2007	-	-	-	3.645	1.48	1.584	4.011	2.03	1.333
Coliform bacteria, 37 °C NMKL method no. 44:2007	-	-	-	3.646	1.21	0.381	4.104	1.74	1.074
Thermotolerant coliform bacteria NMKL method no. 125:2005	-	-	-	3.737	1.36	1.310	4.127	1.45	4.214
Escherichia coli NMKL method no. 125:2005	-	-	-	-	-	-	4.127	1.45	4.214
Presumptive *Bacillus cereus* NMKL method no. 67:2010	4.235	1.71	1.535	-	-	-	-	-	-
Coagulase-positive staphylococci NMKL method no. 66:2009	-	-	-	-	-	-	4.541	1.44	1.179
Enterococci NMKL method no. 68:2011	-	-	-	3.771	1.29	0.972	4.073	1.32	1.170
Gram-negative bacteria in pasteurized milk and cream. Detection of recontamination. NMKL method no. 192:2011	Neg.	-	-	Pos.	-	-	Pos.	-	-

– No target organism and therefore no value
[1] n = 5 vials analysed in duplicate
[2] n = 10 vials analysed in duplicate

References

1. Kelly, K. 1990. Outlier detection in collaborative studies. J. Assoc. Off. Anal. Chem. 73:58-64.
2. Anonymous, 2015. Protocol, Microbiology. Drinking Water & Food, The National Food Agency, Sweden.
3. Peterz, M., Steneryd. A.C. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. J. Appl. Bacteriol. 74:143-148.
4. Mooijman, K.M., During, M. & Nagelkerke, N.J.D. 2003. MICROCRM: Preparation and control of batches of microbiological materials consisting of capsules. RIVM report 250935001/2003. RIVM, Bilthoven, Holland.
5. Heisterkamp, S.H., Hoekstra, J.A., van Strijp-Lockefeer, N.G.W.M., Havelaar, A.H., Mooijman, K.A., in't Veld, P.H., Notermans, S.H.W., Maier, E.A. ; Griepink, B. 1993. Statistical analysis of certification trials for microbiological reference materials. Luxembourg: Commission of the European Communities, Report EUR 15008 EN.

Annex 1 Results of the participating laboratories - October 2018

All results are in log_{10} cfu per ml sample. Results reported as "< value" have been regarded as zero. Results reported as "> value" are exluded from the calculations. A dash indicates the analysis was not performed. Outliers and false results are highlighted and summarized for each analysis at the end of the table.

Lab no.	Vial	Aerobic microorg. 30 °C			Aerobic microorg. 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
1149	1 2 3	5.29	4.29	5.21	-	-	-	-	-	-	<1	3.69	4.64	-	-	-	<1	3.85	4.23	-	-	-	<1	<1	4.23	-	-	-	<1	<1	4.54	-	-	-	-	-	-	1149
1545	2 1 3	5.46	4.37	5.07	-	-	-	-	-	-	<1	3.95	4.63	-	-	-	-	-	-	<1	3.87	4.24	<2	<2	4.24	4.39	<2	<2	<2	<2	4.4	<1	3.68	4.13	-	-	-	1545
1594	1 2 3	5.26	4.3	4.98	5.23	4.3	4.94	-	-	-	0	3.73	4.72	0	3.74	4.54	0	3.78	4.68	0	3.82	4.15	0	0	4.15	**3.08**	0	0	0	0	4.43	0	3.68	4.11	-	-	-	1594
1970	1 2 3	5.14	4.32	4.91	5.07	4.25	4.89	-	-	-	<1	3.74	4.48	<1	3.79	4.43	<1	3.93	4.42	<1	3.76	4.26	<1	<1	4.26	4.09	<2	<2	<2	<2	4.59	<1	3.88	4.04	-	-	-	1970
2035	2 1 3	-	-	-	-	-	-	-	-	-	<1	3.5	**3.8**	<1	3.6	4	-	-	-	-	-	-	<1	<1	4	-	-	-	-	-	-	-	-	-	-	-	-	2035
2043	1 2 3	5.54	4.25	5.08	-	-	-	-	-	-	-	-	-	-	-	-	0	3.47	4.53	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2043
2058	3 1 2	5.18	4.34	5.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.46	**3.3**	0	0	-	-	-	-	-	-	-	-	-	2058
2064	1 2 3	5.27	4.23	4.84	-	-	-	-	-	-	0	3.79	4.52	-	-	-	-	-	-	-	-	-	-	-	-	4.15	0	0	-	-	-	-	-	-	-	-	-	2064
2072	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2072
2109	2 3 1	4.91	3.81	4.69	-	-	-	-	-	-	-	-	-	-	-	-	<1	**<1**	4.15	-	-	-	<1	<1	3.72	-	-	-	-	-	-	-	-	-	-	-	-	2109
2221	2 3 1	5.3	4.2	4.97	-	-	-	**3.65**	3.77	4.74	<1	3.67	4.67	<1	3.73	4.11	<1	3.68	4.21	-	-	-	<2	<2	4	4.16	<2	<2	<2	<2	4.51	<1	3.82	4.18	-	-	-	2221
2324	2 1 3	**4.28**	**2.98**	**3.73**	-	-	-	-	-	-	0	**2.57**	**2.48**	-	-	-	-	-	-	-	-	-	0	0	**3.01**	4	0	0	**3.25**	0	**0**	0	3.72	4.09	-	-	-	2324
2386	2 3 1	5.33	4.2	5.13	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.72	4.04	<1	3.66	4.11	-	-	-	-	-	-	<2	<2	4.52	-	-	-	-	-	-	2386
2402	1 2 3	5.41	4.2	5.11	-	-	-	-	-	-	<1	3.86	4.15	-	-	-	<1	3.92	4.34	-	-	-	<1	<1	4.34	-	-	-	-	-	-	-	-	-	-	-	-	2402
2459	2 1 3	**6.34**	**5.08**	**6.01**	-	-	-	-	-	-	0	**4.75**	**5.54**	-	-	-	0	**0**	**5.64**	-	-	-	0	0	**5.19**	**5.14**	0	0	0	0	**5.4**	-	-	-	-	-	-	2459
2637	1 3 2	5.34	4.23	4.99	-	-	-	5.23	4.08	**3.95**	<1	3.81	4.76	-	-	-	-	-	-	<1	-	4	<1	<1	4.15	4.15	<1	<1	<1	<1	4.57	-	-	-	-	-	-	2637
2659	1 3 2	5.3	4.36	5.16	-	-	-	-	-	-	-	-	-	<1	3.95	4.59	<1	3.95	4.59	-	-	-	<1	<1	4	-	-	-	<1	<1	4.5	-	-	-	Neg	Pos	Pos	2659
2670	1 3 2	5.28	4.23	4.93	-	-	-	-	-	-	-	-	-	-	-	-	<1	4.04	4.04	<1	4.04	4.04	<1	<1	4.04	-	-	-	<1	<1	4.32	-	-	-	-	-	-	2670
2704	3 1 2	5.33	4.25	5.06	-	-	-	-	-	-	<1	3.79	4.66	-	-	-	<1	3.8	4.14	-	-	-	<1	<1	4.14	3.82	<2	<2	<2	<2	4.54	-	-	-	-	-	-	2704
2720	2 1 3	5.25	4.38	4.93	-	-	-	-	-	-	<1	3.99	4.58	-	-	-	-	-	-	-	-	-	-	-	-	4.04	<1	<1	-	-	-	-	-	-	-	-	-	2720
2745	3 2 1	5.17	4.13	4.85	-	-	-	-	-	-	<1	3.63	4.61	-	-	-	-	-	-	<1	3.68	4.05	<1	<1	4.05	4.15	<2	<2	<2	<2	4.4	-	-	-	-	-	-	2745
2757	1 3 2	5.23	4.15	5.04	5.18	3.97	4.95	-	-	-	<1	3.73	4.54	<1	3.65	3.98	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2757
2764	3 2 1	5.3	4.08	5.04	-	-	-	-	-	-	<1	3.74	4.54	-	-	-	<0,60	3.69	4.34	-	-	-	-	-	-	4.2	<1	<1	-	-	-	<2	3.77	4.04	-	-	-	2764
2794	3 2 1	5.03	4.01	**4.49**	-	-	-	-	-	-	-	-	-	-	-	-	0	3.2	3.64	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2794
2941	2 1 3	5.38	4.12	4.91	-	-	-	-	-	-	0	3.63	4.59	0	3.67	4.5	-	-	-	-	-	-	0	0	4.15	4.03	0	0	0	0	4.58	0	3.61	3.92	-	-	-	2941
3031	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.89	4.46	<1	3.92	4.38	-	-	-	-	-	-	-	-	-	<1	3.72	4.04	-	-	-	3031
3055	1 3 2	5.31	4.18	4.94	-	-	-	-	-	-	<1	3.79	4.81	-	-	-	-	-	-	-	-	-	-	-	-	4.02	<1	<1	-	-	-	-	-	-	Neg	Pos	Pos	3055
3155	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.77	4.48	<1	-	3.95	<1	<1	4.01	-	-	-	-	-	-	-	-	-	-	-	-	3155
3159	2 1 3	5.11	4.21	4.97	-	-	-	-	-	-	<1	3.7	4.72	-	-	-	<1	3.71	3.81	<1	3.52	3.84	<1	<1	3.8	4.13	<1	<1	<2	<2	4.46	-	-	-	-	-	-	3159
3243	3 1 2	5.22	4.09	4.95	-	-	-	-	-	-	<1	3.62	4.6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3243
3305	2 1 3	**6.41**	**5.32**	4.97	-	-	-	-	-	-	<1	3.72	4.63	-	-	-	-	-	-	<1	3.77	4.08	<1	<1	4.08	4.11	<2	<2	<2	<2	4.46	-	-	-	-	-	-	3305
3327	1 3 2	5.06	4	4.76	-	-	-	-	-	-	0	3.49	4.39	-	-	-	-	-	-	-	-	-	0	0	3.75	-	-	-	0	0	4.41	-	-	-	-	-	-	3327
3452	2 3 1	**6.2**	**5.33**	**5.86**	-	-	-	-	-	-	-	-	-	**1.3**	**2.86**	**5.68**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3452
3457	1 3 2	-	-	-	5.37	4.07	4.89	-	-	-	<1	3.67	4.35	-	-	-	<1	3.75	4.57	<1	3.66	3.94	<2	<2	3.94	-	-	-	<2	<2	4.78	**4.13**	3.67	4.04	-	-	-	3457
3533	1 2 3	5.16	4.24	5	-	-	-	-	-	-	-	-	-	-	-	-	0	3.66	4.04	0	3.66	4.04	0	0	4.04	-	-	-	0	0	4.32	-	-	-	-	-	-	3533
3543	2 1 3	5.480	4.260	5.200	-	-	-	-	-	-	0.000	3.730	4.740	-	-	-	-	-	-	-	-	-	-	-	-	4	0.000	0.000	0	0.000	4.090	**4.170**	4	4	-	-	-	3543
3587	2 3 1	5.320	4.230	4.890	-	-	-	-	-	-	<1	3.680	4.580	<1	4	5	<1	4	5	-	-	-	<2	<2	4	4	<2	<2	<2	<2	4.500	<1	4	4	-	-	-	3587
3626	2 3 1	5.3	4.2	5	-	-	-	-	-	-	<1	3.7	4.7	<1	3.6	4.1	<1	3.6	4	<1	3.8	4.1	<1	<2	4.1	4.1	<2	<2	<2	<2	4.4	<2	3.6	4.2	-	-	-	3626
3831	1 3 2	5.04	4.04	4.64	-	-	-	-	-	-	-	-	-	-	-	-	0	3.5	4.11	-	-	-	0	0	3.84	-	-	-	-	-	-	-	-	-	-	-	-	3831
3864	2 3 1	5.15	4.48	5.11	-	-	-	-	-	-	<1	3.78	4.51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Pos	Pos	3864
3878	3 2 1	**4.3**	3.94	4.92	-	-	-	-	-	-	-	-	-	<1	3.5	4.12	<1	3.54	4.14	-	-	-	<1	<1	4.14	-	-	-	-	-	-	-	-	-	-	-	-	3878
3923	3 2 1	5.28	4.18	4.87	5.32	4.11	4.8	-	-	-	<1	**3.15**	4.56	0	4.04	4.38	0	4.04	4.04	0	3.66	4.04	0	**3.66**	4.04	4.04	<1	<1	**5.38**	<1	4.36	0	4.04	4.04	-	-	-	3923
4047	1 3 2	5.23	4.22	5.23	-	-	-	-	-	-	<1	3.75	4.6	-	-	-	-	-	-	-	-	-	<1	<1	4.04	4.4	<1	<1	<1	<1	4.45	-	-	-	-	-	-	4047
m		5.262	4.207	4.963	5.262	4.121	4.929	5.125	4.004	4.864	0	3.694	4.541	0	3.693	4.209	0	3.703	4.232	0	3.751	4.168	0	0	4.065	4.120	0	0	0	0	4.461	0	3.727	4.065	neg	pos	pos	**m**
s		0.156	0.107	0.116	0.140	0.127	0.105	0.261	0.223	0.206	0	0.132	0.172	0	0.161	0.331	0	0.191	0.305	0	0.163	0.187	0	0	0.221	0.156	0	0	0	0	0.114	0	0.116	0.096	-	-	-	**s**

Lab no.	Vial	Aerobic microorg. 30 °C			Aerobic microorg. 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
4050	2 3 1	5.32	4.2	4.94	-	-	-	-	-	-	<1	3.74	4.72	<1	3.75	4.47	-	-	-	-	-	-	-	-	-	4	<1	<1	-	-	-	-	-	-	Neg	Pos	Pos	**4050**
4064	2 1 3	5.2	4.15	4.89	-	-	-	-	-	-	0	3.73	4.7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4064**
4100	1 2 3	5.34	4.27	4.8	-	-	-	-	-	-	<1	3.6	4.4	-	-	-	<1	3.6	3.76	-	-	-	<2	<2	3.54	4.03	<2	<2	<2	<2	4.52	<1	3.67	4.06	-	-	-	**4100**
4171	1 3 2	5.28	4.18	4.95	-	-	-	-	-	-	<1	3.69	4.63	-	-	-	<0,60	3.7	4.51	-	-	-	<1	<1	**>1,00**	4.11	<2	<2	<1	<1	**>1,00**	**4.36**	3.73	4.08	-	-	-	**4171**
4246	3 1 2	5.08	4.1	4.88	5.09	4.14	4.91	-	-	-	0	3.72	4.42	0	3.66	3.51	-	-	-	-	-	-	0	0	3.82	-	-	-	0	0	4.65	-	-	-	-	-	-	**4246**
4278	3 1 2	5.18	4.06	4.69	-	-	-	-	-	-	<1	3.53	4.25	-	-	-	-	-	-	-	-	-	-	-	-	**<1**	<1	<1	-	-	-	-	-	-	-	-	-	**4278**
4288	3 2 1	5.37	4.4	5.01	-	-	-	-	-	-	<1	3.91	4.72	-	-	-	<1	3.84	3.48	<1	3.82	4.28	<1	<1	4.3	4.26	<1	<1	<1	<1	4.48	<1	3.79	4.04	-	-	-	**4288**
4339	3 2 1	5.26	4.36	4.92	-	-	-	5.46	3.85	4.9	<1	3.58	4.65	<1	3.73	4.68	<1	3.82	4.78	<1	3.75	3.96	<2	<2	3.96	4.11	<2	<2	<2	<2	4.53	**4.38**	3.8	3.99	-	-	-	**4339**
4352	3 2 1	5.36	**5.04**	**4.36**	-	-	-	5.46	**4.96**	4.45	<1	**4.65**	**3.82**	<1	**4.51**	3.72	<1	4.11	3.68	<1	3.96	**<1**	<1	**4.04**	**<1**	4.08	<2	<2	<2	**4.2**	**<2**	**4.45**	4.08	**3.65**	-	-	-	**4352**
4400	2 1 3	5.33	4.23	5.09	5.2	4.16	4.85	-	-	-	0	3.7	4.53	-	-	-	-	-	-	-	-	-	0	**3.26**	3.27	-	-	-	-	-	-	-	-	-	-	-	-	**4400**
4449	3 1 2	5.18	4.26	4.91	-	-	-	-	-	-	0	3.83	4.62	-	-	-	-	-	-	-	-	-	-	-	-	4.1	0	0	-	-	-	-	-	-	-	-	-	**4449**
4557	2 1 3	5.22	4.11	4.9	-	-	-	-	-	-	0	3.81	4.57	-	-	-	0	3.72	4.14	-	-	-	0	0	4.14	-	-	-	0	0	4.39	0	-	3.85	-	-	-	**4557**
4560	3 1 2	5.36	4.02	4.92	-	-	-	-	-	-	-	-	-	<5	3.75	3.98	-	-	-	-	-	-	<5	<5	3.98	-	-	-	-	-	-	-	-	-	-	-	-	**4560**
4562	3 2 1	5.49	4.23	5	-	-	-	-	-	-	<1	3.7	4.61	-	-	-	<1	3.68	4.28	-	-	-	<1	<1	4.23	4.18	<1	<1	<1	<1	4.49	<1	3.73	4.26	-	-	-	**4562**
4633	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.75	4.51	<1	3.82	4.59	<1	3.77	4.32	<1	<1	4.32	4.01	<2	<2	**5**	<2	4.39	**4.15**	3.74	4.1	-	-	-	**4633**
4635	3 2 1	5.32	4.19	4.98	-	-	-	-	-	-	<1	3.59	4.57	-	-	-	-	-	-	-	-	-	-	-	-	4.01	<1	<1	<1	<1	4.44	<1	3.79	4.12	-	-	-	**4635**
4664	1 2 3	5.2	4.17	5.04	-	-	-	-	-	-	<1	3.52	4.45	-	-	-	<1	3.7	4.12	<1	3.48	4.07	-	-	-	-	-	-	<2	<2	4.34	<1	**5.2**	**<1**	-	-	-	**4664**
4683	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4683**
4710	2 3 1	5.36	4.23	5	5.28	4.15	4.91	-	-	-	<1	3.59	4.57	-	-	-	<1	3.55	4.42	-	-	-	<1	<1	3.85	4.08	<2	<2	<1	<1	4.31	-	-	-	-	-	-	**4710**
4878	3 2 1	5.36	4.16	5	-	-	-	-	-	-	<1	3.75	4.66	-	-	-	-	-	-	-	-	-	-	-	-	4.13	<1	<1	-	-	-	-	-	-	-	-	-	**4878**
4889	2 3 1	5.38	4.2	4.88	5.28	4.18	4.95	-	-	-	0	3.79	4.6	-	-	-	0	3.68	4.18	-	-	-	0	0	4.34	4.28	0	0	0	0	4.46	0	3.72	4.08	-	-	-	**4889**
4951	1 2 3	5.13	4.15	4.93	-	-	-	-	-	-	0	3.49	4.5	-	-	-	0	3.42	**0**	-	-	-	0	0	4.09	-	-	-	-	-	-	-	-	-	-	-	-	**4951**
5018	3 2 1	5.21	4.19	4.93	-	-	-	-	-	-	<1	3.61	4.14	<1	3.65	3.89	<1	3.63	3.92	<1	3.7	3.95	<1	<1	**1.95**	4.08	<1	<1	<1	<1	4.46	<1	3.61	4.19	-	-	-	**5018**
5100	3 2 1	4.74	4.36	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.71	-	-	-	-	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	**5100**
5119	2 1 3	5.23	4.32	5	-	-	-	-	-	-	<1	3.7	4.57	<1	3.65	4.49	-	-	-	-	-	-	<1	<1	4.28	-	-	-	-	-	-	-	-	-	-	-	-	**5119**
5128	1 2 3	5.26	4.22	5.11	-	-	-	-	-	-	-	-	-	<1	3.63	3.95	<1	3.53	4.32	-	-	-	<1	<1	4.04	4.1	<1	<1	<1	<1	4.53	-	-	-	-	-	-	**5128**
5182	3 2 1	-	-	-	-	-	-	-	-	-	<1	3.55	4.41	-	-	-	<1	3.36	4.63	-	-	-	<1	<1	3.44	-	<2	<2	-	-	-	-	-	-	-	-	-	**5182**
5188	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5188**
5200	3 2 1	5.47	4.31	5.08	5.59	4.05	5.07	-	-	-	<1	3.75	4.57	<1	3.15	4.36	<0,477	4.04	4.04	<0,477	4.04	4.04	<3	<3	4.04	-	-	-	<2	<2	4.45	-	-	-	-	-	-	**5200**
5201	2 3 1	4.97	4.15	4.97	-	-	-	-	-	-	<1	3.59	4.76	-	-	-	<1	**<1**	4.2	-	-	-	<2	<2	4.18	4.07	<2	<2	<2	<2	4.45	-	-	-	-	-	-	**5201**
5204	3 1 2	5.3	4.2	5	-	-	-	-	-	-	<1	3.9	4.7	<1	3.8	4.1	<1	3.9	4.2	<1	4	4.3	<1	<1	4.3	4.2	<1	<1	<2	<2	4.5	<1	3.7	4.2	-	-	-	**5204**
5220	3 2 1	4.8	4.2	4.76	-	-	-	-	-	-	0	3.51	4.56	-	-	-	-	-	-	-	-	-	0	0	3.91	4.57	0	0	0	0	4.6	-	-	-	-	-	-	**5220**
5290	3 1 2	5.28	4.24	4.87	-	-	-	-	-	-	0	3.77	4.7	0	3.79	4.23	0	3.86	4.32	-	-	-	0	0	4.07	4.26	0	0	**4.62**	0	4.22	-	-	-	-	-	-	**5290**
5329	1 3 2	5.31	4.2	4.86	-	-	-	-	-	-	<1	3.67	4.38	-	-	-	-	-	-	<1	3.67	4.38	-	-	-	4.11	<2	<2	<3	<2	4.54	**4.19**	3.73	4.08	-	-	-	**5329**
5333	3 1 2	5.36	4.28	5	-	-	-	5.4	4.26	4.97	<1	3.71	4.46	<1	3.64	3.76	<1	3.72	3.99	-	-	-	<2	<2	3.9	4.09	<2	<2	<2	<2	4.49	**4.38**	3.58	4.04	-	-	-	**5333**
5338	2 1 3	5.23	4.21	4.97	-	-	-	-	-	-	0	3.92	4.71	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5338**
5342	1 3 2	5.15	4.25	4.88	-	-	-	-	-	-	<1	3.43	4.44	-	-	-	-	-	-	-	-	-	<1	<1	4.1	-	-	-	**4.92**	<1	4.51	-	-	-	-	-	-	**5342**
5352	1 3 2	5.18	4.18	4.94	-	-	-	-	-	-	0	3.45	4.58	-	-	-	0	3.38	4.34	0	3.59	4.18	0	0	4.18	4.2	0	0	0	0	4.51	**3.94**	**4.58**	**4.76**	-	-	-	**5352**
5419	1 3 2	4.88	4.24	4.79	-	-	-	4.87	4.09	4.85	<1	3.48	4.4	-	-	-	-	-	-	-	-	-	<1	<1	3.94	3.89	<2	<2	<2	<2	4.32	<2	3.71	3.98	-	-	-	**5419**
5446	1 2 3	5.220	4.220	4.990	-	-	-	-	-	-	<1	3.830	4.360	<1	4	5	<1	4	4	-	-	-	<1	<1	4	4	<1	<1	<1	<1	4.270	-	-	-	-	-	-	**5446**
5494	1 3 2	5.190	4.070	4.840	-	-	-	5.070	3.650	4.530	-	-	-	0.000	4	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5494**
5545	2 3 1	-	-	-	-	-	-	-	-	-	-	3.71	4.71	-	-	-	-	-	-	-	-	-	-	-	-	4.23	-	-	-	-	4.61	-	**3.2**	4.11	-	-	-	**5545**
5612	2 3 1	5.7	4.28	5.18	-	-	-	-	-	-	<1	3.87	4.7	-	-	-	<1	3.53	4.48	<1	3.43	4.4	<1	<1	4.7	4.2	<2	<2	<1	<1	4.4	-	-	-	-	-	-	**5612**
5615	3 2 1	5.32	4.3	5.04	-	-	-	-	-	-	<1	3.87	4.68	-	-	-	<1	3.83	4.15	-	-	-	<1	<1	4.15	4.04	<2	<2	<2	<2	4.56	-	-	-	-	-	-	**5615**
5632	1 3 2	5.3	4.2	4.9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	4	**3.4**	<2	<2	<2	<2	4.3	-	-	-	-	-	-	**5632**
5654	2 3 1	5.36	4.26	4.97	-	-	-	-	-	-	<1	3.77	4.65	-	-	-	-	-	-	-	-	-	-	-	-	4.1	<2	<2	-	-	-	-	-	-	-	-	-	**5654**
5701	3 1 2	5.17	4.09	4.91	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5701**
m		5.262	4.207	4.963	5.262	4.121	4.929	5.125	4.004	4.864	0	3.694	4.541	0	3.693	4.209	0	3.703	4.232	0	3.751	4.168	0	0	4.065	4.120	0	0	0	0	4.461	0	3.727	4.065	neg	pos	pos	**m**
s		0.156	0.107	0.116	0.140	0.127	0.105	0.261	0.223	0.206	0	0.132	0.172	0	0.161	0.331	0	0.191	0.305	0	0.163	0.187	0	0	0.221	0.156	0	0	0	0	0.114	0	0.116	0.096	-	-	-	**s**

Lab no.	Vial	Aerobic microorg. 30 °C			Aerobic microorg. 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
5801	3 2 1	4.81	3.93	4.7	-	-	-	-	-	-	<1	3.67	4.51	<1	3.58	4.43	-	-	-	-	-	-	-	-	-	3.78	<2	<2	-	-	-	-	-	-	-	-	-	5801
5808	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5808
5883	1 2 3	5.19	4.21	4.92	-	-	-	-	-	-	<1	3.68	4.5	-	-	-	-	-	-	-	-	-	<2	<2	4.07	4.09	<2	<2	<2	<2	4.41	-	-	-	-	-	-	5883
5950	1 2 3	5.35	4.22	4.87	5.31	4.08	4.98	5.22	4.15	4.93	<1	3.57	4.58	<1	3.38	3.92	<1	3.62	4.02	<1	3.72	4.12	<1	<1	4.12	4.16	<0,1	<0,1	<0,1	<0,1	4.38	<0,1	3.77	4.08	Neg	Pos	Pos	5950
5993	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.28	0	0	**4.94**	0	**3.96**	-	-	-	-	-	-	5993
6109	1 2 3	5.23	4.23	4.85	-	-	-	-	-	-	-	-	-	-	-	-	<0,6	3.8	4.32	-	-	-	-	-	-	4.08	<2	<2	-	-	-	-	-	-	-	-	-	6109
6175	1 2 3	5.35	4.26	5.01	-	-	-	-	-	-	0	3.73	4.54	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6175
6224	1 3 2	5.58	4.35	5.21	-	-	-	-	-	-	<1	3.93	4.77	-	-	-	-	-	-	-	-	-	-	-	-	4.38	<1	**4.08**	-	-	-	-	-	-	-	-	-	6224
6232	3 1 2	5.22	**3.15**	4.92	-	-	-	-	-	-	<1	3.64	4.52	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6232
6253	3 1 2	5.34	4.23	4.88	-	-	-	-	-	-	<1	3.73	4.63	<1	3.71	4.04	-	-	-	-	-	-	<1	<1	4	4.04	<1	<1	<1	<1	4.58	<1	3.71	4.04	-	-	-	6253
6258	3 1 2	5.32	4.29	5.1	-	-	-	-	-	-	-	-	-	0	**5.7**	**1.61**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6258
6343	2 3 1	5.14	4.2	4.87	-	-	-	-	-	-	<1	3.69	4.28	-	-	-	<1	3.85	4.71	-	-	-	<2	<1	4.15	3.6	<2	<2	<2	<2	**4.9**	-	-	-	-	-	-	6343
6352	2 1 3	5.4	4.14	4.82	-	-	-	-	-	-	<1	3.56	4.48	-	-	-	<1	3.43	3.58	-	-	-	<2	<2	3.78	3.93	<2	<2	**4.71**	**2.48**	4.32	<1	3.68	**4.58**	-	-	-	6352
6368	1 3 2	5.26	4	4.92	5.15	3.99	4.9	-	-	-	<1	3.61	4.68	-	-	-	<1	3.6	3.98	<1	3.49	4.2	<1	<1	4.2	4.11	<2	<2	<2	<2	4.46	<1	3.53	3.93	-	-	-	6368
6456	2 3 1	5.27	4.22	4.85	-	-	-	-	-	-	<1	3.7	4.43	<1	3.62	4	<1	3.63	4.02	-	-	-	<1	<1	4.08	4.15	<1	<1	<1	<1	4.48	<1	3.56	**3.71**	-	-	-	6456
6490	3 1 2	5.28	4.19	4.76	-	-	-	-	-	-	0	3.73	4.58	-	-	-	-	-	-	-	-	-	-	-	-	4.23	0	0	0	0	4.48	0	3.69	4.01	-	-	-	6490
6594	2 3 1	5.49	4.32	5	-	-	-	-	-	-	<1	3.53	4.59	-	-	-	<0,60	3.9	4.69	-	-	-	-	-	-	4.15	<2	<2	-	-	-	-	-	-	-	-	-	6594
6658	3 1 2	5.31	4.19	4.86	-	-	-	-	-	-	<1	3.5	**3.77**	-	-	-	-	-	-	-	-	-	-	-	-	4.2	<1	<1	-	-	-	-	-	-	Neg	Pos	Pos	6658
6686	2 3 1	5.26	4.26	5.04	5.36	4.23	5.08	-	-	-	<1	**<1**	4.67	-	-	-	-	-	-	<1	3.82	4.64	<1	<1	4.45	-	-	-	**3.72**	<1	4.48	**4.23**	3.72	4.11	-	-	-	6686
6728	2 1 3	**4.5**	**3.8**	4.8	-	-	-	-	-	-	-	3.4	4.5	-	-	-	0	**2.5**	3.9	-	-	-	0	0	3.9	-	-	-	**3.3**	0	4.5	-	-	-	-	-	-	6728
6762	2 3 1	5.29	4.05	5.05	-	-	-	-	-	-	<1	3.69	4.03	-	-	-	-	-	-	-	-	-	<1	<1	4.05	-	-	-	-	-	-	-	-	-	-	-	-	6762
6801	2 3 1	5.37	4.23	4.96	-	-	-	-	-	-	-	-	-	0	3.92	4.28	0	3.62	4.18	-	-	-	0	0	4.18	-	-	-	**5.2**	0	4.4	-	-	-	-	-	-	6801
6885	2 3 1	5.21	4.23	4.98	-	-	-	-	-	-	0	3.7	4.56	-	-	-	-	-	-	-	-	-	0	0	4.1	4.13	0	0	0	0	4.64	**4.25**	3.7	4.03	Neg	Pos	Pos	6885
6944	3 2 1	-	-	-	5.22	4.11	4.83	-	-	-	-	-	-	-	-	-	0	**4.83**	4.56	-	-	-	0	0	4.12	-	-	-	-	-	-	-	-	-	-	-	-	6944
6958	3 2 1	5.26	4.15	4.83	-	-	-	-	-	-	0	3.53	4.45	-	-	-	-	-	-	-	-	-	-	-	-	3.87	0	0	-	-	-	-	-	-	-	-	-	6958
6971	3 2 1	5.48	4.22	5.07	-	-	-	-	-	-	0	3.86	4.63	-	-	-	-	-	-	-	-	-	-	-	-	3.99	0	0	-	-	-	-	-	-	-	-	-	6971
6992	3 1 2	5.4	4.26	4.92	-	-	-	-	-	-	-	-	-	0	4.04	4.18	-	-	-	-	-	-	<0,477	<0,477	4.18	3.97	<2	<2	<0,477	<0,477	4.7	-	-	-	-	-	-	6992
7182	3 2 1	5.33	4.1	4.95	5.29	4.06	4.89	5.25	4.16	4.95	<1	3.59	4.56	<1	3.52	3.23	<1	3.51	3.72	-	-	-	<1	<1	3.72	-	-	-	-	-	-	-	-	-	-	-	-	7182
7191	2 1 3	5.3	4.1	4.8	-	-	-	-	-	-	-	-	-	-	-	-	<1	4.04	4.04	<1	4.04	4.04	<1	<1	4.04	-	-	-	<1	<1	**<1**	-	-	-	-	-	-	7191
7207	1 2 3	5.46	4.51	5.03	-	-	-	-	-	-	<1	3.6	4.17	-	-	-	-	-	-	-	-	-	-	-	-	4.2	<1	<1	-	-	-	**4.26**	3.68	4.02	-	-	-	7207
7232	3 1 2	5.24	4.18	4.81	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7232
7242	1 3 2	4.86	3.96	4.9	-	-	-	-	-	-	0	3.62	4.54	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7242
7248	2 1 3	5.58	4.41	5.09	5.62	4.28	5.18	-	-	-	0	3.83	4.76	0	4	4.74	0	3.9	4.8	0	3.94	4.26	0	0	4.36	4.32	0	0	0	0	4.57	0	3.78	4.11	-	-	-	7248
7253	2 3 1	5.36	4.26	5.08	-	-	-	-	-	-	<1	3.77	4.71	-	-	-	<1	3.75	4.55	-	-	-	<1	<1	3.97	4.3	<1	<1	<1	<1	4.53	-	-	-	-	-	-	7253
7334	3 1 2	5.3	4.2	4.91	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.59	4.29	-	-	-	<1	<1	**>1**	4.03	<2	<2	<2	<2	4.53	-	-	-	-	-	-	7334
7564	3 2 1	5.29	4.15	5.01	5.27	3.97	4.94	4.43	3.45	**4**	<1	3.62	4.57	-	-	-	<1	3.49	4.11	<1	3.53	4	<1	<1	3.93	-	-	-	-	-	-	<1	3.72	4.03	-	-	-	7564
7617	1 2 3	**4.3**	**5.18**	5.4	-	-	-	-	-	-	-	-	-	-	-	-	**3.75**	4.16	**<1**	-	-	-	<1	**4.16**	**<1**	-	-	-	<1	**3.99**	**4.97**	**3.83**	4.06	4.16	-	-	-	7617
7627	2 3 1	4.96	4.43	4.97	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.59	4.38	-	-	-	-	-	-	4.12	<2	<2	-	-	-	-	-	-	-	-	-	7627
7631	1 2 3	5.21	4.18	4.96	-	-	-	-	-	-	0	3.67	4.61	0	3.69	4.47	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7631
7640	1 3 2	5.340	4.080	4.940	5.330	4.300	5.010	4.760	3.870	4.690	<1	3.830	4.540	<1	4	5	<1	4	5	<1	4	4	<1	<1	4	4	<1	<1	<1	<1	4.410	<1	4	4	-	-	-	7640
7688	1 3 2	5.240	4.190	5.010	-	-	-	-	-	-	<1	3.690	4.670	<1	4	4	<1	4	5	<1	4	4	<1	<1	4	4	<1	<1	<1	<1	4.490	**4.300**	4	4	-	-	-	7688
7728	3 1 2	5.16	4.13	4.96	5.07	4.17	5.05	-	-	-	0	3.59	4.34	-	-	-	0	3.63	4.66	0	3.63	4.66	0	0	4.66	4.41	0	0	0	0	4.58	-	-	-	-	-	-	7728
7750	1 2 3	5.18	4.23	4.94	-	-	-	-	-	-	-	-	-	<0,60	3.61	4.44	-	-	-	-	-	-	-	-	-	4	<2	<2	-	-	-	-	-	-	-	-	-	7750
7825	1 3 2	5.47	4.49	5.13	-	-	-	-	-	-	<1	3.93	4.74	-	-	-	-	-	-	<1	3.76	4.12	<1	<1	4.03	-	-	-	**5.26**	<1	4.48	<1	3.77	3.83	-	-	-	7825
7876	3 2 1	5.3	4.3	5	-	-	-	-	-	-	<1	3.86	4.5	-	-	-	-	-	-	-	-	-	<2	<2	4.1	3.9	<2	<2	<2	<2	4.5	<2	3.61	3.9	-	-	-	7876
7930	1 3 2	5.36	4.3	5.11	-	-	-	-	-	-	<1	3.63	4.71	<1	3.91	4.11	<1	3.99	4.46	<1	3.98	4.2	<1	<1	4.2	4.26	<1	<1	<1	<1	4.48	**4.2**	3.72	4.07	-	-	-	7930
7940	1 2 3	5.17	4.13	4.92	-	-	-	-	-	-	-	-	-	0	3.85	3.91	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7940
m		5.262	4.207	4.963	5.262	4.121	4.929	5.125	4.004	4.864	0	3.694	4.541	0	3.693	4.209	0	3.703	4.232	0	3.751	4.168	0	0	4.065	4.120	0	0	0	0	4.461	0	3.727	4.065	neg	pos	pos	**m**
s		0.156	0.107	0.116	0.140	0.127	0.105	0.261	0.223	0.206	0	0.132	0.172	0	0.161	0.331	0	0.191	0.305	0	0.163	0.187	0	0	0.221	0.156	0	0	0	0	0.114	0	0.116	0.096	-	-	-	**s**

Lab no.	Vial	Aerobic microorg. 30 °C			Aerobic microorg. 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
7962	1 3 2	5.42	4.2	5.04	-	-	-	-	-	-	0	3.79	4.72	0	3.73	4.26	0	3.64	4.08	0	3.67	4.3	0	0	4.3	3.9	0	0	0	0	4.59	0	3.48	**3.58**	-	-	-	**7962**
7968	1 3 2	5.41	4.23	5.05	-	-	-	-	-	-	0	3.77	4.73	0	3.64	4.76	0	3.68	4.67	0	3.81	4.26	0	0	4.26	4.08	0	0	0	0	4.54	0	3.87	4.11	-	-	-	**7968**
7975	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**7975**
7984	3 1 2	5.2	4.18	5.08	-	-	-	-	-	-	0	3.7	4.7	-	-	-	-	-	-	-	-	-	-	-	-	4.3	0	0	-	-	-	-	-	-	Neg	Pos	Pos	**7984**
8019	1 2 3	5.42	4.19	5.08	5.29	3.87	5.01	4.94	4.02	5.38	<1	**2.92**	4.69	<1	**2.95**	3.74	<1	3.06	4.1	<1	**3.02**	**2.93**	<1	<1	**2.84**	4.08	<2	<2	<2	<2	4.45	-	-	-	-	-	-	**8019**
8068	1 2 3	5.34	4.3	5.03	5.29	4.26	5	-	-	-	0	3.81	4.77	0	3.72	4.41	0	3.65	4.23	0	3.92	4.26	0	0	4.26	4.04	0	0	0	0	4.52	0	3.68	4.12	-	-	-	**8068**
8105	3 2 1	5.3	4.22	4.95	-	-	-	-	-	-	-	-	-	-	-	-	0	3.74	4.57	-	-	-	0	0	4.16	4	0	0	0	0	4.4	-	-	-	-	-	-	**8105**
8213	1 3 2	5.27	4.23	5.1	-	-	-	-	-	-	0	3.85	4.56	-	-	-	-	-	-	-	-	-	0	0	4.2	4.5	0	0	-	-	-	-	-	-	Neg	Pos	Pos	**8213**
8228	3 2 1	5.03	4.1	**4.48**	4.99	3.78	4.65	-	-	-	0	3.49	4.37	0	3.59	4.28	-	-	-	-	-	-	-	-	-	**>4,70**	0	0	-	-	-	-	-	-	-	-	-	**8228**
8260	1 2 3	5.18	4.21	4.92	-	-	-	-	-	-	<1	3.64	4.63	<1	3.66	4.41	<1	3.67	4.07	<1	3.67	4.11	<1	<1	4.13	4.05	<1	<1	<1	<1	**<1**	**4.18**	3.69	4.1	-	-	-	**8260**
8313	2 3 1	5.24	4.18	4.89	-	-	-	-	-	-	<1	3.47	4.35	-	-	-	<1	3.56	3.83	-	-	-	<2	<2	3.84	4.16	<2	<2	<2	<2	4.46	**4.16**	3.72	4.08	-	-	-	**8313**
8333	2 3 1	5.37	**4.81**	5.01	-	-	-	-	-	-	<1	3.77	4.09	-	-	-	<0,60	3.76	4.51	-	-	-	-	-	-	3.84	<2	<2	-	-	-	<2	3.67	4.16	-	-	-	**8333**
8397	1 2 3	5.41	4.23	5.02	-	-	-	-	-	-	<1	3.72	**3.52**	-	-	-	-	-	-	-	-	-	<2	<2	3.93	4	<2	<2	<2	<2	4.4	<1	3.72	4	-	-	-	**8397**
8430	3 2 1	5	4.18	4.84	-	-	-	-	-	-	<1	3.62	4.02	<1	3.68	4.36	-	-	-	-	-	-	<1	<1	3.88	-	-	-	**5.01**	<1	4.24	-	-	-	-	-	-	**8430**
8435	1 3 2	5.42	4.23	4.99	5.41	4.2	4.83	-	-	-	<1	3.67	4.57	<1	3.54	4.04	<1	3.57	4.04	<1	3.51	4.12	<1	<1	4.12	4.28	<2	<2	<2	<2	4.54	**4.36**	3.86	4.08	-	-	-	**8435**
8523	2 3 1	5.47	4.41	5.01	-	-	-	-	-	-	<1	3.98	4.72	-	-	-	-	-	-	-	-	-	<1	<1	4	-	-	-	<1	<1	4.47	-	-	-	-	-	-	**8523**
8528	2 3 1	**4.28**	**3.69**	**4.34**	-	-	-	-	-	-	<1	3.6	4.08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**8528**
8568	3 2 1	5.3	4.46	5.06	-	-	-	-	-	-	<1	3.88	4.62	-	-	-	<,60	3.78	3.89	-	-	-	-	-	-	4.05	<2	<2	-	-	-	<2	3.92	4.27	-	-	-	**8568**
8578	3 2 1	5.3	4.15	4.86	-	-	-	-	-	-	-	-	-	-	-	-	<1	**>2,04**	**>2,04**	-	-	-	<1	<1	**>2,04**	-	-	-	-	-	-	-	-	-	-	-	-	**8578**
8626	3 2 1	4.73	**3.78**	5.19	5.18	4.23	5	-	-	-	0	3.62	4.07	-	-	-	0	4.04	4.66	0	4.04	4.66	0	0	4.66	-	-	-	-	-	-	-	-	-	-	-	-	**8626**
8628	2 1 3	5.3	4.23	4.9	5.18	4.23	4.78	-	-	-	<1	3.64	4.28	<1	3.8	3.89	<1	3.69	4	<1	3.73	4.11	<1	<1	4.11	4.26	<2	<2	<2	<2	4.53	**4.15**	3.67	3.98	-	-	-	**8628**
8657	3 2 1	5.29	4.23	4.95	-	-	-	-	-	-	<1	3.77	4.61	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**8657**
8696	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**8696**
8734	1 2 3	5.26	4.03	4.92	-	-	-	5.21	4.02	4.9	<1	3.59	4.44	<1	3.5	3.57	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**8734**
8742	3 2 1	5.21	4.14	4.85	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.66	4.38	<1	3.66	4.38	<1	<1	4.38	-	-	-	<1	<1	4.51	-	-	-	-	-	-	**8742**
8756	3 1 2	5.6	**5.23**	5.09	-	-	-	-	-	-	<2	3.76	4.7	-	-	-	-	-	-	-	-	-	<2	<2	4.16	**5.23**	**3.46**	**4.04**	**5.39**	<2	4.55	**4.07**	3.6	4.1	-	-	-	**8756**
8766	3 1 2	5.25	4.22	4.92	-	-	-	-	-	-	0	3.69	4.34	-	-	-	-	-	-	-	-	-	0	0	3.96	4.06	0	0	0	0	4.49	0	3.64	3.99	-	-	-	**8766**
8891	3 2 1	4.95	4.08	4.89	-	-	-	5.09	4.16	4.86	<1	3.63	4.2	<1	3.41	4.41	-	-	-	-	-	-	<2	<2	4.04	4.11	<2	<2	<2	<2	4.43	-	-	-	-	-	-	**8891**
8909	2 3 1	5.4	4.26	4.97	-	-	-	-	-	-	<1	3.73	4.64	<1	3.72	4.01	-	-	-	-	-	-	<2	<2	3.54	4.16	<2	<2	<2	<2	4.62	<1	3.77	4.03	-	-	-	**8909**
8918	3 1 2	5.2	4.34	4.98	-	-	-	5.26	4.3	4.9	<1	3.72	4.48	-	-	-	<1	3.58	3.92	-	-	-	<2	<2	3.9	4.34	<2	<2	<2	<2	4.49	-	-	-	-	-	-	**8918**
9003	2 3 1	5.28	4.23	5.01	-	-	-	-	-	-	<1	3.83	4.57	-	-	-	<1	3.62	4.18	-	-	-	<2	<2	4.2	-	-	-	<2	<2	4.24	-	-	-	-	-	-	**9003**
9007	2 3 1	5.19	4.13	4.97	-	-	-	-	-	-	0	3.41	4.48	-	-	-	0	3.56	3.9	-	-	-	0	0	4.15	-	-	-	0	0	4.15	-	-	-	-	-	-	**9007**
9025	1 3 2	5.27	**4.69**	5.17	-	-	-	-	-	-	0	3.97	4.59	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Neg	Pos	Pos	**9025**
9034	2 3 1	5.1	4.2	4.9	5.1	4	4.9	-	-	-	<1	3.6	4.6	-	-	-	-	-	-	-	-	-	<1	<1	3.9	-	-	-	-	-	-	-	-	-	-	-	-	**9034**
9078	2 3 1	5.34	4.15	5.11	-	-	-	-	-	-	0	3.95	4.55	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9078**
9217	3 2 1	5.15	4.15	5	-	-	-	-	-	-	<1	3.45	4.56	-	-	-	-	-	-	-	-	-	-	-	-	4.01	<1	<1	<2	<2	4.39	**3.97**	3.7	3.98	-	-	-	**9217**
9429	1 2 3	-	-	-	-	-	-	-	-	-	<1	3.69	4.65	<1	3.72	4.04	<1	3.71	4	<1	3.66	4.04	<2	<2	4.04	-	-	-	-	-	-	<1	3.72	4.08	-	-	-	**9429**
9436	2 3 1	5.36	4.2	4.85	-	-	-	-	-	-	<1	3.67	4.22	<1	3.5	4.54	<1	3.5	4.67	<1	3.6	4.16	<2	<2	4	4.1	<2	<2	<2	<2	4.21	<1	3.67	3.98	-	-	-	**9436**
9453	3 1 2	5.2	4.26	4.89	-	-	-	5.1	4.06	4.88	<1	3.82	4.64	-	-	-	-	-	-	-	-	-	-	-	-	4.24	<1	<1	<1	<1	4.48	<1	3.8	3.9	-	-	-	**9453**
9512	1 2 3	5.100	4.100	4.860	-	-	-	-	-	-	0.00	3.700	4.500	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9512**
9559	3 2 1	5.320	4.200	4.930	5.280	4.170	4.840	5.190	4.010	4.910	<1	3.720	4.680	-	-	-	<1	4	5	-	-	-	<2	<2	4	4	<2	<2	<2	<2	4.600	-	-	-	Neg	Pos	Pos	**9559**
9662	2 1 3	5.3	4.16	4.98	-	-	-	-	-	-	<1	3.71	4.72	<1	3.71	4.11	<1	3.66	3.85	-	-	-	<2	<2	4	4.38	<2	<2	<2	<2	4.37	<1	3.66	4.08	-	-	-	**9662**
9747	3 1 2	5.11	**5.06**	4.74	-	-	-	-	-	-	-	**3.2**	**3.98**	-	-	-	-	-	-	-	-	-	-	-	-	3.94	-	-	-	-	-	-	-	-	-	-	-	**9747**
9890	3 1 2	5.48	4.3	4.91	5.38	4.15	4.96	-	-	-	0	3.3	4.43	-	-	-	0	3.6	4.41	-	-	-	0	0	4.41	3.95	0	0	0	0	4.4	-	-	-	-	-	-	**9890**
9903	2 1 3	5.21	4.09	4.81	-	-	-	-	-	-	<1	3.6	4.2	-	-	-	-	-	-	-	-	-	<2	<2	3.89	4.02	<2	<2	<2	<2	**4.03**	<1	3.47	4.22	-	-	-	**9903**
9950	3 2 1	-	-	-	5.26	4.05	4.95	5.19	4.16	4.98	-	-	-	-	-	-	0	3.51	3.9	-	-	-	0	0	3.9	4.15	0	0	-	-	-	-	-	-	-	-	-	-	**9950**
m		5.262	4.207	4.963	5.262	4.121	4.929	5.125	4.004	4.864	0	3.694	4.541	0	3.693	4.209	0	3.703	4.232	0	3.751	4.168	0	0	4.065	4.120	0	0	0	0	4.461	0	3.727	4.065	neg	pos	pos	**m**
s		0.156	0.107	0.116	0.140	0.127	0.105	0.261	0.223	0.206	0	0.132	0.172	0	0.161	0.331	0	0.191	0.305	0	0.163	0.187	0	0	0.221	0.156	0	0	0	0	0.114	0	0.116	0.096	-	-	-	**s**

Lab no.	Vial	Aerobic microorg. 30 °C			Aerobic microorg. 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
N		166	166	165	29	29	29	18	18	18	137	140	140	57	57	57	94	93	92	48	46	48	119	119	115	109	109	109	105	105	105	66	66	67	11	11	11	**N**
Min		4.28	2.98	3.73	4.99	3.78	4.65	3.65	3.45	3.95	0	0	2.48	0	2.86	1.61	0	0	0	0	3.02	0	0	0	0	0	0	0	0	0	0	0	3.2	0	-	-	-	**Min**
Max		6.41	5.33	6.01	5.62	4.30	5.18	5.46	4.96	5.38	0	4.75	5.54	1.30	5.70	5.68	3.75	4.83	5.64	0	4.04	4.66	0	4.16	5.19	5.23	3.46	4.08	5.39	4.20	5.40	4.45	5.20	4.76	-	-	-	**Max**
Med		5.28	4.21	4.96	5.28	4.15	4.94	5.19	4.06	4.90	0	3.70	4.57	0	3.69	4.23	0	3.70	4.20	0	3.75	4.12	0	0	4.05	4.11	0	0	0	0	4.48	0	3.72	4.07	-	-	-	**Med**
m		5.262	4.207	4.963	5.262	4.121	4.929	5.125	4.004	4.864	0	3.694	4.541	0	3.693	4.209	0	3.703	4.232	0	3.751	4.168	0	0	4.065	4.120	0	0	0	0	4.461	0	3.727	4.065	neg	pos	pos	**m**
s		0.156	0.107	0.116	0.140	0.127	0.105	0.261	0.223	0.206	0	0.132	0.172	0	0.161	0.331	0	0.191	0.305	0	0.163	0.187	0	0	0.221	0.156	0	0	0	0	0.114	0	0.116	0.096	-	-	-	**s**
F+		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	4	0	0	1	2	13	3	0	21	0	0	0	0	0	**F+**
F-		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3	2	0	0	1	0	0	2	1	0	0	0	0	4	0	0	1	0	0	0	**F-**
<		5	5	5	0	0	0	1	0	2	0	4	6	0	2	1	0	1	0	0	1	1	0	0	3	3	0	0	0	0	2	0	1	3	-	-	-	**<**
>		3	9	2	0	0	0	0	1	0	0	2	1	0	2	1	0	1	1	0	0	0	0	0	1	2	0	0	0	0	3	0	2	2	-	-	-	**>**
< OK		4.73	3.81	4.64	4.99	3.78	4.65	4.43	3.45	4.45	0	3.30	4.02	0	3.15	3.23	0	3.06	3.48	0	3.43	3.84	0	0	3.27	3.60	0	0	0	0	4.09	0	3.47	3.82	-	-	-	**< OK**
> OK		5.69	4.51	5.40	5.62	4.30	5.18	5.46	4.30	5.38	0	3.99	4.81	0	4.05	4.76	0	4.17	4.80	0	4.05	4.66	0	0	4.69	4.57	0	0	0	0	4.78	0	4.08	4.34	-	-	-	**> OK**

N = number of analyses performed
Min = lowest reported result
Max = highest reported result
Median = median value
m = mean value
s = standard deviation
F+ = false positive
F- = false negative
< = low outlier
> = high outlier
< OK = lowest accepted value
> OK = highest accepted value

The results are not evaluated

Annex 2 Z-scores of all participants - October 2018

Z-scores are calculated according to: z = (x-m)/s, where x = result of the individual laboratory, m = mean of the results of all participating laboratories, s = standard deviation of the results of all participating laboratories. Correct negative results in quantitative analyses have obtained a z-score of zero. False results do not generate a z-score. Z-scores from outliers are not real z-scores, but are a practical means to express the results from outliers. Very low and high z-scores are limited to -4 and +4 respectively.

2 < |z| ≤ 3, |z|>3

Lab nr.	Provnr.	Aerobic microorganisms 30 °C			Aerobic microorganisms 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
1149	1 2 3	0.182	0.778	**2.123**							0	-0.027	0.574				0	0.771	-0.008				0	0	0.744				0	0	0.691								1149
1545	2 1 3	1.271	1.527	0.921							0	1.941	0.515							0	0.729	0.385	0	0	0.789	1.735	0	0	0	0	-0.539		-0.403	0.678				1545
1594	1 2 3	-0.011	0.871	0.149	-0.227	1.406	0.103				0	0.276	1.039	0	0.296	1.002	0	0.403	1.468	0	0.423	-0.095	0	0	0.382	**-4.000**	0	0	0	0	-0.276		-0.403	0.469				1594
1970	1 2 3	-0.780	1.059	-0.452	-1.371	1.013	-0.374				0	0.351	-0.357	0	0.607	0.669	0	1.190	0.615	0	0.056	0.492	0	0	0.879	-0.192	0	0	0	0	1.130		1.324	-0.263				1970
2035	2 1 3										0	-1.466	**-4.000**	0	-0.576	-0.631							0	0	-0.295													2035
2043	1 2 3	1.784	0.403	1.007													0	-1.224	0.976																			2043
2058	3 1 2	-0.523	1.246	**2.037**																			0	0	1.782	**-4.000**	0	0										2058
2064	1 2 3	0.054	0.216	-1.053							0	0.730	-0.125													0.194	0	0										2064
2072	2 1 3																																						2072
2109	2 3 1	**-2.254**	**-3.718**	**-2.341**													0		-0.270				0	0	-1.560													2109
2221	2 3 1	0.246	-0.065	0.063				**-4.000**	-1.049	-0.600	0	-0.179	0.748	0	0.233	-0.299	0	-0.122	-0.074				0	0	-0.295	0.258	0	0	0	0	0.427		0.806	1.200				2221
2324	2 1 3	**-4.000**	**-4.000**	**-4.000**							0	**-4.000**	**-4.000**										0	0	**-4.000**	-0.770	0	0		0			-0.057	0.260				2324
2386	2 3 1	0.438	-0.065	1.436													0	0.088	-0.631	0	-0.556	-0.308							0	0	0.515							2386
2402	1 2 3	0.951	-0.065	1.265							0	1.260	**-2.277**				0	1.138	0.353				0	0	1.240													2402
2459	2 1 3	**4.000**	**4.000**	**4.000**							0	**4.000**	**4.000**				0		**4.000**				0	0	**4.000**	**4.000**	0	0	0	0	**4.000**							2459
2637	1 3 2	0.502	0.216	0.235				0.402	0.344	**-4.000**	0	0.881	1.272							0		-0.895	0	0	0.382	0.194	0	0	0	0	0.954							2637
2659	1 3 2	0.246	1.433	1.694										0	1.603	1.153	0	1.295	1.173				0	0	-0.295				0	0	0.339				0	0	0	2659
2670	1 3 2	0.118	0.216	-0.280													0	1.768	-0.631	0	1.769	-0.682	0	0	-0.115				0	0	-1.242							2670
2704	3 1 2	0.438	0.403	0.836							0	0.730	0.690				0	0.508	-0.303				0	0	0.337	-1.926	0	0	0	0	0.691							2704
2720	2 1 3	-0.075	1.621	-0.280							0	**2.244**	0.225													-0.513	0	0										2720
2745	3 2 1	-0.587	-0.721	-0.967							0	-0.481	0.399							0	-0.434	-0.628	0	0	-0.069	0.194	0	0	0	0	-0.539							2745
2757	1 3 2	-0.203	-0.534	0.664	-0.584	-1.187	0.199				0	0.276	-0.008	0	-0.265	-0.692																						2757
2764	3 2 1	0.246	-1.189	0.664							0	0.351	-0.008				0	-0.069	0.353							0.515	0	0				0.374	-0.263						2764
2794	3 2 1	-1.515	-1.858	**-4.000**													0	**-2.633**	-1.932																			2794
2941	2 1 3	0.759	-0.815	-0.452							0	-0.481	0.283	0	-0.140	0.881							0	0	0.382	-0.577	0	0	0	0	1.042		-1.007	-1.517				2941
3031	3 1 2																0	0.992	0.754	0	1.061	1.133											-0.021	-0.248				3031
3055	1 3 2	0.310	-0.253	-0.195							0	0.730	1.563													-0.642	0	0							0	0	0	3055
3155	1 2 3																0	0.325	0.812	0		-1.162	0	0	-0.250													3155
3159	2 1 3	-0.972	0.028	0.063							0	0.049	1.039				0	0.036	-1.386	0	-1.413	-1.748	0	0	-1.198	0.065	0	0	0	0	-0.012							3159
3243	3 1 2	-0.267	-1.096	-0.109							0	-0.557	0.341																									3243
3305	2 1 3	**4.000**	**4.000**	0.063							0	0.200	0.515							0	0.117	-0.468	0	0	0.066	-0.063	0	0	0	0	-0.012							3305
3327	1 3 2	-1.292	-1.939	-1.740							0	-1.541	-0.881										0	0	-1.424				0	0	-0.451							3327
3452	2 3 1	**4.000**	**4.000**	**4.000**											**-4.000**	**4.000**																							3452
3457	1 3 2				0.775	-0.401	-0.374				0	-0.179	-1.114				0	0.246	1.107	0	-0.556	-1.215	0	0	-0.566				0	0	**2.799**		-0.489	-0.263				3457
3533	1 2 3	-0.651	0.309	0.321													0	-0.226	-0.631	0	-0.556	-0.682	0	0	-0.115				0	0	-1.242							3533
3543	2 1 3	1.400	0.497	**2.037**							0	0.276	1.155													1.671	0	0	0	0	**-3.262**		1.151	-0.054				3543
3587	2 3 1	0.374	0.216	-0.624							0	-0.103	0.225	0	-0.016	1.032	0	0.298	1.206				0	0	-0.611	0.258	0	0	0	0	0.339		0.115	-1.099				3587
3626	2 3 1	0.246	-0.065	0.321							0	0.049	0.923	0	-0.576	-0.329	0	-0.541	-0.763	0	0.301	-0.362	0	0	0.156	-0.128	0	0	0	0	-0.539		-1.093	1.409				3626
3831	1 3 2	-1.421	-1.564	**-2.770**													0	-1.066	-0.402				0	0	-1.018													3831
3864	2 3 1	-0.741	**2.529**	1.291							0	0.639	-0.212																								0	0	0	3864
3878	3 2 1	**-4.000**	**-2.473**	-0.358										0	-1.211	-0.262	0	-0.856	-0.313				0	0	0.324													3878
3923	3 2 1	0.118	-0.253	-0.795	0.417	-0.087	-1.234				0	**-4.000**	0.108	0	**2.163**	0.518	0	1.768	-0.631	0	-0.556	-0.682	0		-0.115	-0.513	0	0		0	-0.890		**2.705**	-0.263				3923
4047	1 3 2	-0.203	0.122	**2.295**							0	0.427	0.341										0	0	-0.115	1.799	0	0	0	0	-0.100							4047
4050	2 3 1	0.374	-0.065	-0.195							0	0.351	1.039	0	0.358	0.790										-0.770	0	0							0	0	0	4050
4064	2 1 3	-0.395	-0.534	-0.624							0	0.276	0.923																									4064
4100	1 2 3	0.502	0.590	-1.396							0	-0.709	-0.823				0	-0.541	-1.550				0	0	**-2.373**	-0.577	0	0	0	0	0.515		-0.489	-0.054				4100
4171	1 3 2	0.118	-0.253	-0.109							0	-0.027	0.515				0	-0.017	0.911				0	0		-0.063	0	0	0	0			0.029	0.155				4171

Lab nr.	Provnr.			Aerobic microorganisms 30 °C			Aerobic microorganisms 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
4246	3	1	2	-1.164	-1.002	-0.710	-1.228	0.149	-0.183				0	0.200	-0.706	0	-0.202	-2.114							0	0	-1.108				0	0	1.657							4246
4278	3	1	2	-0.523	-1.377	-2.341							0	-1.238	-1.696														0	0								4278
4288	3	2	1	0.695	1.808	0.406							0	1.638	1.039				0	0.718	-2.468	0	0.423	0.599	0	0	1.060	0.900	0	0	0	0	0.164		0.547	-0.263				4288
4339	3	2	1	-0.011	1.433	-0.366				1.283	-0.690	0.176	0	-0.860	0.632	0	0.233	1.426	0	0.613	1.796	0	-0.005	-1.108	0	0	-0.476	-0.063	0	0	0	0	0.603		0.633	-0.785				4339
4352	3	2	1	0.631	4.000	-4.000				1.283	4.000	-2.007	0	4.000	-4.000	0	4.000	-1.478	0	2.135	-1.812	0	1.280		0			-0.256	0	0	0				3.050	-4.000				4352
4400	2	1	3	0.438	0.216	1.093	-0.441	0.306	-0.757				0	0.049	-0.066										0		-3.592													4400
4449	3	1	2	-0.523	0.497	-0.452							0	1.033	0.457													-0.128	0	0										4449
4557	2	1	3	-0.267	-0.908	-0.538							0	0.881	0.166				0	0.088	-0.313				0	0	0.324				0	0	-0.627			-2.248				4557
4560	3	1	2	0.631	-1.751	-0.366										0	0.358	-0.692							0	0	-0.386													4560
4562	3	2	1	1.464	0.216	0.321							0	0.049	0.399				0	-0.122	0.156				0	0	0.744	0.386	0	0	0	0	0.252		0.029	2.036				4562
4633	1	2	3													0	0.358	0.911	0	0.613	1.173	0	0.117	0.812	0	0	1.150	-0.706	0	0		0	-0.627		0.115	0.364				4633
4635	3	2	1	0.374	-0.159	0.149							0	-0.784	0.166													-0.706	0	0	0	0	-0.188		0.547	0.573				4635
4664	1	2	3	-0.395	-0.346	0.664							0	-1.314	-0.532				0	-0.017	-0.369	0	-1.658	-0.522							0	0	-1.066		4.000					4664
4683	1	2	3																																						4683
4710	2	3	1	0.631	0.216	0.321	0.131	0.228	-0.183				0	-0.784	0.166				0	-0.804	0.615				0	0	-0.973	-0.256	0	0	0	0	-1.330							4710
4878	3	2	1	0.631	-0.440	0.321							0	0.427	0.690													0.065	0	0										4878
4889	2	3	1	0.759	-0.065	-0.710	0.131	0.463	0.199				0	0.730	0.341				0	-0.122	-0.172				0	0	1.240	1.029	0	0	0	0	-0.012		-0.057	0.155				4889
4951	1	2	3	-0.844	-0.534	-0.280							0	-1.541	-0.241				0	-1.486					0	0	0.111													4951
5018	3	2	1	-0.331	-0.159	-0.280							0	-0.633	-2.335	0	-0.265	-0.964	0	-0.384	-1.025	0	-0.311	-1.162	0	0	-4.000	-0.256	0	0	0	0	-0.012		-1.007	1.305				5018
5100	3	2	1	-3.343	1.433														0	0.036					0	0														5100
5119	2	1	3	-0.203	1.059	0.321							0	0.049	0.166	0	-0.265	0.851							0	0	0.969													5119
5128	1	2	3	-0.011	0.122	1.265										0	-0.389	-0.783	0	-0.909	0.287				0	0	-0.115	-0.128	0	0	0	0	0.603							5128
5182	3	2	1										0	-1.087	-0.765				0	-1.801	1.304				0	0	-2.824		0	0										5182
5188	2	1	3																																						5188
5200	3	2	1	1.334	0.967	1.047	2.316	-0.549	1.381				0	0.442	0.156	0	-3.372	0.469	0	1.775	-0.627	0	1.778	-0.674	0	0	-0.108				0	0	-0.111							5200
5201	2	3	1	-1.869	-0.534	0.063							0	-0.784	1.272				0		-0.106				0	0	0.518	-0.320	0	0	0	0	-0.100							5201
5204	3	1	2	0.246	-0.065	0.321							0	1.562	0.923	0	0.669	-0.329	0	1.033	-0.106	0	1.524	0.705	0	0	1.060	0.515	0	0	0	0	0.339		-0.230	1.409				5204
5220	3	2	1	-2.959	-0.065	-1.740							0	-1.390	0.108										0	0	-0.702	2.891	0	0	0	0	1.218							5220
5290	3	1	2	0.118	0.309	-0.795							0	0.578	0.923	0	0.607	0.064	0	0.823	0.287				0	0	0.021	0.900	0	0		0	-2.120							5290
5329	1	3	2	0.335	-0.078	-0.853							0	-0.163	-0.938							0	-0.482	1.133				-0.081	0	0	0	0	0.727		0.050	0.184				5329
5333	3	1	2	0.631	0.684	0.321				1.053	1.152	0.515	0	0.124	-0.474	0	-0.327	-1.357	0	0.088	-0.795				0	0	-0.747	-0.192	0	0	0	0	0.252		-1.266	-0.263				5333
5338	2	1	3	-0.203	0.028	0.063							0	1.714	0.981																									5338
5342	1	3	2	-0.716	0.403	-0.710							0	-1.995	-0.590										0	0	0.156					0	0.427							5342
5352	1	3	2	-0.523	-0.253	-0.195							0	-1.844	0.225				0	-1.696	0.353	0	-0.985	0.065	0	0	0.518	0.515	0	0	0	0	0.427		4.000	4.000				5352
5419	1	3	2	-2.446	0.309	-1.482				-0.977	0.388	-0.067	0	-1.617	-0.823										0	0	-0.566	-1.477	0	0	0	0	-1.242		-0.144	-0.890				5419
5446	1	2	3	-0.267	0.122	0.235							0	1.033	-1.056	0	0.918	1.516	0	0.298	-0.861				0	0	-0.386	-1.348	0	0	0	0	-1.681							5446
5494	1	3	2	-0.459	-1.283	-1.053				-0.211	-1.588	-1.619				0	0.109	1.063																						5494
5545	2	3	1											0.124	0.981													0.707				1.306		-4.000	0.469				5545
5612	2	3	1	2.746	0.684	1.866							0	1.335	0.864				0	-0.909	0.812	0	-1.964	1.239	0	0	2.821	0.386	0	0	0	0	-0.539							5612
5615	3	2	1	0.374	0.871	0.664							0	1.335	0.806				0	0.666	-0.270				0	0	0.382	-0.513	0	0	0	0	0.866							5615
5632	1	3	2	0.246	-0.065	-0.538																			0	0	-0.295	-4.000	0	0	0	0	-1.417							5632
5654	2	3	1	0.631	0.497	0.063							0	0.578	0.632													-0.128	0	0										5654
5701	3	1	2	-0.587	-1.096	-0.452																																		5701
5801	3	2	1	-2.895	-2.594	-2.255							0	-0.179	-0.183	0	-0.700	0.669										-2.183	0	0										5801
5808	3	2	1																																						5808
5883	1	2	3	-0.459	0.028	-0.366							0	-0.103	-0.241										0	0	0.021	-0.192	0	0	0	0	-0.451							5883
5950	1	2	3	0.566	0.122	-0.795	0.346	-0.322	0.486	0.364	0.658	0.321	0	-0.936	0.225	0	-1.945	-0.873	0	-0.436	-0.697	0	-0.189	-0.255	0	0	0.247	0.258	0	0	0	0	-0.715		0.374	0.155	0	0	0	5950
5993	2	3	1																									1.029	0	0		0	-4.000							5993
6109	1	2	3	-0.203	0.216	-0.967													0	0.508	0.287							-0.256	0	0										6109
6175	1	2	3	0.566	0.497	0.406							0	0.276	-0.008																									6175
6224	1	3	2	2.041	1.340	2.123							0	1.790	1.330													1.671	0											6224
6232	3	1	2	-0.267	-4.000	-0.375							0	-0.383	-0.130																									6232
6253	3	1	2	0.502	0.216	-0.710							0	0.276	0.515	0	0.109	-0.510							0	0	-0.295	-0.513	0	0	0	0	1.042		-0.144	-0.263				6253
6258	3	1	2	0.355	0.747	1.182										0	4.000	-4.000																						6258
6343	2	3	1	-0.780	-0.065	-0.795							0	-0.027	-1.521				0	0.771	1.567				0	0	0.382	-3.339	0	0	0	0	3.853							6343
6352	2	1	3	0.887	-0.627	-1.225							0	-1.011	-0.357				0	-1.433	-2.140				0	0	-1.289	-1.220	0	0			-1.242		-0.403	4.000				6352

Lab nr.	Provnr.			Aerobic microorganisms 30 °C			Aerobic microorganisms 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
6368	1	3	2	-0.011	-1.939	-0.366	-0.799	-1.029	-0.279				0	-0.633	0.806				0	-0.541	-0.828	0	-1.596	0.172	0	0	0.608	-0.063	0	0	0	0	-0.012		-1.697	-1.412				6368
6456	2	3	1	0.054	0.122	-0.967							0	0.049	-0.648	0	-0.451	-0.631	0	-0.384	-0.697				0	0	0.066	0.194	0	0	0	0	0.164		-1.438	**-3.711**				6456
6490	3	1	2	0.118	-0.159	-1.740							0	0.276	0.225													0.707	0	0	0	0	0.164		-0.316	-0.576				6490
6594	2	3	1	1.464	1.059	0.321							0	-1.238	0.283				0	1.033	1.501							0.194	0	0										6594
6658	3	1	2	0.310	-0.159	-0.881							0	-1.466	**-4.000**													0.515	0	0							0	0	0	6658
6686	2	3	1	-0.011	0.497	0.664	0.703	0.856	1.441				0		0.748							0	0.423	**2.519**	0	0	1.737					0	0.164		-0.057	0.469				6686
6728	2	1	3	**-4.000**	**-3.812**	-1.396								**-2.222**	-0.241				0	**-4.000**	-1.091				0	0	-0.747					0	0.339							6728
6762	2	3	1	0.182	-1.470	0.750							0	-0.027	**-2.975**										0	0	-0.069													6762
6801	2	3	1	0.689	0.219	-0.031										0	1.410	0.205	0	-0.420	-0.185				0	0	0.500					0	-0.558							6801
6885	2	3	1	-0.331	0.216	0.149							0	0.049	0.108										0	0	0.156	0.065	0	0	0	0	1.569		-0.230	-0.367	0	0	0	6885
6944	3	2	1				-0.298	-0.087	-0.948										0	**4.000**	1.075				0	0	0.247													6944
6958	3	2	1	-0.011	-0.534	-1.139							0	-1.238	-0.532													-1.605	0	0										6958
6971	3	2	1	1.400	0.122	0.921							0	1.260	0.515													-0.834	0	0										6971
6992	3	1	2	0.874	0.450	-0.375										0	**2.169**	-0.099							0	0	0.500	-0.976	0	0	0	0	**2.087**							6992
7182	3	2	1	0.438	-1.002	-0.109	0.203	-0.480	-0.374	0.479	0.703	0.418	0	-0.784	0.108	0	-1.074	**-2.961**	0	-1.014	-1.681				0	0	-1.560													7182
7191	2	1	3	0.246	-1.002	-1.396													0	1.768	-0.631	0	1.769	-0.682	0	0	-0.115				0	0								7191
7207	1	2	3	1.271	**2.838**	0.578							0	-0.709	**-2.161**													0.515	0	0					-0.403	-0.472				7207
7232	3	1	2	-0.126	-0.225	-1.328																																		7232
7242	1	3	2	**-2.592**	**-2.285**	-0.536							0	-0.572	-0.026																									7242
7248	2	1	3	**2.041**	1.902	1.093	**2.563**	1.249	**2.397**				0	1.033	1.272	0	1.914	1.607	0	1.033	1.862	0	1.157	0.492	0	0	1.331	1.286	0	0	0	0	0.954		0.461	0.469				7248
7253	2	3	1	0.631	0.497	1.007							0	0.578	0.981				0	0.246	1.042				0	0	-0.431	1.157	0	0	0	0	0.603							7253
7334	3	1	2	0.246	-0.065	-0.452													0	-0.594	0.189				0	0		-0.577	0	0	0	0	0.603							7334
7564	3	2	1	0.182	-0.534	0.406	0.060	-1.187	0.103	**-2.663**	**-2.486**	**-4.000**	0	-0.557	0.166				0	-1.119	-0.402	0	-1.352	-0.895	0	0	-0.611								-0.057	-0.367				7564
7617	1	2	3	**-4.000**	**4.000**	**3.721**														**2.405**					0						0		**4.000**		**2.883**	0.942				7617
7627	2	3	1	-1.933	**2.089**	0.063													0	-0.594	0.484							0.001	0	0										7627
7631	1	2	3	-0.331	-0.253	-0.023							0	-0.179	0.399	0	-0.016	0.790																						7631
7640	1	3	2	0.502	-1.189	-0.195	0.489	1.406	0.772	-1.398	-0.600	-0.843	0	1.033	-0.008	0	0.980	1.123	0	0.403	1.107	0	0.362	-1.215	0	0	-0.657	0.515	0	0	0	0	-0.451		0.719	**2.872**				7640
7688	1	3	2	-0.139	-0.159	0.406							0	-0.027	0.748	0	-0.327	-0.329	0	0.928	0.878	0	0.117	-0.682	0	0	-0.250	0.194	0	0	0	0	0.252		0.547	-0.576				7688
7728	3	1	2	-0.651	-0.721	-0.023	-1.371	0.385	1.155				0	-0.784	-1.172				0	-0.384	1.403	0	-0.740	**2.625**	0	0	**2.685**	1.864	0	0	0	0	1.042							7728
7750	1	2	3	-0.523	0.216	-0.195										0	-0.514	0.700										-0.770	0	0										7750
7825	1	3	2	1.342	**2.623**	1.436							0	1.812	1.167							0	0.037	-0.260	0	0	-0.173					0	0.181		0.366	**-2.468**				7825
7876	3	2	1	0.502	0.871	0.321							0	1.260	-0.357										0	0	-0.024	-1.669	0	0	0	0	-0.012		-1.007	-1.517				7876
7930	1	3	2	0.631	0.871	1.265							0	-0.481	0.981	0	1.354	-0.299	0	1.505	0.747	0	1.402	0.172	0	0	0.608	0.900	0	0	0	0	0.164		-0.057	0.051				7930
7940	1	2	3	-0.587	-0.721	-0.366										0	0.980	-0.904																						7940
7962	1	3	2	1.015	-0.065	0.664							0	0.730	1.039	0	0.233	0.155	0	-0.331	-0.500	0	-0.495	0.705	0	0	1.060	-1.412	0	0	0	0	1.130		**-2.129**	**-4.000**				7962
7968	1	3	2	0.951	0.216	0.750							0	0.578	1.097	0	-0.327	1.668	0	-0.122	1.435	0	0.362	0.492	0	0	0.879	-0.256	0	0	0	0	0.691		1.237	0.469				7968
7975	3	1	2																																				7975
7984	3	1	2	-0.395	-0.253	1.007							0	0.049	0.923													1.157	0	0							0	0	0	7984
8019	1	2	3	1.015	-0.159	1.007	0.203	-1.972	0.772	-0.709	0.074	**2.504**	0	**-4.000**	0.864	0	**-4.000**	-1.418	0	**-3.375**	-0.435	0	**-4.000**	**-4.000**	0	0	**-4.000**	-0.256	0	0	0	0	-0.100							8019
8068	1	2	3	0.502	0.871	0.578	0.203	1.092	0.677				0	0.881	1.330	0	0.171	0.609	0	-0.279	-0.008	0	1.035	0.492	0	0	0.879	-0.513	0	0	0	0	0.515		-0.403	0.573				8068
8105	3	2	1	0.246	0.122	-0.109													0	0.193	1.107				0	0	0.427	-0.770	0	0	0	0	-0.539							8105
8213	1	3	2	0.054	0.216	1.179							0	1.184	0.108										0	0	0.608	**2.442**	0	0							0	0	0	8213
8228	3	2	1	-1.485	-1.002	**-4.000**	-1.943	**-2.679**	**-2.668**				0	-1.541	-0.997	0	-0.638	0.216											0	0										8228
8260	1	2	3	-0.523	0.028	-0.366							0	-0.406	0.515	0	-0.202	0.609	0	-0.174	-0.533	0	-0.495	-0.308	0	0	0.292	-0.449	0	0	0	0			-0.316	0.364				8260
8313	2	3	1	-0.171	-0.272	-0.658							0	-1.708	-1.108				0	-0.746	-1.307				0	0	-1.022	0.277	0	0	0	0	0.023		-0.066	0.113				8313
8333	2	3	1	0.695	**4.000**	0.406							0	0.578	**-2.626**				0	0.298	0.911							-1.798	0	0						-0.489	0.991				8333
8397	1	2	3	0.983	0.220	0.502							0	0.170	**-4.000**										0	0	-0.614	-0.798	0	0	0	0	-0.557		-0.092	-0.636				8397
8430	3	2	1	-1.677	-0.253	-1.053							0	-0.557	**-3.034**	0	-0.078	0.458							0	0	-0.837					0	-1.945							8430
8435	1	3	2	1.036	0.219	0.245	1.084	0.610	-0.924				0	-0.163	0.156	0	-0.924	-0.506	0	-0.708	-0.627	0	-1.504	-0.269	0	0	0.235	1.021	0	0	0	0	0.727		1.128	0.108				8435
8523	2	3	1	1.336	1.902	0.406							0	**2.168**	1.039										0	0	-0.295				0	0	0.076							8523
8528	2	3	1	**-4.000**	**-4.000**	**-4.000**							0	-0.709	**-2.685**																									8528
8568	3	2	1	0.246	**2.370**	0.836							0	1.411	0.457				0	0.403	-1.123							-0.449	0	0						1.669	**2.140**				8568
8578	3	2	1	0.246	-0.534	-0.881													0						0	0														8578
8626	3	2	1	**-3.407**	**-3.999**	1.951	-0.584	0.856	0.677				0	-0.557	**-2.743**				0	1.768	1.403	0	1.769	**2.625**	0	0	**2.685**													8626
8628	2	1	3	0.246	0.216	-0.538	-0.584	0.856	-1.426				0	-0.406	-1.521	0	0.669	-0.964	0	-0.069	-0.763	0	-0.128	-0.308	0	0	0.202	0.900	0	0	0	0	0.603		-0.489	-0.890				8628
8657	3	2	1	0.182	0.216	-0.109							0	0.578	0.399																									8657

Lab nr.	Provnr.			Aerobic microorganisms 30 °C			Aerobic microorganisms 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-neg bacteria in dairy prod.			Lab nr.
	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	A	B	C	
8696	2	1	3																																					8696
8734	1	2	3	-0.011	-1.658	-0.366				0.325	0.074	0.176	0	-0.784	-0.590	0	-1.198	-1.932																					8734
8742	3	2	1	-0.331	-0.627	-0.967													0	-0.226	0.484	0	-0.556	1.132	0	0	1.421				0	0	0.427							8742
8756	3	1	2	**2.169**	**4.000**	1.093							0	0.503	0.923										0	0	0.427	**4.000**				0	0.779		-1.093	0.364				8756
8766	3	1	2	-0.075	0.122	-0.366							0	-0.027	-1.172										0	0	-0.476	-0.385	0	0	0	0	0.252		-0.748	-0.785				8766
8891	3	2	1	-1.972	-1.189	-0.624				-0.150	0.703	-0.018	0	-0.481	-1.986	0	-1.759	0.609							0	0	-0.115	-0.038	0	0	0	0	-0.276							8891
8909	2	3	1	0.887	0.497	0.063							0	0.276	0.574	0	0.171	-0.601							0	0	**-2.373**	0.258	0	0	0	0	1.394		0.374	-0.367				8909
8918	3	1	2	-0.395	1.246	0.149				0.517	1.332	0.176	0	0.200	-0.357				0	-0.646	-1.025				0	0	-0.747	1.414	0	0	0	0	0.252							8918
9003	2	3	1	0.124	0.219	0.394							0	1.003	0.156				0	-0.420	-0.157				0	0	0.627				0	0	-1.918							9003
9007	2	3	1	-0.459	-0.721	0.063							0	**-2.147**	-0.357				0	-0.751	-1.091				0	0	0.382				0	0	**-2.735**							9007
9025	1	3	2	0.054	**4.000**	1.780							0	**2.092**	0.283																						0	0	0	9025
9034	2	3	1	-1.036	-0.065	-0.538	-1.156	-0.951	-0.279				0	-0.709	0.341										0	0	-0.747													9034
9078	2	3	1	0.502	-0.534	1.265							0	1.941	0.050																									9078
9217	3	2	1	-0.716	-0.534	0.321							0	-1.844	0.108													-0.706	0	0	0	0	-0.627		-0.230	-0.890				9217
9429	1	2	3										0	-0.027	0.632	0	0.171	-0.510	0	0.036	-0.763	0	-0.556	-0.682	0	0	-0.115								-0.057	0.155				9429
9436	2	3	1	0.631	-0.065	-0.967							0	-0.179	-1.870	0	-1.198	1.002	0	-1.066	1.435	0	-0.923	-0.042	0	0	-0.295	-0.128	0	0	0	0	**-2.208**		-0.489	-0.890				9436
9453	3	1	2	-0.395	0.497	-0.624				-0.096	0.254	0.079	0	0.957	0.574													0.772	0	0	0	0	0.164		0.633	-1.726				9453
9512	1	2	3	-1.036	-1.002	-0.881							0	0.049	-0.241																									9512
9559	3	2	1	0.374	-0.065	-0.280	0.131	0.385	-0.852	0.249	0.029	0.224	0	0.200	0.806				0	0.141	1.468				0	0	-0.927	1.992	0	0	0	0	1.218							9559
9662	2	1	3	0.246	-0.440	0.149							0	0.124	1.039	0	0.109	-0.299	0	-0.226	-1.255				0	0	-0.295	1.671	0	0	0	0	-0.803		-0.575	0.155				9662
9747	3	1	2	-0.972	**4.000**	-1.911								**-3.736**	**-3.266**													-1.155													9747
9890	3	1	2	1.400	0.871	-0.452	0.846	0.228	0.295				0	**-2.979**	-0.648				0	-0.541	0.583				0	0	1.556	-1.091	0	0	0	0	-0.539							9890
9903	2	1	3	-0.331	-1.096	-1.310							0	-0.709	-1.986										0	0	-0.792	-0.642	0	0	0	0	**-3.789**		**-2.215**	1.618				9903
9950	3	2	1				-0.012	-0.558	0.199	0.249	0.703	0.564							0	-1.014	-1.091				0	0	-0.747	0.194	0	0										9950

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

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

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

The National Food Agency's PT program offers

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

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

The National Food Agency's reference material

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

More information is available on our website: www.livsmedelsverket.se/en/rm-micro