

Proficiency testing Food Microbiology

April 2024

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Abbreviations

Media

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

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

TEMPO YM	TEMPO® Yeast/Mould
TGE	Tryptone glucose extract agar
TS	Tryptose sulphite agar
TSA	Tryptic soya agar
TSC	Tryptose sulphite cycloserine agar
TSBY	Tryptone soya broth with yeast extract
XLD	Xylose lysine deoxycholate agar
VIDAS CAM	VIDAS® Campylobacter
VIDAS ECPT	VIDAS® UP E. coli O157 (including H7)
VIDAS LMX	VIDAS® Listeria monocytogens Xpress
VRB	Violet red bile agar
VRBG	Violet red bile glucose agar
YGC	Yeast extract glucose chloramphenicol agar

Organisations

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

Analyses in this PT round

Quantitative analyses

Aerobic microorganisms, 30 °C

Psychrotrophic microorganisms

Enterobacteriaceae

Escherichia coli

Presumptive *Bacillus cereus*

Coagulase-positive staphylococci

Lactic acid bacteria

Clostridium perfringens

Anaerobic sulphite-reducing bacteria

Aerobic microorganisms in fish products

H₂S-reducing bacteria in fish products

Yeasts

Moulds

Method

Reporting of results and method information

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

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

Standard deviation and assigned value

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

A robust statistical approach is used to determine the mean value and standard deviation. Algorithm A with iterated scale as described in ISO 13528:2022 [1] is used to determine the robust mean (m_{PT}) and robust standard deviation (s_{PT}) of the participants’ results. Results that are obviously erroneous are excluded prior to determining m_{PT} and s_{PT} (blunder removal). For evaluated parameters, the assigned value consists of m_{PT} . It is regarded as the true, normative value.

For small datasets, there is an increased uncertainty associated with determining the robust mean (m_{PT}) and robust standard deviation (s_{PT}) of the participants’ results. Therefore, when fewer than 12 participants have reported evaluated results, the statistical measures for performance evaluation will be provided *only as an information* to the participants.

Outliers

Outliers are results that deviate from the other results in a way that cannot be explained by normal variation. Results within $m_{PT} \pm 3s_{PT}$ are considered acceptable, whereas results outside this interval are considered as outliers. When fewer than 12 participants have reported results, as well as in some individual cases, subjective adjustments are made to set acceptance limits based on prior knowledge of the samples contents.

Results from different methods

Non-robust median values (*Med*) and standard deviations (*s*) are calculated to assist in the evaluation of the results from different methods. These are shown in tables in the report, in connection with the respective analyses. In these instances, *Med* and *s* are calculated from the respective method groups' results, with outliers and false results excluded. For method groups with fewer than 5 results, only the number of false results and outliers are provided.

Measurement uncertainty for the assigned values

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

$$u_{PT} = 1.25 \times \frac{s_{PT}}{\sqrt{n}}$$

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

$$u_{PT} < 0.3s_{PT}$$

Z-scores

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

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

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

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

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

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

Table legends

- N number of participants that reported results for the analysis
- n number of participants with satisfactory result (false results and outliers excluded)
- m_{PT} assigned value, robust mean value in \log_{10} cfu ml⁻¹
- s_{PT} robust standard deviation
- u_{PT} standard uncertainty of the assigned value

- F number of false positive or false negative results
- $<$ number of low outliers
- $>$ number of high outliers
- results deviating more than $1 s_{PT}$ from m , or unusually many deviating results.

Figure legends

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

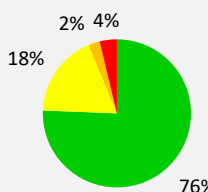
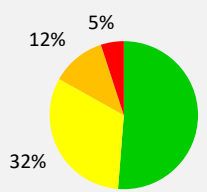
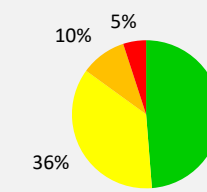
Results

General outcome

Samples were sent to 167 participants: 39 in Sweden, 114 in Europe, and 14 outside of Europe. In total, 160 participants (96 %) reported results, of which 98 (61 %) provided at least one result with a remark.

Individual results are listed in Appendix 1. Z-scores for individual results are listed in Appendix 2.

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

	Sample A				Sample B				Sample C			
% participants with												
Microorganisms	<i>Bacillus cereus</i> <i>Enterococcus durans</i> <i>Escherichia coli</i> <i>Hafnia alvei</i> <i>Staphylococcus aureus</i>				<i>Aeromonas hydrophila</i> <i>Candida glabrata</i> <i>Clostridium perfringens</i> <i>Penicillium roquefortii</i> <i>Staphylococcus aureus</i>				<i>Aeromonas hydrophila</i> <i>Candida glabrata</i> <i>Clostridium perfringens</i> <i>Penicillium roquefortii</i> <i>Staphylococcus aureus</i>			
Analysis	Target organism	N	F	X	Target organism	N	F	X	Target organism	N	F	X
Aerobic micro-organisms 30 °C	All	148	0	13	All	148	0	7	All	148	0	4
Psychrotrophic microorganisms	All	20	1	0	All	20	4	0	All	20	6	0
Enterobacteriaceae	<i>E. coli</i> <i>H. alvei</i>	125	0	7	(<i>A. hydrophila</i>)	122	49	0	(<i>A. hydrophila</i>)	122	50	0
<i>Escherichia coli</i>	<i>E. coli</i>	95	3	7	-	94	0	0	-	94	2	0
Preumptive <i>Bacillus cereus</i>	<i>B. cereus</i>	98	0	4	(<i>S. aureus</i>)	95	2	0	(<i>S. aureus</i>)	96	5	0
Coagulase-positive staphylococci	<i>S. aureus</i>	87	1	6	<i>S. aureus</i>	89	8	6	<i>S. aureus</i>	87	7	4
Lactic acid bacteria	<i>E. durans</i>	44	6	2	(<i>S. aureus</i>) (<i>C. glabrata</i>)	44	15	0	(<i>S. aureus</i>) (<i>C. glabrata</i>)	46	15	0
<i>Clostridium perfringens</i>	-	48	1	0	<i>C. perfringens</i>	46	2	2	<i>C. perfringens</i>	47	1	3
Anaerob. sulphite-red. bacteria	-	56	1	0	<i>C. perfringens</i>	53	1	4	<i>C. perfringens</i>	54	1	4
Aerobic microorg. in fish products	All	21	0	0	All	21	0	3	All	21	0	1
H ₂ S-prod. bacteria in fish products	<i>H. alvei</i>	18	1	1	(<i>A. hydrophila</i>)	18	0	0	(<i>A. hydrophila</i>)	18	0	0
Yeasts	-	126	5	0	<i>C. glabrata</i>	123	2	11	<i>C. glabrata</i>	124	0	10
Moulds	-	124	2	0	<i>P. roquefortii</i>	122	6	3	<i>P. roquefortii</i>	123	5	3

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

□ The results are not evaluated.

Aerobic microorganisms, 30 °C

Sample A

All strains in the sample are capable of forming colonies on PCA and were present in similar concentrations.

In total, 148 participants reported results. Ten low and three high outliers were reported.

Sample B

The strains of *A. hydrophila* and *S. aureus* were present in the highest concentrations.

In total, 148 participants reported results. Five low and two high outliers were reported.

Sample C

The sample was identical to sample B.

In total, 148 participants reported results. Two low and two high outliers were reported.

General remarks

Most participants followed either NMKL 86:2013, ISO 4833-1:2013 or used 3M Petrifilm AC. The withdrawn NMKL 86:2006 and ISO 4833:2003 were still used by ten and six participants, respectively. ISO 4833-1:2013 was last reviewed by ISO in 2019 and remains current. An amendment with a clarification on the scope of the method is available (ISO 4833-1:2013/Amd 1:2022). NMKL 86:2013 was last reviewed by NMKL in 2022 and remains current.

Both NMKL 86:2013 and ISO 4833-1:2013 are based on incubation on PCA or MPCA at 30 °C for 72 h. Users of Petrifilm AC can use different incubation times/temperatures, depending on the method validation. For example, AOAC[®] prescribes incubation at 35 °C for 48 h while AFNOR prescribes 30 °C for either 48 h or 72 h, depending on which product that is analysed.

Most participants incubated on either PCA or Petrifilm AC. Incubation on MPCA was mainly done by laboratories within the dairy industry. Incubation on TSA was mainly done by users of a company-specific method.

A few participants used TEMPO AC, which is based on MPN (Most Probable Number). With this method, the sample is incubated in a card that contains different-sized wells. A substrate in the medium emits fluorescence when hydrolysed by the microorganisms. The number of microorganisms is determined statistically by the number and size of the fluorescing wells.

One participant followed IDF 100B:1991. This has been withdrawn and replaced by ISO 4833-1:2013 and ISO 4833-2:2013.

One participant followed ISO 13559:2002/IDF 153:2020, which is adapted for the enumeration of contaminating microorganisms in butter, fermented milks and fresh cheese. The method is similar to

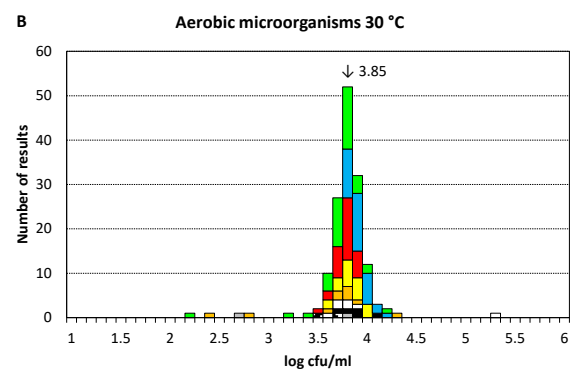
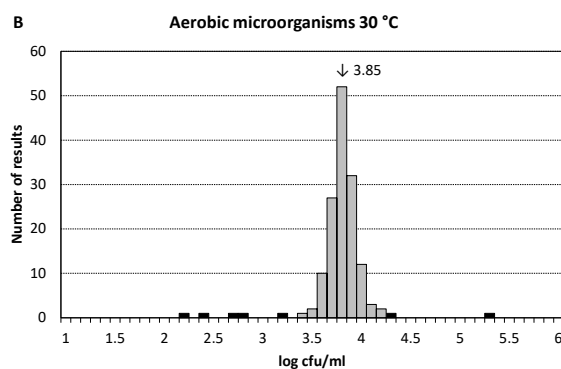
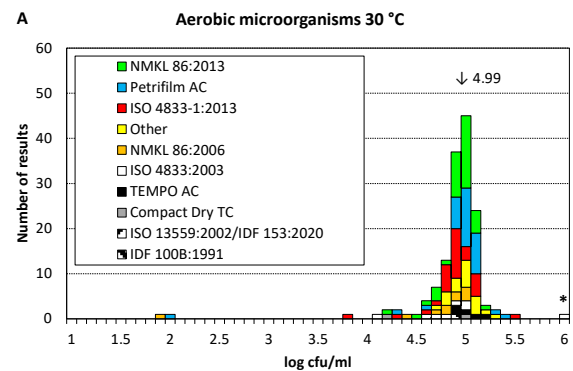
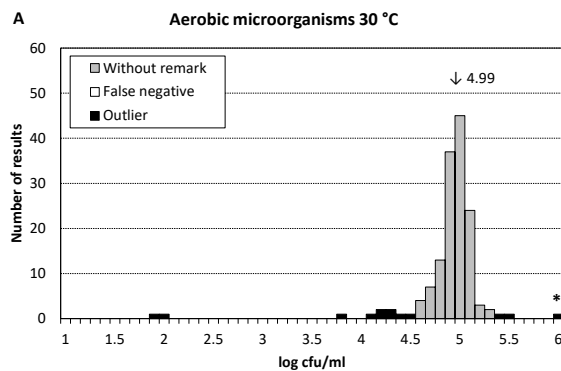
e.g. NMKL 86 and ISO 4833-1, but incubation is on SFA instead of PCA. Since the participant incubated on PCA, the results are as an exception included in the evaluation, but the parameter is otherwise to be performed in PT Food October round.

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

Method	Sample A							Sample B							Sample C						
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>
All results	148	135	4.99	0.14	0	10	3	148	141	3.85	0.13	0	5	2	148	144	3.87	0.14	0	2	2
NMKL 86:2013	39	37	5.02	0.12	0	2	0	39	37	3.81	0.13	0	2	0	39	38	3.83	0.12	0	0	1
Petrifilm AC ¹	34	31	5.04	0.11	0	2	1	34	34	3.96	0.10	0	0	0	34	34	3.97	0.11	0	0	0
ISO 4833-1:2013	30	27	4.94	0.13	0	2	1	30	30	3.83	0.09	0	0	0	30	30	3.81	0.09	0	0	0
Other	19	19	5.03	0.14	0	0	0	19	19	3.86	0.11	0	0	0	19	19	3.88	0.11	0	0	0
NMKL 86:2006	10	8	4.95	0.11	0	2	0	10	7	3.80	0.11	0	2	1	10	9	3.80	0.13	0	1	0
ISO 4833:2003	7	5	4.97	0.14	0	1	1	7	6	3.80	0.11	0	0	1	7	6	3.82	0.16	0	0	1
TEMPO AC	5	5	5.04	0.15	0	0	0	5	5	3.96	0.14	0	0	0	5	5	4.00	0.12	0	0	0
Compact Dry TC	2	1	-	-	0	1	0	2	1	-	-	0	1	0	2	1	-	-	0	1	0
ISO 13559:2002/ IDF 153:2020	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
IDF 100B:1991	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

¹ "Petrifilm AC" includes one participant that incubated on Petrifilm RAC.



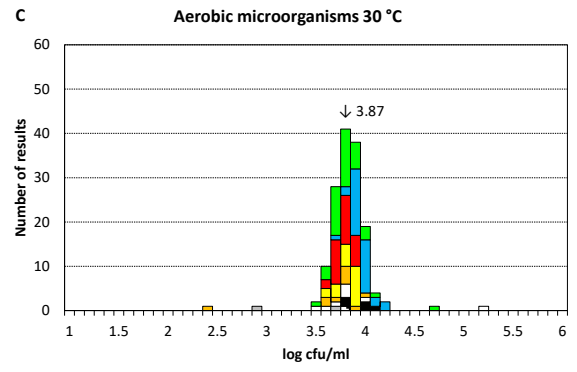
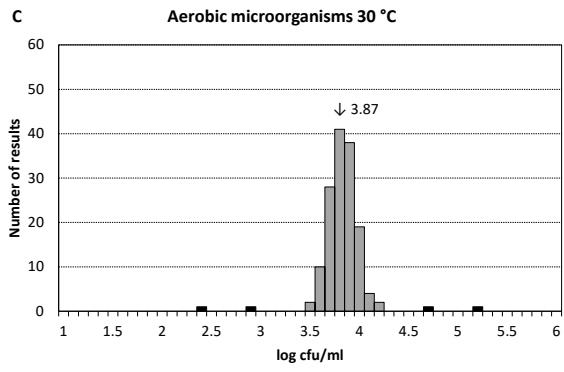


Figure 1. Results from analysis of aerobic microorganisms, 30 °C.

Psychrotrophic microorganisms

Sample A

In total, 20 participants reported results. One false-negative result was reported.

Sample B

In total, 20 participants reported results. Four false-negative results were reported.

Note: The measurement uncertainty of the assigned value is not negligible. The evaluation of the results could therefore be affected. Z-scores should be interpreted with caution, and only be used as a guidance.

Sample C

The sample was identical to sample B.

In total, 20 participants reported results. Six false-negative results were reported.

Note: The measurement uncertainty of the assigned value is not negligible. The evaluation of the results could therefore be affected. Z-scores should be interpreted with caution, and only be used as a guidance.

General remarks

In summary, the results are difficult to evaluate. This is mainly due to the differences between the methods, but also due to the fact that participants often used modified or withdrawn methods. In addition, several methods were used only by 1–2 participants.

Users of NMKL 86:2013 typically incubated for 10 days at 6.5 °C, but 20 h at 17 °C followed by 3 days at 7 °C was also used. For psychrotrophic microorganisms in milk, ISO 6730:2005/IDF 101:2005 stipulates incubation at 6.5 °C. The other method for milk, ISO 8552:2004/IDF 132:2004, instead estimates the number of psychrotrophic microorganisms in a rapid method based on incubation at 21 °C. Both of these have been replaced by ISO 17410:2019, which stipulates 6.5 °C as the primary incubation temperature.

NMKL 74:2000 was used by one participant; the method has been replaced by NMKL 86:2013. NMKL 184 was also used only by one participant. This method is mainly adapted for analysis of aerobic count and specific spoilage organisms in fish and fish products.

Fourteen of the 21 participants incubated on PCA, two on MPCA, two on Petrifilm AC and two on Long & Hammer agar.

Table 3. Results from analysis of psychrotrophic microorganisms.

Method	Sample A							Sample B							Sample C						
	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>
All results	20	19	4.58	0.35	1	0	0	20	16	2.99	0.70	4	0	0	20	14	2.92	0.78	6	0	0
NMKL 86:2013	11	10	4.43	0.40	1	0	0	11	7	2.75	0.90	4	0	0	11	6	2.19	0.86	5	0	0
ISO 17410:2019	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
ISO 8552:2004/ IDF 132:2004	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
ISO 6730:2005/ IDF 101:2005	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
NMKL 184:2006	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
Petrifilm AC	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
Other	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
NMKL 74:2000	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	0	-	-	1	0	0

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

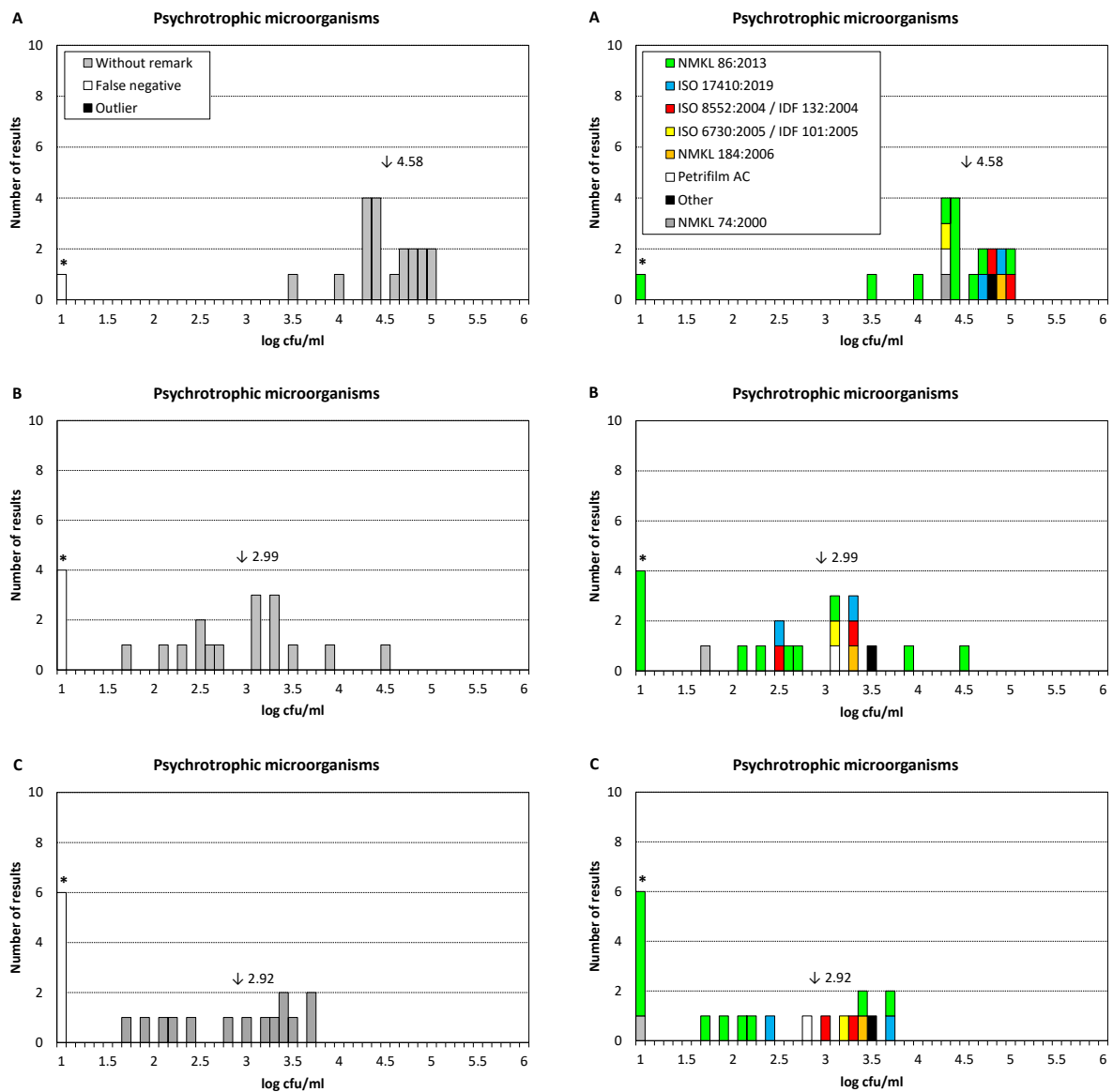


Figure 2. Results from analysis of psychrotrophic microorganisms.

Enterobacteriaceae

Sample A

The strains of *E. coli* and *H. alvei* were target organisms. On VRB, both form typical red colonies that are surrounded by a bile salt precipitation zone. Both strains are oxidase-negative. *H. alvei* was present in a slightly higher concentration than *E. coli*.

Results in the lower acceptance range may be due to problems with detecting *H. alvei*, as it is sometimes associated with low outliers in previous PT rounds.

In total, 125 participants reported results. Five low and two high outliers were reported.

Sample B

No target organism was present in the sample. The oxidase-positive strain of *A. hydrophila* was present as a false-positive organism for the analysis. On VRBG, it forms purple colonies with a small bile salt precipitation zone. It may also form colonies on other similar media, for example Compact Dry ETB and Petrifilm EB.

In total, 122 participants reported results. Forty-nine (49) false-positive results were reported.

False-positive results were reported by almost all of the methods that were used and were distributed more or less proportionally among the methods. The median of the false-positive results was $2.58 \log_{10} \text{ cfu ml}^{-1}$, which is somewhat less than the concentration of *A. hydrophila* in the sample. Participants that reported performing a confirmation test appear to have reported false-positive results to a lesser extent.

Sample C

The sample was identical to sample B.

In total, 122 participants reported results. Fifty (50) false-positive results were reported.

For the false-positive results, similar observations as for sample B were made. Participants that reported false-positive results for sample B, also in general reported false-positive results for sample C.

General remarks

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

The most common methods were NMKL 144:2005 or a method with Petrifilm EB. Many participants also followed ISO 21528-2:2017 or – to a lesser extent – the withdrawn ISO 21528-2:2004 and ISO 21528-1:2004. ISO 21528-2:2017 is based on colony-count, whereas ISO 21528-1:2017 is based on

MPN. The latter method is recommended when the expected level of Enterobacteriaceae is lower than 100 cfu g⁻¹. Both ISO standards were last reviewed by ISO in 2022 and remain current.

Confirmation was performed by 57 % of the participants, and most often consisted of an oxidase test. False results were reported both by participants that performed a confirmation and those that did not. Still, the majority (69 %) of the 99 false results for samples B and C were reported by participants that did not perform a confirmation.

Table 4. Results from analysis of Enterobacteriaceae.

Method	Sample A							Sample B							Sample C						
	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>
All results	125	118	4.53	0.14	0	5	2	122	73	-	-	49	-	-	122	72	-	-	50	-	-
NMKL 144:2005	50	48	4.55	0.14	0	1	1	50	36	-	-	14	-	-	50	37	-	-	13	-	-
Petrifilm EB	33	31	4.58	0.08	0	2	0	31	15	-	-	16	-	-	31	15	-	-	16	-	-
ISO 21528-2:2017	15	15	4.55	0.18	0	0	0	15	9	-	-	6	-	-	14	8	-	-	6	-	-
Other	9	9	4.58	0.15	0	0	0	8	3	-	-	5	-	-	9	2	-	-	7	-	-
ISO 21528-2:2004	6	5	4.51	0.05	0	1	0	6	4	-	-	2	-	-	6	4	-	-	2	-	-
ISO 21528-1:2004	5	4	-	-	0	0	1	5	3	-	-	2	-	-	5	3	-	-	2	-	-
TEMPO EB	5	5	4.48	0.20	0	0	0	5	3	-	-	2	-	-	5	3	-	-	2	-	-
Compact Dry ETB	1	0	-	-	0	1	0	1	0	-	-	1	-	-	1	0	-	-	1	-	-
ISO 21528-1:2017	1	1	-	-	0	0	0	1	0	-	-	1	-	-	1	0	-	-	1	-	-

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

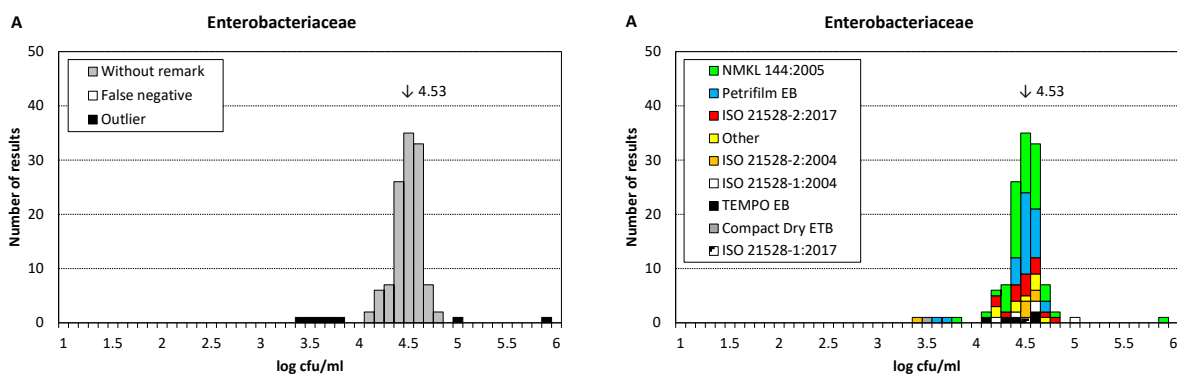


Figure 3. Results from analysis of Enterobacteriaceae.

Escherichia coli

Sample A

The strain of *E. coli* was target organism. On TSA/VRB, it forms typical red colonies surrounded by a bile salt precipitation zone. The strain is positive for indole production and β -glucuronidase activity, and produces gas in LTL5B.

In total, 95 participants reported results. Six low and one high outlier were reported, as well as three false-negative results.

Sample B

No target organism was present in the sample. At the Swedish Food Agency, no colonies were observed on TSA/VRB.

In total, 94 participants reported results. All reported results were correct negative.

Sample C

The sample was identical to sample B.

In total, 94 participants reported results. Two false-positive results were reported.

General remarks

Most participants (45 %) used a method based on 3M™ Petrifilm™, either Petrifilm EC/CC or Petrifilm SEC. NMKL 125:2005 and ISO 16649-2:2001 were in comparison used by 22 % and 13 % of the participants, respectively. A few of the participants that followed NMKL 125:2005 and ISO 16649-2:2001 used media other than those stipulated by the respective standards, for example Petrifilm EC/CC or Brilliance EC/CC. 16649-2:2001 was last reviewed by ISO in 2019 and remains current.

Three participants followed ISO 7251:2005, which is an MPN-based method for the detection *E. coli*. It was last reviewed by ISO in 2019 and remains current. An amendment with performance testing of culture media and reagents was published in 2023.

The definition of *E. coli* differs between methods, which may sometimes cause problems with non-typical strains. Users of ISO 16649-2:2001 typically count as *E. coli* those bacteria that form blue (i.e. β -glucuronidase positive) colonies on TBX, without further confirmation. Similarly, Petrifilm EC/CC and Petrifilm SEC are also based on media that detect *E. coli* by the activity of β -glucuronidase. The latter media however also have a plastic film that facilitates detection of gas production due to lactose fermentation. In comparison, users of NMKL 125:2005 typically count as *E. coli* those bacteria that form typical dark red colonies surrounded by a red precipitation zone on VRB. Users often, but not always, perform further confirmation test, for example tests for the production of gas and indole. Other media, e.g. Brilliance™ EC/CC, facilitate detection and distinction between coliform bacteria and

E. coli, based their differences in β -glucuronidase and β -galactosidase activity. Despite these differences, altogether, the results from the different methods and media were similar.

Table 5. Results from analysis of *Escherichia coli*.

Method	Sample A							Sample B							Sample C						
	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>
All results	95	85	3.97	0.26	3	6	1	94	94	-	-	0	-	-	94	92	-	-	2	-	-
Petrifilm EC/CC	24	21	4.05	0.13	0	3	0	22	22	-	-	0	-	-	22	21	-	-	1	-	-
NMKL 125:2005	21	20	4.11	0.16	1	0	0	21	21	-	-	0	-	-	21	21	-	-	0	-	-
Petrifilm SEC	18	17	4.07	0.13	0	1	0	18	18	-	-	0	-	-	18	18	-	-	0	-	-
ISO 16649-2:2001	13	10	3.81	0.25	1	2	0	13	13	-	-	0	-	-	13	13	-	-	0	-	-
Other	8	8	3.62	0.21	0	0	0	8	8	-	-	0	-	-	8	8	-	-	0	-	-
TEMPO EC	4	4	-	-	0	0	0	4	4	-	-	0	-	-	4	4	-	-	0	-	-
ISO 7251:2005 (MPN)	2	1	-	-	0	0	1	3	3	-	-	0	-	-	3	3	-	-	0	-	-
Compact Dry EC	2	2	-	-	0	0	0	2	2	-	-	0	-	-	2	1	-	-	1	-	-
Petrifilm REC	1	1	-	-	0	0	0	1	1	-	-	0	-	-	1	1	-	-	0	-	-
NMKL 96:2009 (MPN)	1	1	-	-	0	0	0	1	1	-	-	0	-	-	1	1	-	-	0	-	-

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

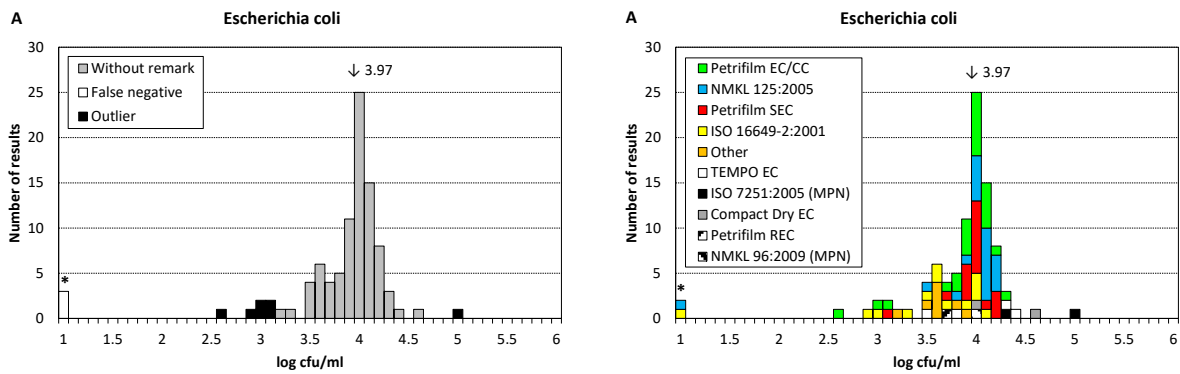


Figure 4. Results from analysis of *Escherichia coli*.

Presumptive *Bacillus cereus*

Sample A

The strain of *B. cereus* was target organism. On BA, it forms typical grey colonies surrounded by a zone of haemolysis. On BcsA, it forms typical blue colonies surrounded by a blue zone of precipitation.

In total, 98 participants reported results. Four low outliers were reported.

Sample B

No target organism was present in the sample. At the Swedish Food Agency, two types of atypical colonies were observed on BcsA/BA. Notably, no blue colonies were observed on BcsA.

In total, 95 participants reported results. Two false-positive results were reported.

Sample C

The sample was identical to sample B.

In total, 96 participants reported results. Five false-positive results were reported.

General remarks

Most participants followed either NMKL 67:2010 (34 %) or ISO 7932:2004 (30 %). The new NMKL 67:2021 – which replaces NMKL 67:2010 – was in contrast only followed by 18 participants (18 %).

ISO 7932:2004 was last reviewed by ISO in 2021 and remains current. An amendment with optional test was published in 2020. The new version of NMKL 67 stipulates a different primary incubation medium. Notably, users of the new NMKL 67:2021 in total only reported one deviating result, whereas users of the old NMKL 67:2010 in total reported eight false results and outliers.

The most common selective media were MYP and BcsA. On BcsA, presumptive *B. cereus* form bluish colonies that are surrounded by a blue zone of precipitation, due to lecithinase activity on egg yolk present in the medium. On MYP, presumptive *B. cereus* form large pink colonies that are normally surrounded by a zone of precipitation, again as a consequence of lecithinase activity. MYP and BcsA were often used together with a non-selective medium, typically BA. On BA, *B. cereus* forms large, irregular grey colonies, surrounded by a distinct zone of haemolysis.

Other selective media that were used included Brilliance™ *B. cereus* agar (CBC), Compact Dry X-BC and BACARA™, and PEMBA. Brilliance™ *B. cereus* contains the substrate X-Gluc, which is cleaved by *B. cereus* β -glucuronidase. Colonies of *B. cereus* are therefore white with a blue/green centre on this medium. Similarly, the chromogenic and selective agents in Compact Dry X-BC cause *B. cereus* to form blue/green colonies, whereas other bacteria normally form white colonies. Compact Dry X-BC may give somewhat lower results compared to the reference method ISO 7932:2004, something that is mentioned in both the NordVal 045 and MicroVal 2011-LR41 validations. PEMBA is almost identical to BcsA in

its composition, and was similarly often used together with BA. In contrast, Brilliance™ *B. cereus* and Compact Dry X-BC were most often used as standalone media.

Overall, the results for the identical samples A and C were highly similar.

Table 6. Results from analysis of presumptive *Bacillus cereus*.

Method	Sample A							Sample B							Sample C						
	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>
All results	98	94	4.32	0.29	0	4	0	95	93	-	-	2	-	-	96	91	-	-	5	-	-
NMKL 67:2010	33	31	4.41	0.28	0	2	0	32	30	-	-	2	-	-	32	28	-	-	4	-	-
ISO 7932:2004	29	27	4.24	0.28	0	2	0	27	27	-	-	0	-	-	28	28	-	-	0	-	-
NMKL 67:2021	18	18	4.24	0.23	0	0	0	18	18	-	-	0	-	-	18	17	-	-	1	-	-
Other	13	13	4.31	0.40	0	0	0	13	13	-	-	0	-	-	13	13	-	-	0	-	-
TEMPO BC	2	2	-	-	0	0	0	2	2	-	-	0	-	-	2	2	-	-	0	-	-
Compact Dry X-BC	2	2	-	-	0	0	0	2	2	-	-	0	-	-	2	2	-	-	0	-	-
RAPID®B.cereus	1	1	-	-	0	0	0	1	1	-	-	0	-	-	1	1	-	-	0	-	-

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

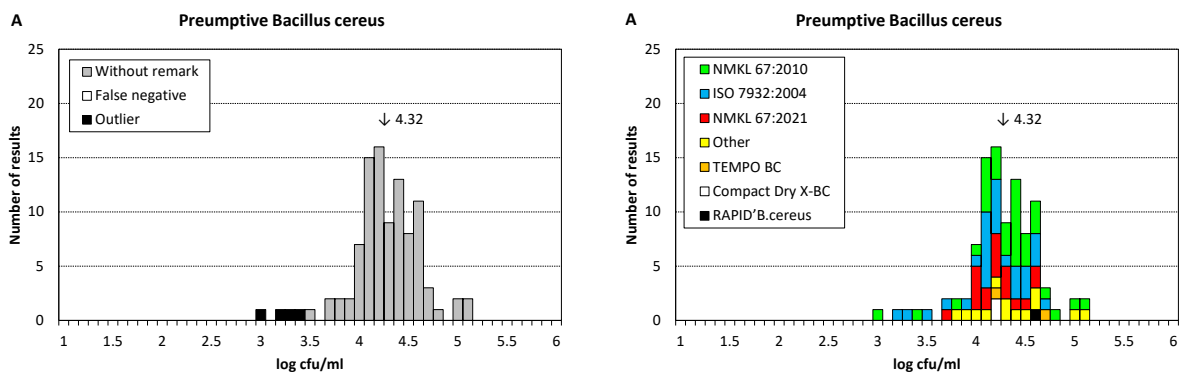


Figure 5. Results from analysis of presumptive *Bacillus cereus*.

Coagulase-positive staphylococci

Sample A

The strain of *S. aureus* was target organism. On RPFAs, it forms typical grey colonies surrounded by a precipitation zone.

In total, 87 participants reported results. Five low and one high outlier were reported, as well as one false-negative result.

Sample B

The strain of *S. aureus* (not identical to that in sample A) was target organism. It forms typical colonies on RPFAs, but the surrounding coagulase zone is often very weak, and may appear to be missing completely.

In total, 89 participants reported results. Five low and one high outlier were reported, as well as eight false-negative results.

Sample C

The sample was identical to sample B.

In total, 87 participants reported results. Three low and one high outlier were reported, as well as seven false-negative results.

General remarks

Most participants (41 %) followed NMKL 66:2009, where incubation is done either with BP and/or RPFAs. In comparison, ISO 6888-1:2021 stipulates BP, whereas 6888-2:2021 stipulates the use of RPFAs. By far however, most participants that followed an ISO method referenced the withdrawn versions ISO 6888-1:1999 and ISO 6888-2:1999. Amendments with clarifications to ISO 6888-1:2021 and ISO 6888-2:2021 were published in 2023.

Four participants used a method with TEMPO STA. Three of these participants reported low outliers or false-negative results for the identical samples A and C. For sample A, the results were however similar to other methods. This has been seen previously for this strain, and likely reflects difficulties with detecting this particular strain of *S. aureus* with TEMPO STA.

Most participants (47 %) incubated on BP. On this medium, *S. aureus* form characteristic convex, shiny colonies that have a grey/black colour due to reduction of tellurite in the medium. The colonies are usually surrounded by a clear zone, due to proteolysis of egg yolk in the medium (lecithinase activity). An opaque halo may also form near the colony, due to precipitation caused by lipase activity. Participants that used BP typically perform a confirmation based on coagulase activity, for example a tube coagulase test or the use of RPFAs as a secondary medium.

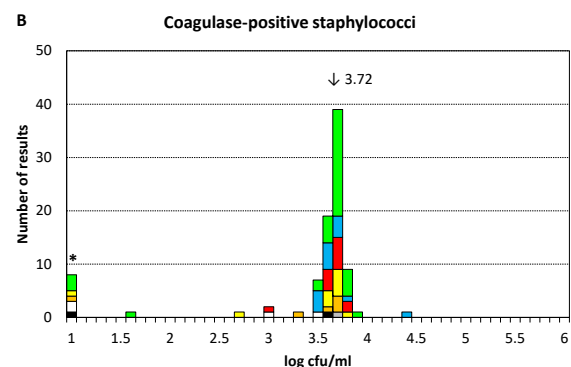
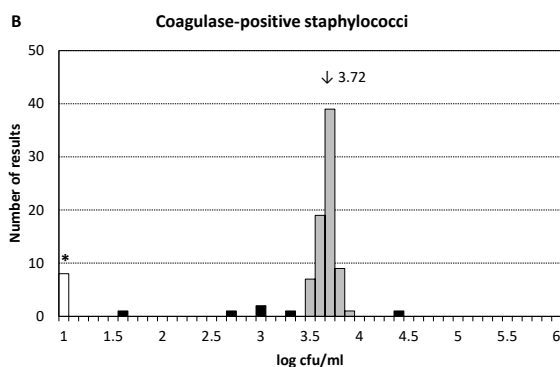
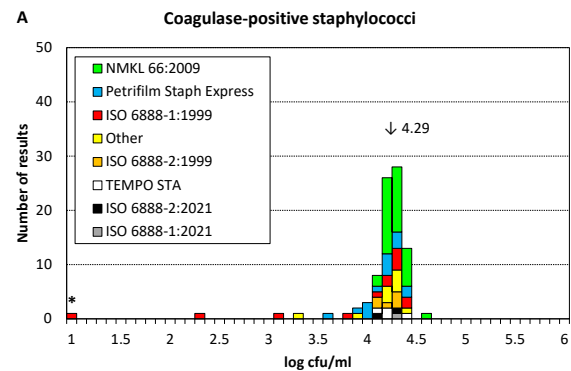
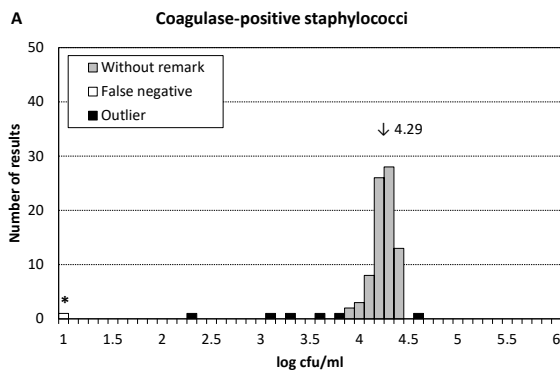
The second most common media were RPFA and Petrifilm Staph Express. With RPFA, the coagulase activity is tested directly in the medium. Petrifilm Staph Express is based on a modified Baird-Parker agar. It also contains a chromogenic indicator that causes *S. aureus* to form red/purple colonies. Participants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

Overall, the results for the identical samples A and C were highly similar.

Table 7. Results from analysis of coagulase-positive staphylococci.

Method	Sample A							Sample B							Sample C						
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>
All results	87	80	4.29	0.12	1	5	1	89	75	3.72	0.09	8	5	1	87	76	3.70	0.11	7	3	1
NMKL 66:2009	36	35	4.32	0.09	0	0	1	37	33	3.76	0.08	3	1	0	36	32	3.70	0.09	3	0	1
Petrifilm Staph Express	15	14	4.26	0.15	0	1	0	15	14	3.68	0.09	0	0	1	15	15	3.68	0.13	0	0	0
ISO 6888-1:1999	13	9	4.35	0.12	1	3	0	13	12	3.74	0.06	0	1	0	13	13	3.70	0.09	0	0	0
Other	10	9	4.33	0.13	0	1	0	11	9	3.72	0.06	1	1	0	11	9	3.73	0.09	1	1	0
ISO 6888-2:1999	6	6	4.30	0.08	0	0	0	6	4	-	-	1	1	0	6	4	-	-	1	1	0
TEMPO STA	4	4	-	-	0	0	0	4	1	-	-	2	1	0	4	1	-	-	2	1	0
ISO 6888-2:2021	2	2	-	-	0	0	0	2	1	-	-	1	0	0	1	1	-	-	0	0	0
ISO 6888-1:2021	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).



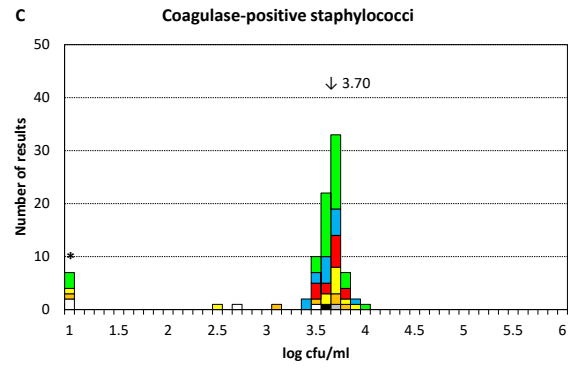
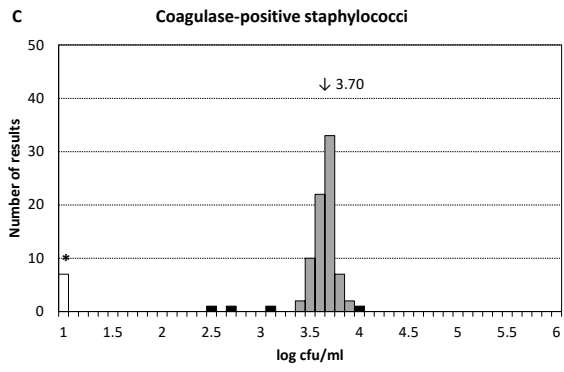


Figure 6. Results from analysis of coagulase-positive staphylococci.

Lactic acid bacteria

Sample A

The strain of *E. durans* was target organism. On MRS-aB, it forms typical white/grey colonies. The strain is catalase-negative and Gram-positive.

In total, 44 participants reported results. Two low outliers were reported, as well as six false-negative results.

Sample B

No target organism was present in the sample. At the Swedish Food Agency, small white colonies (likely *S. aureus*) were observed on MRS-aB. They were catalase-positive and could thus be distinguished from lactic acid bacteria. It has also been reported that *C. glabrata* formed colonies on MRS-S agar.

In total, 44 participants reported results. Fifteen false-positive results were reported.

Sample C

The sample was identical to sample B.

In total, 46 participants reported results. Fifteen false-positive results were reported.

Participants that reported false-positive results for sample B, also in general reported false-positive results for sample C.

General remarks

Most of the participants followed NMKL 140, either NMKL 140:2007 or NMKL 140:1991. Both of these have been replaced by NMKL 140:2023, which contains changes in the incubation time and the introduction of mandatory confirmation tests.

ISO 15214:1998 was reviewed by ISO in 2021 and remains current. ISO 7889/IDF 117:2003, which is a method for characteristic microorganisms in yoghurt at 37 °C, is scheduled to be replaced by ISO/CD 7889, which is under development.

Lactic acid bacteria constitute a heterogeneous group of microorganisms, and therefore have different optimal medium, pH and incubation conditions. Therefore, the choice of media will often have an impact on the results. For example, MRS-aB (pH 6.2) is a less selective medium that allows the growth of a more wide range of lactic acid bacteria. This may however also result in the appearance of more false-positive colonies compared to the more acid media MRS and MRS-S (pH 5.7). Such differences between media and incubation conditions underline the importance of performing a confirmation test in uncertain cases, especially when using a less selective medium.

ISO 15214:1998 recommends confirmation of uncertain colonies, and with NMKL 140:2023 confirmation is mandatory. Lactic acid bacteria are Gram positive and normally catalase-negative.

Confirmation of some kind was here performed by roughly half (48 %) of the participants. Confirmation does not appear to have had an impact on the results for samples B/C, since similar numbers of false results were reported by participants that performed a confirmation, and those that did not.

Notably, no outliers or false results were reported by participants that used Petrifilm LAB or TEMPO LAB. On Petrifilm LAB, lactic acid bacteria form red colonies. The plates also facilitate distinction between gas producing (heterofermentative) and non-gas producing (homofermentative) lactic acid bacteria.

Table 8. Results from analysis of lactic acid bacteria.

Method	Sample A							Sample B							Sample C						
	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>
All results	44	36	4.45	0.20	6	2	0	44	29	-	-	15	-	-	46	31	-	-	15	-	-
NMKL 140:2007	15	13	4.54	0.17	1	1	0	15	11	-	-	4	-	-	15	11	-	-	4	-	-
Other	9	5	4.39	0.12	4	0	0	9	4	-	-	5	-	-	9	5	-	-	4	-	-
ISO 15214:1998	5	5	4.42	0.13	0	0	0	5	4	-	-	1	-	-	7	5	-	-	2	-	-
Petrifilm LAB	5	5	4.33	0.06	0	0	0	5	5	-	-	0	-	-	5	5	-	-	0	-	-
TEMPO LAB	4	4	-	-	0	0	0	4	4	-	-	0	-	-	4	4	-	-	0	-	-
ISO 7889/IDF 117:2003	3	1	-	-	1	1	0	3	1	-	-	2	-	-	3	1	-	-	2	-	-
NMKL 140:1991	3	3	-	-	0	0	0	3	0	-	-	3	-	-	3	0	-	-	3	-	-

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

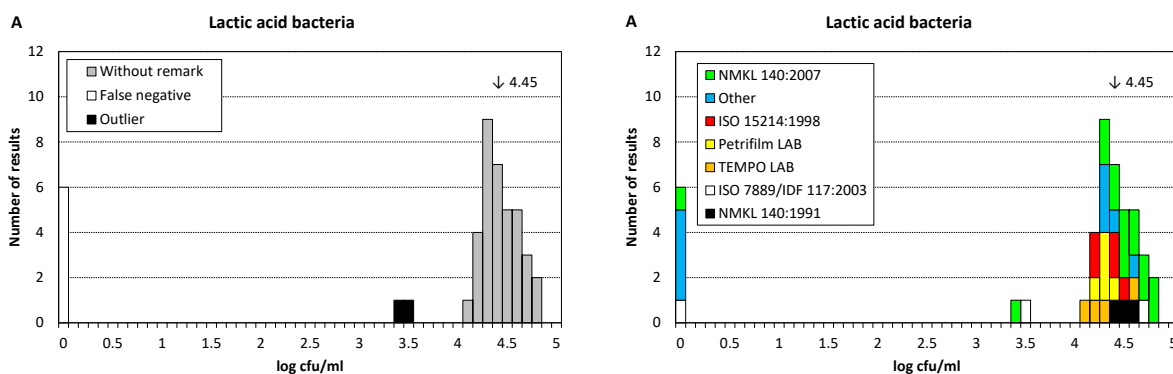


Figure 7. Results from analysis of lactic acid bacteria.

Clostridium perfringens

Sample A

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on TSC.

In total, 48 participants reported results. One false-positive result was reported.

Sample B

The strain of *C. perfringens* was target organism. It forms black colonies on TSC. The strain is non-motile and ferments lactose. It grows on BA under anaerobic conditions, but not under aerobic conditions.

In total, 46 participants reported results. Two low outliers were reported, as well as two false-negative results.

Sample C

The sample was identical to sample B.

In total, 47 participants reported results. Three low outliers were reported, as well as one false-negative result.

General remarks

Most participants followed either NMKL 95:2009 or the recently withdrawn ISO 7937:2004. One participant followed the withdrawn NMKL 95:1997 and one participant analysed according to NMKL 56:2015 (Sulphite-reducing Clostridia). ISO 7937:2004 is replaced by ISO 15213-2:2023 ("Detection and enumeration of *Clostridium* spp."). No obvious differences could be seen in the results from the different methods.

In line with ISO 7937:2004 and NMKL 95:2009, the majority (94 %) of the participants reported the use of TSC. On TSC, *C. perfringens* form black colonies after anaerobic incubation at 37 °C.

Two common methods for confirmation of *C. perfringens* are motility test and test for lactose fermentation; *C. perfringens* is non-motile and forms acid and gas as a consequence of lactose fermentation. *C. perfringens* can also be confirmed since it forms a double haemolytic zone upon anaerobic incubation on BA. In total, 92 % of the participants stated they performed some kind of confirmation.

C. perfringens normally grows both at 37 °C and at 44 °C. Here, the majority of the participants (96 %) incubated at 37 °C. It is therefore difficult to say if the choice of incubation temperature had an impact on the outcome.

Table 9. Results from analysis of *Clostridium perfringens*.

Method	Sample A						Sample B						Sample C					
	N	n	m _{PT}	s _{PT}	F	< >	N	n	m _{PT}	s _{PT}	F	< >	N	n	m _{PT}	s _{PT}	F	< >
All results	48	47	-	-	1	- -	46	42	2.34	0.23	2	2 0	47	43	2.39	0.20	1	3 0
NMKL 95:2006	33	33	-	-	0	- -	32	31	2.40	0.21	0	1 0	32	31	2.45	0.20	0	1 0
ISO 7937:2004	12	11	-	-	1	- -	11	10	2.41	0.27	1	0 0	12	10	2.40	0.23	1	1 0
NMKL 95:1997	1	1	-	-	0	- -	1	0	-	-	1	0 0	1	1	-	-	0	0 0
NMKL 56:2015	1	1	-	-	0	- -	1	0	-	-	0	1 0	1	0	-	-	0	1 0
Other	1	1	-	-	0	- -	1	1	-	-	0	0 0	1	1	-	-	0	0 0

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

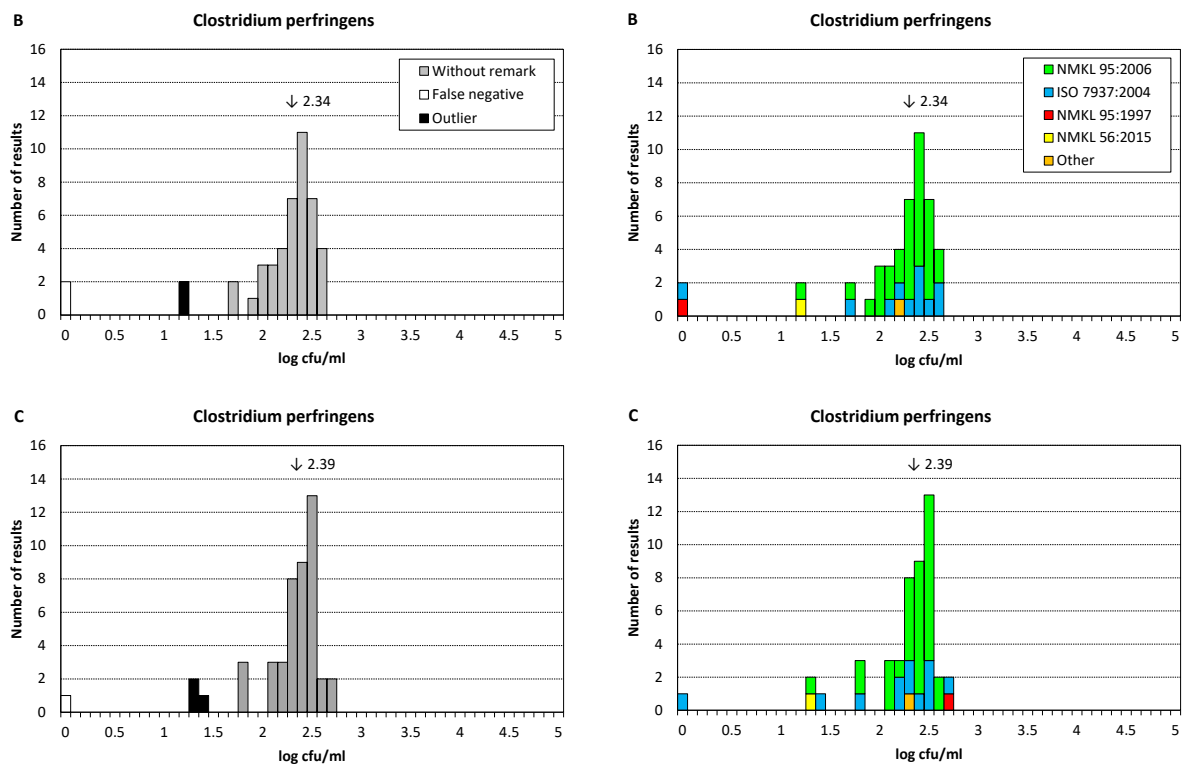


Figure 8. Results from analysis of *Clostridium perfringens*.

Anaerobic sulphite-reducing bacteria

Sample A

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on ISA.

In total, 56 participants reported results. One false-positive result was reported.

Sample B

The strain of *C. perfringens* was target organism. It forms black colonies on ISA. The black colour may be more distinct after 48 h incubation, compared to after 24 h incubation.

In total, 53 participants reported results. Four low outliers were reported, as well as one false-negative result.

Sample C

The sample was identical to sample B.

In total, 54 participants reported results. Four low outliers were reported, as well as one false-negative result.

Participants that reported deviating results for sample B, in all instances also reported a similar deviating result for sample C.

General remarks

The majority of the participants followed a version of NMKL 56. However most followed the withdrawn NMKL 56:2008 or even NMKL 56:1994, instead of the existing NMKL 56:2015. The latter was reviewed by NMKL in 2019 and remains current. Nine participants followed ISO 15213:2003, which was recently replaced by ISO 15213-1:2023 ("Enumeration of sulfite-reducing *Clostridium* spp. by colony-count technique"). One participant followed ISO 7937:2004, which was also recently replaced by ISO 15213-2:2023 ("Detection and enumeration of *Clostridium* spp").

Both NMKL 56:2015 and ISO 15213-1:2023 prescribe pour-plate methods with ISA, which was consequently the medium most frequently used by the participants (43 %). With ISA, black colonies (possibly surrounded by a black zone) are considered as sulphite-reducing bacteria. The black colour of the colonies comes from iron sulphide, which is formed as a precipitate of Fe^{3+} in the medium, and H_2S that is produced by the reduction of sulphite. Growth of anaerobic bacteria that only produce hydrogen (and not H_2S) may sometimes result in a diffuse and unspecific blackening of the medium.

Other media that were used were TSC (20 %), SFP (16 %), TS (9 %) and PAB (5 %). These media are often used when identifying *C. perfringens*, and it should therefore be mentioned that for that purpose, colonies should be confirmed using the methods in for example NMKL 95.

Table 10. Results from analysis of anaerobic sulphite-reducing bacteria.

Method	Sample A						Sample B						Sample C					
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >
All results	56	55	-	-	1	- -	53	48	2.39	0.15	1	4 0	54	49	2.39	0.20	1	4 0
NMKL 56:2008	21	21	-	-	0	- -	21	19	2.46	0.17	0	2 0	21	19	2.50	0.18	0	2 0
NMKL 56:2015	16	16	-	-	0	- -	16	15	2.40	0.14	0	1 0	16	15	2.49	0.16	0	1 0
ISO 15213:2003	9	9	-	-	0	- -	8	7	2.43	0.12	0	1 0	9	8	2.41	0.18	0	1 0
Other	6	6	-	-	0	- -	5	5	2.32	0.08	0	0 0	5	5	2.37	0.18	0	0 0
NMKL 56:1994	3	3	-	-	0	- -	2	2	-	-	0	0 0	2	2	-	-	0	0 0
ISO 7937:2004	1	0	-	-	1	- -	1	0	-	-	1	0 0	1	0	-	-	1	0 0

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

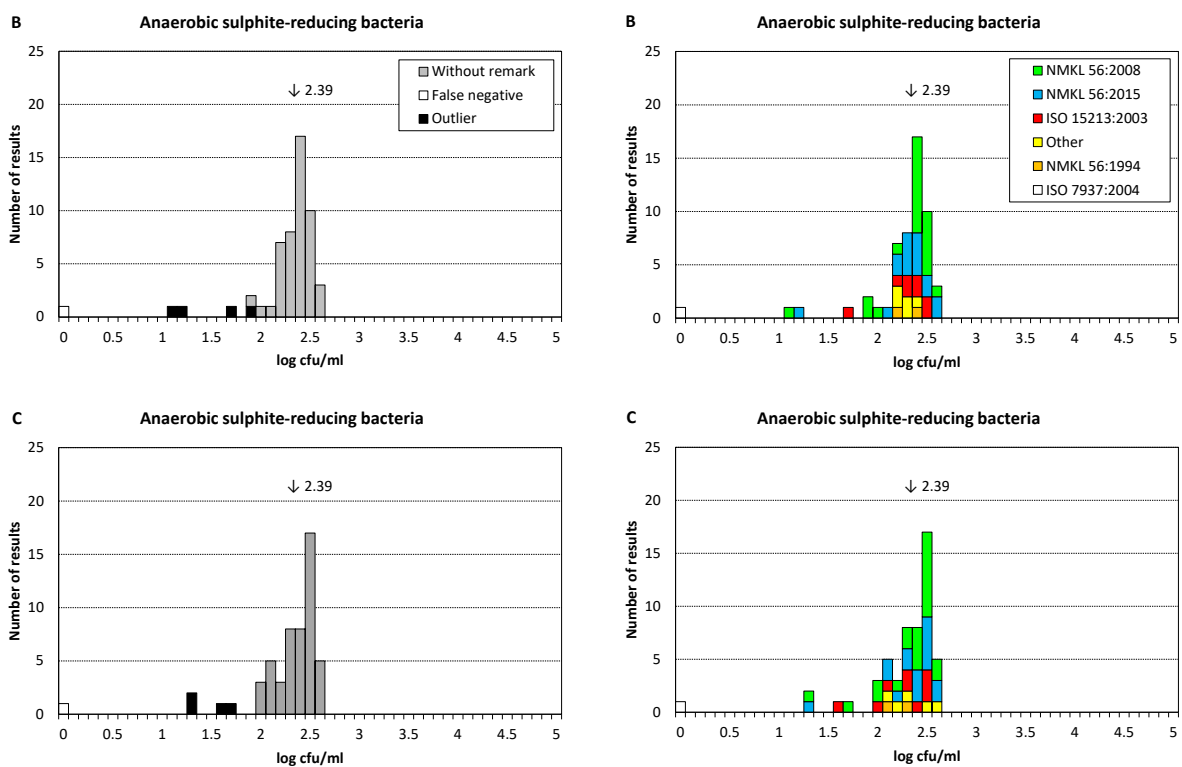


Figure 9. Results from analysis of anaerobic sulphite-reducing bacteria.

Aerobic microorganisms in fish products

Sample A

In total, 21 participants reported results. The results varied between 3.28 and 5.11 log₁₀ cfu ml⁻¹.

The statistical test failed to identify a robust standard deviation. The analysis has therefore been excluded from evaluation, **and all reported results are considered acceptable.**

Sample B

In total, 21 participants reported results. Two low and one high outlier were reported.

Sample C

The sample was identical to sample B.

In total, 21 participants reported results. One high outlier was reported.

General remarks

Seventeen of the 21 participants followed the method for aerobic microorganisms and specific spoilage organisms in fish and fish products, NMKL 184:2006. This prescribes a pour-plate method with IA, which was consequently the medium most frequently used by the participants (81 %). The participants that followed ISO 4833-1:2013 and NMKL 86:2006 incubated on PCA.

One participant reported the use of NMKL 96:2003, which is assumed to be an error, since that method is adapted for analysis of coliform bacteria, thermotolerant coliform bacteria and *E. coli* in fish and seafood.

Table 11. Results from analysis of aerobic microorganisms in fish products.

Method	Sample A*							Sample B							Sample C						
	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>
All results	21	21	-	-	-	-	-	21	18	3.83	0.15	0	2	1	21	20	3.77	0.15	0	1	0
NMKL 184: 2006	17	17	-	-	-	-	-	17	15	3.86	0.13	0	1	1	17	16	3.80	0.12	0	1	0
Petrifilm AC	1	1	-	-	-	-	-	1	1	-	-	0	0	0	1	1	-	-	0	0	0
ISO 4833-1:2013	1	1	-	-	-	-	-	1	0	-	-	0	1	0	1	1	-	-	0	0	0
NMKL 96:2003	1	1	-	-	-	-	-	1	1	-	-	0	0	0	1	1	-	-	0	0	0
NMKL 86:2006	1	1	-	-	-	-	-	1	1	-	-	0	0	0	1	1	-	-	0	0	0

* The sample is not evaluated.

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

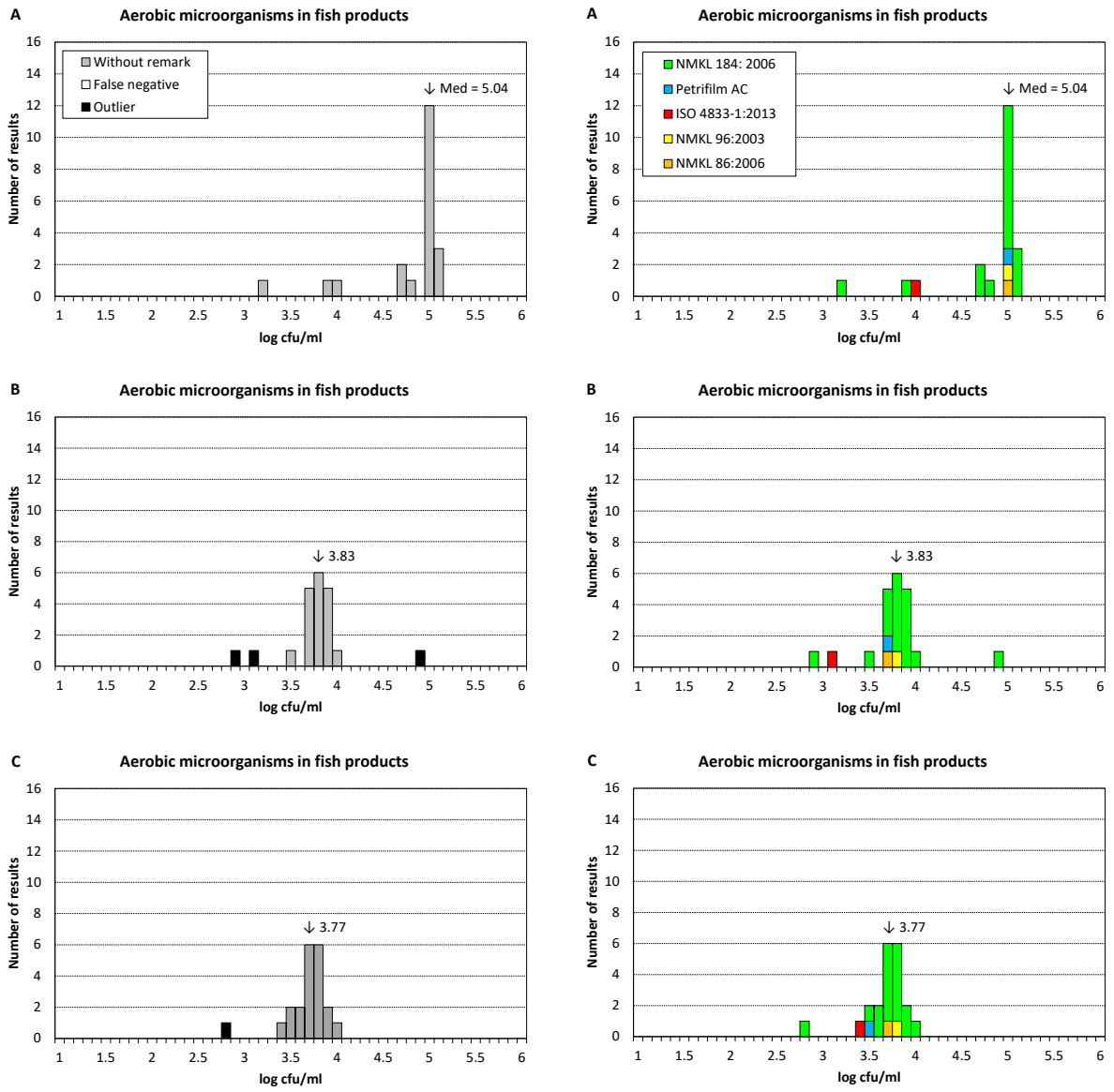


Figure 10. Results from analysis of aerobic microorganisms in fish products.

H₂S-reducing bacteria in fish products

Sample A

The strain of *H. alvei* was target organism. It forms black colonies on IA.

In total, 18 participants reported results. One low outlier was reported, as well as one false-negative result.

Note: The measurement uncertainty of the assigned value is not negligible. The evaluation of the results could therefore be affected. Z-scores should be interpreted with caution, and only be used as a guidance.

Sample B

No target organism was present in the sample. The strain of *A. hydrophila* was present as a false-positive organism for the analysis. It may form colonies with a slight grey/brown colour on IA.

In total, 18 participants reported results. All reported results were correct negative.

Sample C

The sample was identical to sample B.

In total, 18 participants reported results. All reported results were correct negative.

General remarks

All of the 18 participants followed the method for aerobic microorganisms and specific spoilage organisms in fish and fish products, NMKL 184:2006, and all of the participants incubated on IA. NMKL 184 was reviewed by NMKL in 2022 and remains current.

With IA, H₂S-producing bacteria form black colonies. It is important to read the plates immediately after the incubation, since the colour of the colonies may fade after a few days storage in a fridge.

Table 12. Results from analysis of H₂S-reducing bacteria in fish products.

Method	Sample A							Sample B							Sample C						
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>
All results	18	16	4.52	0.10	1	1	0	18	18	-	-	0	-	-	18	18	-	-	0	-	-
NMKL 184: 2006	18	16	4.53	0.11	1	1	0	18	18	-	-	0	-	-	18	18	-	-	0	-	-

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

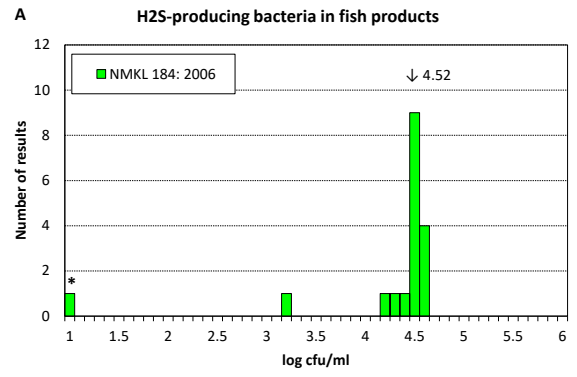
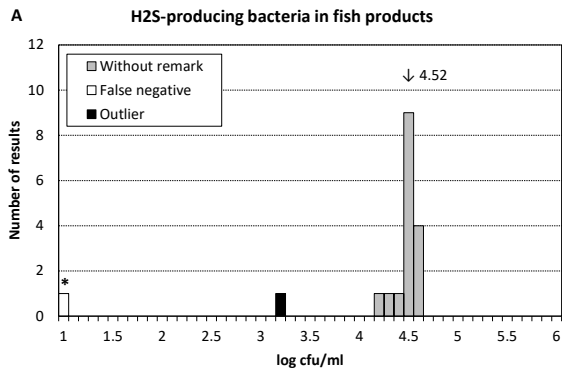


Figure 11. Results from analysis of H₂S-reducing bacteria in fish products.

Yeasts and moulds

Sample A

No target organism was present, neither for yeasts nor for moulds.

In total, 126 participants reported results for yeasts. Five false-positive results were reported.

In total, 124 participants reported results for moulds. Two false-positive results were reported.

Sample B

The strains of *C. glabrata* and *P. roquefortii* and were target organisms for yeasts and moulds, respectively.

In total, 123 participants reported results for yeasts. Seven low and four high outliers were reported, as well as two false-negative results.

In total, 122 participants reported results for moulds. Two low and one high outlier were reported, as well as six false-negative results.

Sample C

The sample was identical to sample B.

In total, 124 participants reported results for yeasts. Seven low and three high outliers were reported.

In total, 123 participants reported results for moulds. Two low and one high outlier were reported, as well as five false-negative results.

General remarks

In essence, the same participants analysed both yeasts and moulds, and they generally reported identical method information for both parameters. The most common methods were NMKL 98:2005, ISO 6611:2004/IDF 94:2004 or a method with 3M™ Petrifilm™.

NMKL 98:2005 was last reviewed by NMKL in 2019 and remains current. ISO 6611:2004/IDF 94:2004 and ISO 21527-1:2008/ISO 21527-2:2008 were last reviewed by ISO in 2020 and 2018, respectively, and remain current. They are however scheduled to be replaced by ISO/CD 21527, which is currently under development. Two participants followed the withdrawn ISO 7954:1987 which has been replaced by ISO 21527-1:2008 and ISO 21527-2:2008.

With NMKL 98:2005, participants mainly used either DRBC and/or DG18. With ISO 6611:2004 / IDF 94:2004, which describes the enumeration of yeasts and moulds in milk and milk products, participants instead mainly used YGC. ISO 21527-1:2008 and ISO 21527-2:2008 stipulate the use of DRBC and DG18, respectively. In general, DRBC is recommended for food with water activity $a_w > 0.95$ (e.g. fresh fruit, vegetables, meat and milk products) while DG18 is recommended for food with $a_w \leq 0.95$ (e.g.

dried fruit, dried meat, grains and nuts). Outliers and false results were for the most part evenly distributed between the main methods and media that were used.

Note: Four participants used TEMPO YM, which gives a combined value for yeasts and moulds. These results were excluded from calculations of the assigned value and standard deviations for samples B and C. Due to the low number of participants that use this method, results from TEMPO YM need to be evaluated by the individual participants themselves.

Table 13. Results from analysis of yeasts.

Method	Sample A						Sample B						Sample C							
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >		
All results	126	121	-	-	5	- -	123	110	2.63	0.11	2	7	4	124	114	2.63	0.11	0	7	3
NMKL 98:2005	43	42	-	-	1	- -	43	40	2.65	0.10	1	2	0	43	39	2.64	0.10	0	4	0
Other	26	25	-	-	1	- -	26	24	2.62	0.09	0	1	1	26	25	2.61	0.08	0	0	1
ISO 6611:2004/ IDF 94:2004	22	21	-	-	1	- -	23	20	2.65	0.13	0	2	1	23	22	2.66	0.10	0	1	0
Petrifilm YM	12	12	-	-	0	- -	13	13	2.68	0.09	0	0	0	13	13	2.67	0.10	0	0	0
ISO 21527:2008	8	7	-	-	1	- -	7	5	2.62	0.05	0	0	2	8	6	2.59	0.10	0	0	2
Petrifilm RYM	8	7	-	-	1	- -	8	6	2.64	0.13	1	1	0	8	7	2.71	0.12	0	1	0
TEMPO	4	4	-	-	0	- -	0	0	-	-	0	0	0	0	0	-	-	0	0	0
ISO 7954:1987	2	2	-	-	0	- -	2	2	-	-	0	0	0	2	2	-	-	0	0	0
Compact Dry YM	1	1	-	-	0	- -	1	0	-	-	0	1	0	1	0	-	-	0	1	0

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

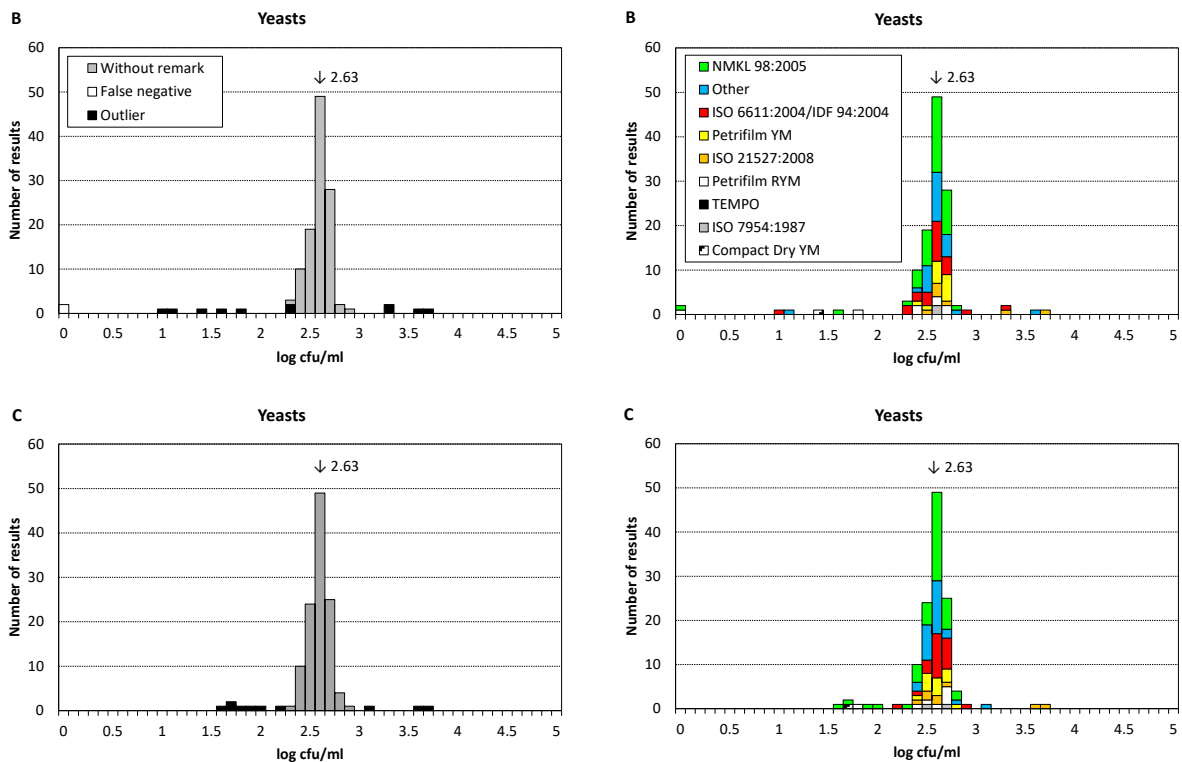


Figure 12. Results from analysis of yeasts.

Table 14. Results from analysis of moulds.

Method	Sample A						Sample B						Sample C					
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >
All results	124	122	-	-	2	- -	122	113	2.12	0.33	6	2 1	123	115	2.13	0.30	5	2 1
NMKL 98:2005	42	41	-	-	1	- -	42	42	2.15	0.30	0	0 0	42	42	2.18	0.30	0	0 0
Other	28	28	-	-	0	- -	28	25	2.18	0.32	3	0 0	28	26	2.13	0.25	2	0 0
ISO 6611:2004/ IDF 94:2004	21	20	-	-	1	- -	22	21	1.93	0.45	0	1 0	22	22	1.97	0.31	0	0 0
Petrifilm YM	13	13	-	-	0	- -	14	13	2.00	0.26	1	0 0	14	12	2.10	0.22	1	1 0
ISO 21527:2008	8	8	-	-	0	- -	7	6	2.37	0.14	0	0 1	8	7	2.36	0.18	0	0 1
Petrifilm RYM	6	6	-	-	0	- -	6	4	-	-	2	0 0	6	4	-	-	2	0 0
TEMPO	3	3	-	-	0	- -	0	0	-	-	0	0 0	0	0	-	-	0	0 0
ISO 7954:1987	2	2	-	-	0	- -	2	2	-	-	0	0 0	2	2	-	-	0	0 0
Compact Dry YM	1	1	-	-	0	- -	1	0	-	-	0	1 0	1	0	-	-	0	1 0

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

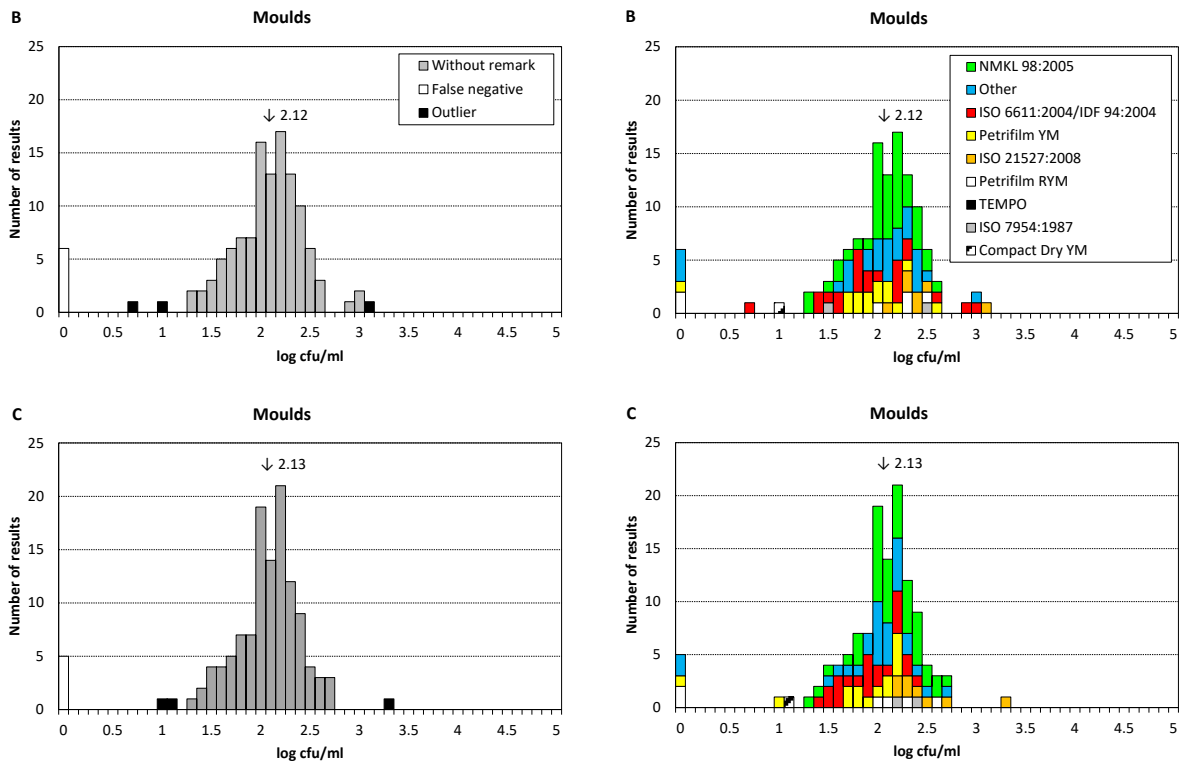


Figure 13. Results from analysis of moulds.

Outcome of the results of individual participants - assessment

Reporting and evaluation of results

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

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

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

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

Box plots and numbers of deviating results for each participant

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

The different parts of a box plot are shown in figure 5.

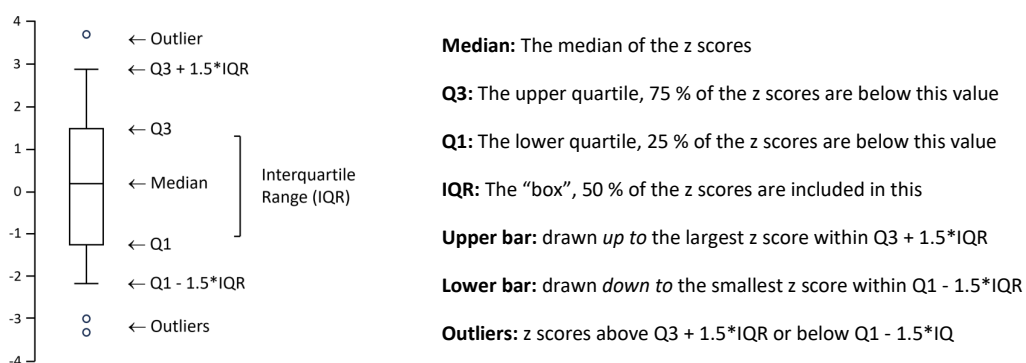
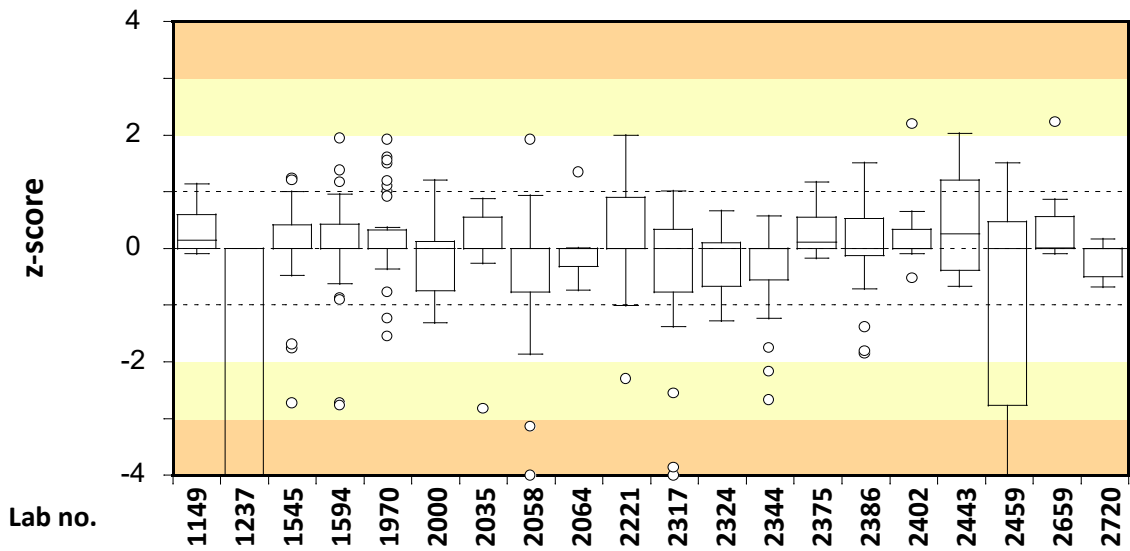
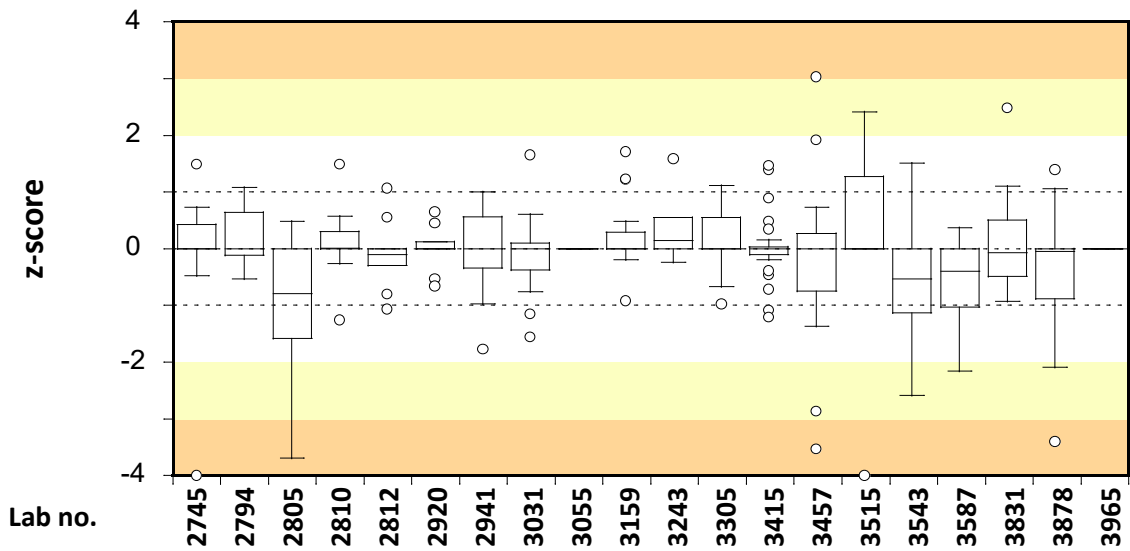


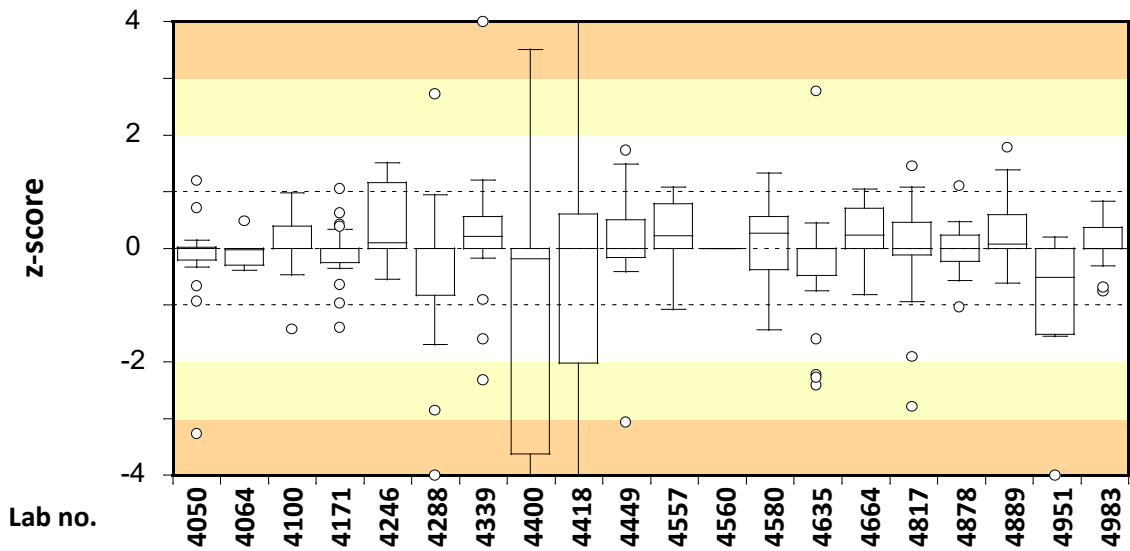
Figure 5. Schematic explanation of a box plot.



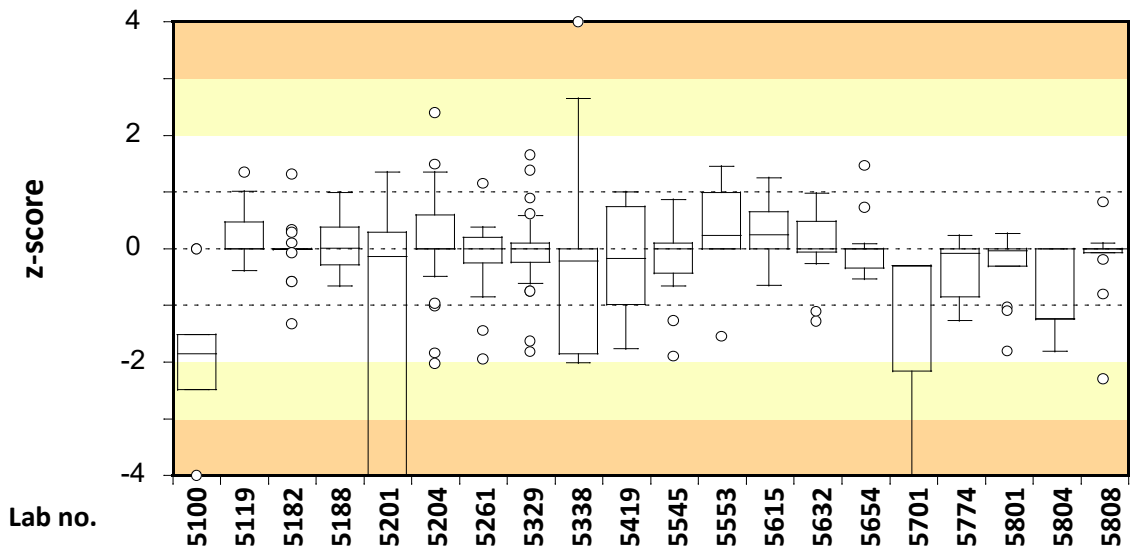
Lab no.	1149	1237	1545	1594	1970	2000	2035	2058	2064	2221	2317	2324	2344	2375	2386	2402	2443	2459	2659	2720
No. of results	18	35	30	33	38	22	15	24	15	30	27	19	23	12	24	15	15	9	9	15
False positive	2	4	0	0	0	0	0	2	0	2	2	0	0	2	2	0	4	0	2	1
False negative	0	2	0	1	2	0	0	1	0	0	0	0	0	0	0	0	1	2	0	0
Low outliers	0	20	0	0	0	0	0	2	0	0	3	0	0	0	0	0	0	2	0	0
High outliers	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0



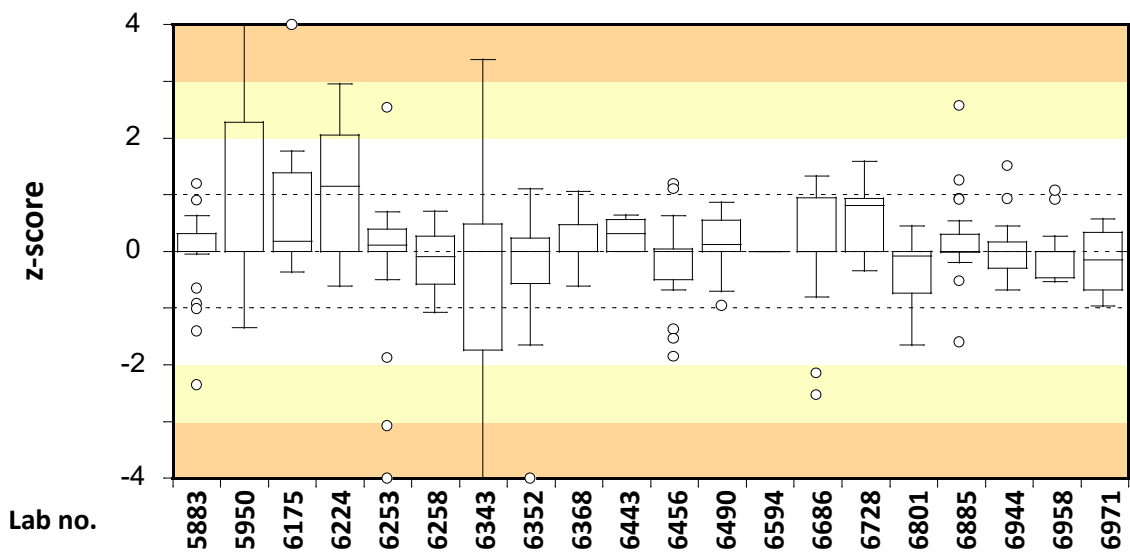
Lab no.	2745	2794	2805	2810	2812	2920	2941	3031	3055	3159	3243	3305	3415	3457	3515	3543	3587	3831	3878	3965
No. of results	27	9	9	9	9	9	27	17	0	18	6	35	27	24	18	16	24	15	23	0
False positive	0	0	2	0	0	0	4	2	0	0	0	0	0	4	0	2	2	3	3	0
False negative	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0
Low outliers	1	0	1	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	1	0
High outliers	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0



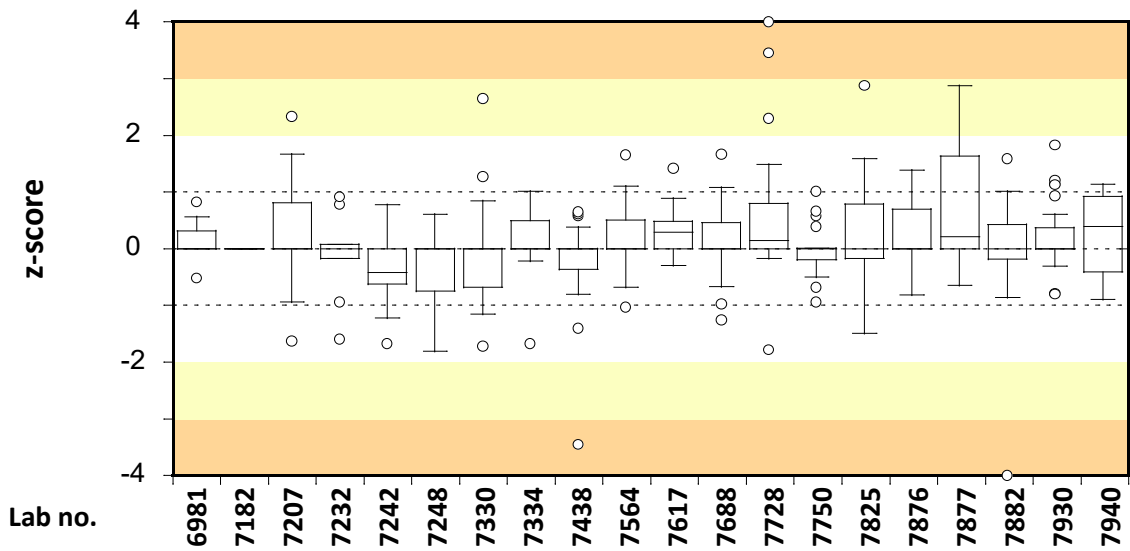
No. of results	16	6	30	24	12	27	35	18	29	16	12	0	9	22	18	19	15	23	15	15	
False positive	1	0	0	2	2	0	2	0	3	0	2	0	0	0	0	0	0	1	0	2	0
False negative	0	0	2	1	2	0	0	0	4	0	0	0	0	1	0	0	0	0	0	1	0
Low outliers	1	0	0	0	0	1	0	6	5	1	0	0	0	0	0	0	0	0	0	2	0
High outliers	0	0	0	0	0	0	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0



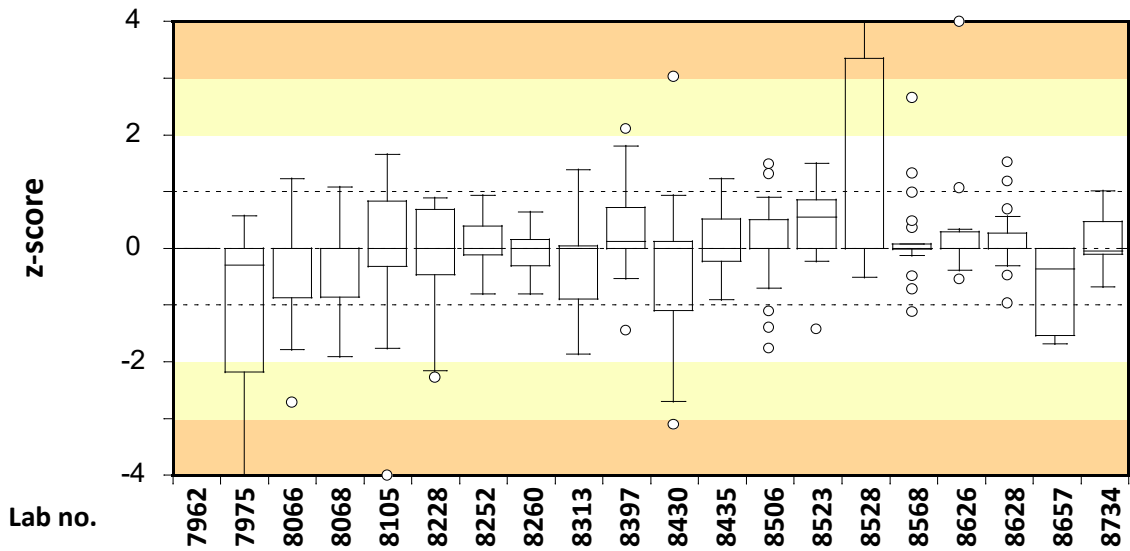
No. of results	9	11	18	8	15	33	18	24	12	12	18	18	27	19	15	3	6	15	6	15
False positive	0	0	0	0	2	0	4	2	2	2	0	0	2	1	0	0	0	2	0	0
False negative	0	0	1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	2
Low outliers	2	0	0	0	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
High outliers	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0



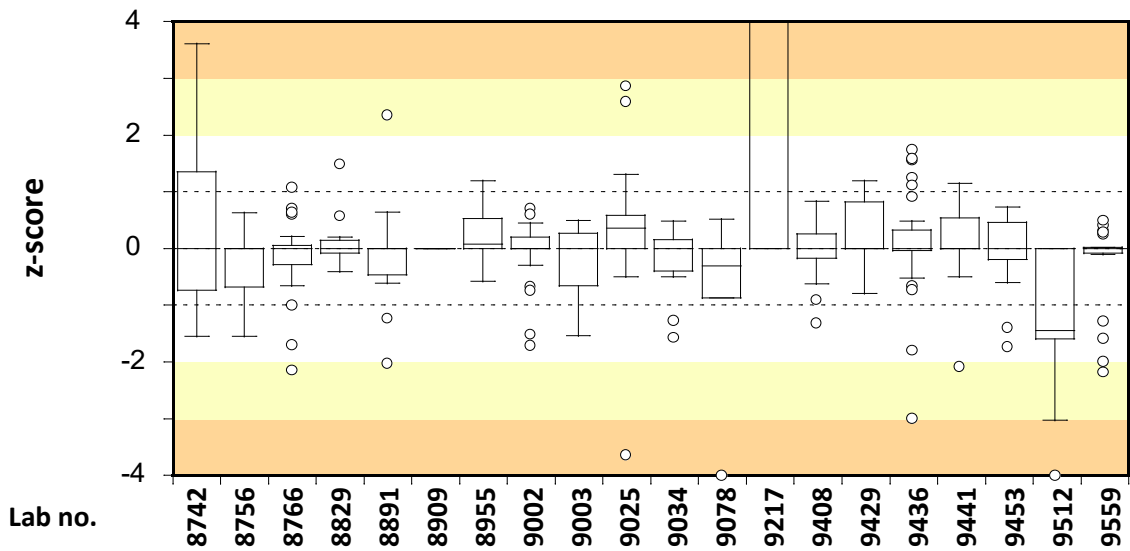
No. of results	30	8	12	9	18	12	30	30	35	6	21	21	0	29	12	9	24	18	15	6	
False positive	0	0	1	2	0	0	4	4	0	0	0	0	0	0	2	0	0	0	0	2	2
False negative	0	3	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Low outliers	0	0	0	0	2	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0
High outliers	0	1	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0



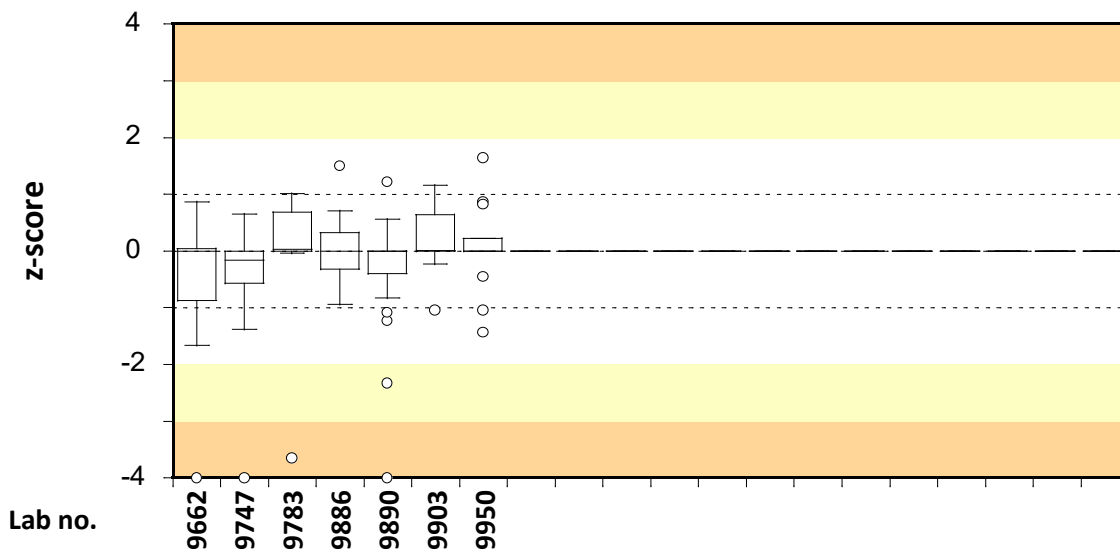
No. of results	6	0	18	9	12	38	21	20	27	21	12	29	27	21	18	24	15	30	29	6
False positive	0	0	1	0	2	0	2	0	0	0	2	0	0	2	4	0	2	2	0	2
False negative	0	0	1	0	0	0	0	0	0	0	0	2	0	1	1	0	0	0	0	0
Low outliers	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	4	0	0
High outliers	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0



No. of results	0	15	20	27	15	15	12	24	21	24	18	22	21	21	15	24	11	21	12	15	
False positive	0	0	0	0	0	0	0	0	0	0	3	1	0	2	0	2	0	0	0	0	5
False negative	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	3
Low outliers	0	3	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
High outliers	0	0	0	0	0	0	0	0	0	0	1	0	0	0	5	0	1	0	0	0	0



No. of results	9	15	24	12	21	0	32	30	16	15	12	6	9	32	21	33	20	18	15	24
False positive	0	2	0	0	1	0	2	0	0	2	0	0	2	0	0	0	0	0	2	2
False negative	0	2	0	0	0	0	0	2	0	0	0	0	1	0	0	1	0	0	0	1
Low outliers	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0
High outliers	1	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0



Lab no.	9662	9747	9783	9886	9890	9903	9950
No. of results	24	15	12	12	24	24	15
False positive	2	2	0	0	0	2	2
False negative	0	0	0	0	0	0	0
Low outliers	3	1	1	0	1	0	0
High outliers	0	0	0	0	0	0	0

Test material and quality control

Test material

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

Table 15. Microorganisms and approximate concentrations in the samples.

Sample	Microorganism	Strain			
		SLV no. ¹	Origin	Reference ²	log ₁₀ cfu ml ⁻¹
A	<i>Bacillus cereus</i>	SLV-518	Couscous	CCUG 44741	4.3
	<i>Enterococcus durans</i>	SLV-078	Fresh meat	CCUG 44816	4.5
	<i>Escherichia coli</i>	SLV-524	Chicken	CCUG 47554	4.2
	<i>Hafnia alvei</i>	SLV-015	Minced meat	CCUG 45642	4.6
	<i>Staphylococcus aureus</i>	SLV-280	Egg	-	4.4
B	<i>Aeromonas hydrophila</i>	SLV-467	Drinking water	CCUG 44811	3.0
	<i>Candida glabrata</i>	SLV-052	-	-	2.8
	<i>Clostridium perfringens</i>	SLV-442	-	CCUG 43593	2.4
	<i>Penicillium roquefortii</i>	SLV-510	Malt	-	2.8
	<i>Staphylococcus aureus</i>	SLV-185	Chicken	CCUG 48090	3.8
C	<i>Aeromonas hydrophila</i>	SLV-467	Drinking water	CCUG 44811	3.0
	<i>Candida glabrata</i>	SLV-052	-	-	2.8
	<i>Clostridium perfringens</i>	SLV-442	-	CCUG 43593	2.4
	<i>Penicillium roquefortii</i>	SLV-510	Malt	-	2.8
	<i>Staphylococcus aureus</i>	SLV-185	Chicken	CCUG 48090	3.8

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

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

Quality control of the samples

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

Table 16. Concentration mean (m), I_2 and T 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 ¹		
	m	I_2	T	m	I_2	T	m	I_2	T
Aerobic microorganisms, 30 °C NMKL method no. 86:2013	5.03	0.71	1.26	3.87	1.26	1.30	3.87	1.26	1.30
Psychrotrophic microorganisms NMKL method no. 86:2013	4.83	0.41	1.17	2.49	1.92	1.56	2.49	1.92	1.56
Enterobacteriaceae NMKL method no. 144:2005	4.61	1.43	1.43	-	-	-	-	-	-
<i>Escherichia coli</i> NMKL method no. 125:2005	4.24	0.48	1.16	-	-	-	-	-	-
Presumptive <i>Bacillus cereus</i> NMKL method no. 67:2021	4.35	0.52	1.34	-	-	-	-	-	-
Coagulase-positive staphylococci NMKL method no. 66:2009	4.38	0.88	1.18	3.79	2.86	1.55	3.79	2.86	1.55
Lactic acid bacteria NMKL method no. 140:2007	4.48	0.65	1.35	-	-	-	-	-	-
<i>Clostridium perfringens</i> NMKL method no. 95:2009	-	-	-	2.42	1.59	1.66	2.42	1.59	1.66
Anaerobic sulphite-reducing bacteria NMKL method no. 56:2015	-	-	-	2.44	0.68	1.36	2.44	0.68	1.36
Aerobic microorganisms in fish products NMKL method no. 184:2006	4.87	1.88	1.37	3.98	1.53	1.30	3.98	1.53	1.30
H ₂ S-producing bacteria in fish products NMKL method no. 184:2006	4.60	1.40	1.53	-	-	-	-	-	-
Yeasts NMKL method no. 98:2005 (DG18)	-	-	-	2.75	0.58	1.34	2.75	0.58	1.34
Moulds NMKL method no. 98:2005 (DG18)	-	-	-	2.56	1.67	1.90	2.56	1.67	1.90

– No target organism or no value

¹ n = 10 vials analysed in duplicate

References

1. ISO 13528:2022 Statistical methods for use in proficiency testing by interlaboratory comparison.
2. Ilbäck J and Blom L. 2023. Protocol – Microbiological Proficiency Testing, Swedish Food Agency.
3. Peterz M and Steneryd AC. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. *Journal of Applied Bacteriology*. 74:143–148.
4. Heisterkamp SH, Hoekstra JA, van Strijp-Lockefeer NGWM, Havelaar AH, Mooijman KA, in't Veld PH, Notermans SHW, Maier EA and Griepink B. 1993. Statistical analysis of certification trials for microbiological reference materials. Luxembourg: Commission of the European Communities, Report EUR 15008 EN.
5. Mooijman KM, During M and Nagelkerke NJD 2003. MICROCRM: Preparation and control of batches of microbiological materials consisting of capsules. RIVM report 250935001/2003. RIVM, Bilthoven, Holland.

Appendix 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Preumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	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	4.99	3.98	3.97	-	-	-	4.69	2.98	3.03	3.95	0	0	4.4	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.66	2.73	0	2.28	2.26	
1237	4.29	2.79	2.97	3.53	<1	<1	3.51	1.45	1.48	2.67	<1	<1	-	-	-	3.36	2.76	2.53	3.56	2.48	2.59	<1	1.23	1.36	<1	1.15	1.32	3.9	2.9	2.81	3.26	<1	<1	<1	1.48	1.79	<1	1	1.18
1545	5.13	3.86	3.91	-	-	-	4.57	<1	<1	4.1	<1	<1	4.34	<1	<1	4.23	3.56	3.68	4.39	<1	<1	<0	2.53	2.64	<0	2.53	2.64	-	-	-	<0	2.45	2.33	<0	2.35	2.25			
1594	5.11	3.83	3.75	-	-	-	4.61	0	0	4.08	0	0	4.41	0	0	4.18	0	3.69	4.85	0	0	0	1.72	1.83	0	2.53	2.59	-	-	4.66	0	0	0	2.64	2.56	0	2.51	2.26	
1970	5.04	3.65	3.7	4.45	0	0	4.57	0	0	4	0	0	4.61	0	0	4.32	3.86	3.68	4.76	0	0	0	2.34	2.41	0	2.28	2.62	5.08	3.86	3.81	4.51	0	0	0	2.76	2.8	0	2.43	2.7
2000	4.8	3.7	3.7	-	-	-	4.7	0	-	3.7	0	0	4.1	0	0	4.3	3.6	-	-	-	-	0	2.4	2.5	-	-	-	-	-	-	-	0	2.6	2.6	0	2.4	2.4		
2035	-	-	-	-	-	-	-	-	-	4.2	<1	<1	3.5	<1	<1	-	-	-	-	-	-	-	-	-	<1	2.5	2.5	-	-	-	-	<1	2.7	2.6	<1	2.2	2.3		
2058	4.54	3.2	4	-	-	-	4.59	2.5	2.5	4	0	0	4.1	0	0	-	-	-	4.43	0	0	0	0	0	2.78	-	-	-	-	-	-	0	2.43	2.51	0	1.85	1.9		
2064	4.96	3.85	3.84	-	-	-	4.72	0	0	-	-	-	4.14	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.59	2.58	0	1.88	2.05			
2221	5.11	3.74	3.73	-	-	-	4.64	1.12	1.37	3.39	<1	<1	4.61	<1	<1	4.39	3.73	3.81	4.54	<1	<1	<1	2.68	2.7	<0	2.26	2.29	-	-	-	<1	2.61	2.73	<1	2.59	2.72			
2317	4.97	3.75	3.68	-	-	-	4.63	1.28	2.15	4.06	0	0	4.31	0	0	4.33	3.7	3.58	-	-	-	0	1.76	1.43	0	1.71	1.61	-	-	-	-	0	2.71	2.74	0	2.33	2.36		
2324	5.03	3.75	3.75	-	-	-	4.41	<1	<1	-	-	-	4.51	<1	<1	4.22	3.75	3.7	-	-	-	-	-	<1	>1	>1	-	-	-	-	<1	2.65	2.7	<1	1.7	1.79			
2344	4.91	3.57	3.79	-	-	-	4.46	0	0	3.66	0	0	4.15	-	0	4.35	3.72	3.74	-	-	0	0	-	1.85	0	-	2.04	-	-	-	0	-	2.58	0	-	2.3			
2375	5.04	3.85	3.9	-	-	-	4.51	2.42	2.73	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.62	2.69	0	2.51	2.29			
2386	5.04	3.99	4.08	-	-	-	4.69	3.04	3.28	4.11	<1	<1	3.78	<1	<1	4.46	3.77	3.75	-	-	-	0	2.18	2.11	-	-	-	-	-	-	<1	2.6	2.43	<1	2.08	2.11			
2402	5.3	3.84	3.91	-	-	-	4.52	0	0	3.84	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.64	2.7	0	2.25	2.25				
2443	5.06	3.8	3.97	-	-	-	4.7	2.65	2.42	-	-	-	-	-	-	-	-	-	4.32	3.57	0	-	-	-	-	-	-	-	-	4.63	2.85	2.83	0	0	2				
2459	2.09	3.97	4.08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	1.18	2.46	0	0	0				
2659	5.11	3.85	4.18	-	-	-	4.52	2.67	2.82	4.04	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
2720	4.94	3.86	3.89	-	-	-	4.44	<1	2.43	-	-	-	4.13	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	2.65	2.6	<1	1.93	1.98			
2745	5.08	3.94	3.93	-	-	-	4.52	0	0	4.09	0	0	4.18	0	0	4.29	0	0	4.51	0	0	0	2.51	2.52	-	-	-	-	-	-	0	2.62	2.02	0	2.11	2.57			
2794	4.97	3.78	3.82	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.7	2.63	0	2.48	2.34				
2805	4.68	3.72	3.76	-	-	-	4.6	3.32	3.33	3.03	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
2810	5.03	4.04	3.95	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.66	2.63	0	1.71	2.05			
2812	5.14	3.92	3.83	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.62	2.54	0	1.77	2.04				
2920	5.08	3.78	3.78	-	-	-	4.55	<1	<1	4.09	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
2941	4.91	3.91	3.79	-	-	-	4.47	2.57	2.48	4.23	<1	<1	4.25	<1	<1	4.33	3.79	3.78	4.33	3.62	3.7	-	-	-	<1	2.5	2.56	-	-	-	<1	2.65	2.7	<1	1.8	1.6			
3031	5.04	3.82	3.71	-	-	-	4.52	1.96	1.73	3.78	0	0	-	-	-	4.48	3.67	3.53	-	-	-	-	-	-	-	-	-	5.04	3.86	3.76	4.58	0	0	-	-	-	-		
3055	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
3159	5.16	4.07	3.9	-	-	-	4.6	<1	<1	4.05	<1	<1	4.26	<2	<2	4.43	3.74	3.7	4.27	<2	<2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
3243	5.03	3.92	4.09	-	-	-	4.5	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
3305	4.92	3.9	3.88	-	-	-	4.63	<1	<1	4.11	<1	<1	4.48	<1	<1	4.34	3.77	3.7	4.6	<1	<1	<1	2.6	2.51	<1	2.48	2.54	5.04	3.79	3.71	4.45	<1	<1	<1	2.71	2.66	<1	2.2	1.84
3415	4.96	3.79	3.72	-	-	-	4.48	<	<	3.98	<	<	4.11	<	<	4.45	3.76	3.79	-	-	-	<	2.38	2.46	<	2.4	2.15	-	-	-	<	2.79	2.63	<	2.11	2.08			
3457	5	3.89	4.29	-	-	-	4.56	3.16	3.03	4.03	<1	<1	-	-	-	3.95	3.77	3.9	4.24	1	1.48	<1	2.03	2.12	-	-	-	-	-	<1	2.71	2.58	<1	2.15	1.08				
3515	5.27	4.16	4.14	-	-	-	4.66	0	0	4.3	0	0	4.73	0	0	4.29	3.08	2.73	4.64	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
3543	5.04	3.78	4.08	-	-	-	4.18	1.76	1.66	4.23	<1	<1	3.99	<1	<1	<1	3.63	3.58	-	-	-	-	-	<1	2.01	2.02	-	-	-	<1	2.94	2.9	-	-	-	-			
3587	4.82	3.72	3.72	-	-	-	4.51	2.41	2.28	4.07	0	0	4.02	0	0	4.19	3.72	3.72	-	-	-	-	-	0	2.28	2.19	-	-	-	0	2.47	2.56	0	1.41	1.51				
3831	4.88	3.73	3.8	-	-	-	-	-	-	4.61	0	1.63	-	-	-	4.36	3.34	2.19	-	-	-	-	-	-	-	-	-	-	-	0	2.74	2.75	0	2.08	2				
3878	5.076	3.833	3.74	-	-	-	4.519	2.097	2.255	3.106	<1	1.903	4.423	0	0	4.041	3.681	3.602	-	-	-	-	-	-	-	-	5.021	3.771	3.58	-	<1	2.746	2.782	<1	<1	<1			
3965	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
4050	4.94	3.73	3.89	-	-	-	4.54	0	0	-	-	3.37	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.56	2.76	0	2.36	2.1				
4064	4.98	3.8	3.83	-	-	-	4.6	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
4100	5.04	3.85	3.9	4.41	<1	<1	4.57	<1	<1	3.61	<1	<1	4.57	<1	<1	-	-	-	4.42	<1	<1	<1	2.47	2.54	<1	2.54	2.48	-	-	<1	2.69	2.67	<1	2.22	2.4				
4171	4.85	3.93	3.93	-	-	-	4.58	3.08	3.26	3.62	<0,60	<0,60	4.43	<1	<1	>0,01	>0,01	>0,01	<1	<1	<1	-	-	<0	2.38	2.61	-	-	<0	2.6	2.59	<0	2.04	1.94					
4246	4.91	4.02	4.08	-	-	-	4.67	3.06	3.06	4.02	0	0	4.29	0	0	4.29	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
4288	1.96	3.89	3.84	-	-	-	4.45	0	0	3.98	0	0	5.11	0	0	4.33	3.65	3.54	-	-	-	0	2.09	2.25	0	1.97	2.05	-	-	0	2.53	2.53	0	2.36	2.41				
4339	5.11	3.92	3.94	-	-	-	4.51	<1	<1	4.08	<1	<1	4.48	&																									

Appendix 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Preumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	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
4889	5.04	3.77	3.88	-	-	-	4.48	0	0	4.15	0	0	4.45	0	0	4.4	3.74	3.82	-	-	-	-	-	-	0	2.6	2.62	5.11	3.85	4.04	4.57	0	0	-	-	-	-	-	-
4951	4.34	3.65	3.74	-	-	-	4.56	2.91	3.04	3.93	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	<1	1.6	<1	1.63	1.88	
4983	5.03	3.92	3.93	-	-	-	4.43	0	0	-	-	-	4.23	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.72	2.72	0	1.9	2.18		
5100	4.77	3.61	3.66	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	1.6	1.99	0	1.3	1.56			
5119	5.18	3.98	4	-	-	-	4.48	<1	<1	3.89	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<2	2.52	2.64	<2	2.52	2.64			
5182	5.035	3.862	3.79	-	-	-	4.573	<1	<1	<1	<1	<1	4.314	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	2.569	2.483	<1	2.1	2.519			
5188	-	-	-	4.79	2.53	2.48	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.87	3.98	3.79	4.52	<2	<2	-	-	-	-	-		
5201	4.97	2.4	4.03	-	-	-	4.49	1.48	2.28	4.32	-	-	4.18	-	-	4.27	1.66	3.69	-	-	-	-	-	-	-	-	-	-	-	-	1	2.66	-	0.77	2.24				
5204	4.93	3.72	3.59	4.71	2.65	2.18	4.72	<1	<1	3.99	<1	<1	4.58	<1	<1	4.46	3.93	3.5	4.54	<2	<2	<1	2.43	2.51	<1	2.44	2.39	-	-	-	<1	2.71	2.74	<1	2.53	2.53			
5261	4.71	3.74	3.67	-	-	-	4.56	3.16	3.14	4.03	0	0	4.65	3.28	3.23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.64	2.67	0	2.04	2.18				
5329	5.07	3.77	3.84	-	-	-	4.43	<1	<1	3.56	<1	<1	4.25	<1	<1	4.48	3.84	3.79	4.58	3.54	3.6	-	-	-	-	-	-	-	-	-	<1	2.55	2.64	<1	1.52	2.08			
5338	4.7	3.61	3.82	-	-	-	4.43	2.35	2.27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	3.38	2.62	0	3	1.53				
5419	4.85	3.8	3.73	4.92	3.36	3.7	4.29	1.57	2.56	-	-	-	-	-	-	4.29	<2	<2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
5545	4.95	3.79	3.99	-	-	-	4.6	0	0	-	-	-	3.95	0	0	4.24	0	0	-	-	-	-	-	-	-	-	-	-	-	-	0	2.56	2.42	0	2.2	2.19			
5553	5.18	3.91	3.9	-	-	-	4.67	<1	<1	3.58	<1	<1	4.74	<1	<1	4.45	3.74	3.73	-	-	-	<1	2.6	2.58	-	-	-	-	-	-	-	-	-	-	-	-	-		
5615	5.08	4	4.04	-	-	-	4.59	2.18	2.64	4.23	<1	<1	4.65	<1	<1	4.32	3.67	3.73	-	-	-	<1	2.2	2.26	<0	2.58	2.54	-	-	-	<0	2.59	2.68	<0	2.26	2.2			
5632	5.1	3.9	3.9	-	-	-	4.6	-	2.3	4.1	<1	<1	4.3	<2	<2	-	3.7	3.8	-	-	-	-	-	-	-	-	-	-	-	<1	2.7	2.6	<1	1.7	1.8				
5654	4.94	3.86	3.87	-	-	-	4.46	0	0	-	-	-	4.22	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.71	2.79	0	2	2				
5701	3.89	3.81	3.83	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
5774	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
5801	4.84	3.85	3.62	-	-	-	4.49	2.6	2.78	-	-	-	4	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.54	2.49	0	2.2	2.08				
5804	4.81	3.69	3.62	-	-	-	-	-	-	3.66	<0,48	<0,48	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	2.66	2.6	<1	2.11	2.08				
5808	4.66	3.85	3.86	-	-	-	-	-	-	4	<1	<1	4.26	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	2.72	2.54	<1	<1	<1				
5883	4.98	3.89	3.88	-	-	-	4.21	<1	<1	4.28	<1	<1	4.13	<1	<1	4.36	3.75	3.76	4.27	<1	<1	0	2.55	2.4	0	2.46	2.19	-	-	0	2.48	2.64	0	2.24	2.16				
5950	-	-	-	<2	4.59	<2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3.28	4.93	3.56	<1	<1	<1	-	-	-	-	-		
6175	5.24	3.84	3.82	-	-	-	4.6	<1	1.48	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	3.63	3.15	0	2.45	2.18				
6224	5.15	4.23	4.2	-	-	-	4.77	2.06	1.95	-	-	-	4.14	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6253	4.72	3.88	3.9	-	-	-	-	-	-	-	-	-	4.43	<1	<1	3.81	3.74	3.77	-	-	-	-	-	-	<1	2.32	2.53	-	-	<1	2.3	2.67	<1	2.96	2.28				
6258	4.96	3.94	3.95	4.37	3.12	3.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	2.32	2.53	-	-	0	2.57	2.53	0	1.97	1.81					
6343	5.17	3.86	3.83	-	-	-	5	2.41	1.4	3.53	0	0	4.65	0	0	3.15	3.76	3.69	4.61	2.4	2.4	0	1.98	1.89	0	1.9	1.72	-	-	0	2.74	2.76	0	1.3	1.4				
6352	5.02	3.71	3.83	-	-	-	4.68	2.99	3.13	4.2	<1	<1	4.07	<1	<1	4.32	3.57	3.6	3.43	2.49	2.8	<1	2.1	2.46	<1	2.31	2.35	-	-	<1	2.62	2.75	<1	2.31	2				
6368	4.99	3.77	3.9	4.91	3.34	3.44	4.57	<1	<1	4.09	<1	<1	4.2	<1	<1	4.37	3.7	3.68	4.43	<1	<1	-	-	-	<1	2.41	2.45	5	3.92	3.93	4.51	<1	<1	<1	2.24	2.29			
6443	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.42	2.45	0	2.49	2.51	-	-	-	-	-	-	-	-		
6456	4.89	3.77	3.81	-	-	-	-	-	-	-	-	-	3.78	<1	<1	4.36	3.72	3.7	-	-	-	<1	2.36	2.29	<1	2.33	2.32	-	-	0	2.76	2.75	0	1.67	1.67				
6490	4.9	3.93	3.99	-	-	-	4.55	<1	<1	-	-	-	4.56	<1	<1	4.35	3.74	3.71	-	-	-	-	-	<1	2.52	2.52	-	-	<1	2.65	2.65	<1	1.81	1.92					
6594	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6686	5.15	4	3.81	5.04	3.93	3.78	4.58	0	0	4.08	0	0	-	-	-	3.99	3.77	3.66	-	-	-	0	2.52	2.52	-	-	-	5.11	3.95	3.96	4.64	0	0	0	2.4	2.54	0	0	0
6728	5.11	3.97	4.09	-	-	-	4.62	3.02	3.1	4.17	0	0	-	-	-	4.39	3.82	3.66	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6801	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.2	3.57	3.53	-	-	-	-	-	-	-	-	-	-	-	-	<1	2.6	2.62	<1	2.15	2.26			
6885	4.96	4.18	4	-	-	-	4.52	0	0	4.02	0	0	4.31	0	0	4.1	3.67	3.83	-	-	-	0	2.42	2.36	-	-	-	-	-	0	2.66	2.73	0	2.3	2.23				
6944	5.01	3.97	4.08	-	-	-	-	-	-	4.05	0	0	-	-	-	4.27	3.68	3.68	4.33	0	0	-	-	-	-	-	-	-	-	0	2.68	2.57	0	1.9	2.04				
6958	4.92	3.8	3.8	-	-	-	4.66	2.3	2.26	-	-	-	4.63	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.66	2.57	0	2.1	1.98					
6971	5	3.8	3.95	-	-	-	4.4	1.85	1.3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6981	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.72	2.69	0	1.95	2.15				
7182	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
7207	5.32	3.95	3.91	-	-	-	4.44	<1	<1	-	-	-	4.8	<1	3.6	-	-	-	<1	<1	<1	-	-	-	-	-	-	-	<1	2.53	2.45	<1	2.4	2.6					
7232	4.76	3.83	3.88	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.53	2.61	0	2.38	2.4					
7242	4.93	3.78	3.81	-	-	-	4.64	1.85	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.39	2.5	2.56	0	1.57	2.35					
7248	4.88	3.72	3.62	4.65	2.75	2.2	4.3	0	0	4.04	0	0	4.03	0	0																								

Appendix 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Preumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	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
7825	5.1	4.22	4.09	-	-	-	4.65	2.96	2.74	<1	<1	<1	-	-	-	-	-	-	4.48	2.51	2.34	-	-	-	-	-	-	-	-	-	-	<1	2.54	2.61	<1	1.63	2.02		
7876	5.05	3.96	3.92	-	-	-	4.42	<1	<1	4.19	<1	<1	4.24	<1	<1	4.2	3.79	3.8	-	-	-	<1	2.24	2.34	-	-	-	-	-	-	<1	2.72	2.67	<1	2.58	2.3			
7877	5.16	4.06	4.12	4.35	3.14	2.89	4.7	1.78	1.3	-	-	-	5.15	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	2.64	2.93	-	-	-				
7882	4.99	3.91	3.95	-	-	-	4.64	2.55	2.75	4.21	0	0	4.07	0	0	4.32	3.78	3.63	4.38	0	0	0	1.28	1.39	0	1.28	1.39	-	-	0	2.74	2.67	0	2.65	2.24				
7930	5.03	3.85	3.76	-	-	-	4.69	0	0	4.07	0	0	4.25	0	0	4.25	3.77	3.89	-	-	-	0	2.62	2.58	-	-	-	5.1	4	3.86	4.5	0	0	0	2.67	2.63	0	2.16	1.89
7940	4.86	3.94	3.88	-	-	-	4.69	2.48	2.28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
7962	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
7975	4.35	3.86	3.95	-	-	-	3.72	0	0	-	-	-	-	-	-	3.69	3.56	3.42	-	-	-	-	-	-	-	-	-	-	-	0	2.6	2.49	0	2.02	2.15				
8066	-	-	-	-	-	-	-	-	-	3.86	0	0	3.8	0	0	4.43	0	0	4.3	0	0	0	2.06	2.15	-	-	-	4.72	3.7	3.77	4.24	0	0	-	-	-			
8068	5.04	3.83	3.76	-	-	-	4.34	<1	<1	4.2	<1	<1	4.04	<1	<1	4.18	3.78	3.79	-	-	-	0	2.59	2.32	0	2.11	2.18	-	-	0	2.57	2.54	0	1.78	1.78				
8105	5.11	4.03	3.98	-	-	-	-	-	-	4.17	0	0	-	-	-	4.08	3.66	3.78	-	-	-	-	-	-	-	-	-	-	-	0	1.82	1.82	0	2.56	2.62				
8228	4.68	3.75	3.76	4.89	3.57	3.54	4.22	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.71	2.61	0	2.18	2.32				
8252	5.04	3.96	4	-	-	-	-	-	-	4.08	<1	<1	4.2	<1	<1	4.26	3.74	3.61	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
8260	4.93	3.89	3.91	-	-	-	4.53	0	0	-	-	-	4.13	0	0	4.26	3.68	3.72	-	-	-	0	2.23	2.37	0	2.29	2.41	-	-	0	2.7	2.54	0	2.3	2.23				
8313	4.85	3.83	3.91	-	-	-	4.41	<1	<1	-	-	-	4	<1	<1	4.18	3.63	3.7	-	-	-	-	-	-	-	-	-	-	-	<1	2.43	2.71	<1	2.3	2.11				
8397	5.04	4.12	4.09	-	-	-	4.46	0	0	4.22	0	0	4.48	0	0	4.33	3.86	3.78	4.82	0	0	-	-	-	-	<1	2.6	2.53	-	-	0	2.68	2.47	0	2.34	2.2			
8430	5.42	3.86	4	-	-	-	4.43	2.16	1.9	3.18	<1	<1	-	-	-	4.35	3.73	3.68	-	-	-	-	-	-	-	-	-	-	<1	2.34	2.6	1	1.4	1.7					
8435	5.06	3.76	4.04	-	-	-	4.67	<1	<1	4.14	<1	<1	4.53	<1	3.78	4.25	3.68	3.6	-	-	-	0	2.36	2.32	5.02	3.87	3.86	-	<1	2.59	2.97	<1	2.59	2.97					
8506	5.11	4.04	3.94	-	-	-	4.29	0	0	3.62	0	0	4.58	0	0	-	-	-	-	-	-	0	2.29	2.17	-	-	-	-	0	2.65	2.61	0	2.42	2.52					
8523	5.03	3.92	3.96	5.03	3.38	3.31	4.74	3.08	3.04	3.61	<1	<1	-	-	-	4.26	3.75	3.79	-	-	-	-	-	-	-	-	-	-	<1	2.69	2.72	<1	2.6	2.48					
8528	5.5	3.87	3.8	-	-	-	4.6	<1	<1	-	-	-	4.19	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.71	3.74	<1	3.15	3.31					
8568	4.98	4.02	3.88	-	-	-	4.67	2.7	2.96	3.85	0	0	5.09	0	0	-	-	-	0	0	0	-	-	-	0	2.45	2.37	-	-	0	2.51	2.55	0	2.12	2.27				
8626	5.14	3.8	4.78	-	-	-	4.58	0	0	4.04	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5.04	3.75	3.77	-	-	-	-	-	-				
8628	-	-	-	-	-	-	-	-	-	-	-	-	4.23	0	0	4.23	3.69	3.77	4.26	0	0	0	2.45	2.41	0	2.62	2.45	-	-	0	2.66	2.69	0	2.08	2.48				
8657	4.98	3.81	3.81	-	-	-	4.33	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.45	2.45	0	1.9	1.65					
8734	4.98	3.97	4.01	-	-	-	4.44	2.58	2.76	-	-	-	-	-	-	-	-	4.43	3.21	3.28	-	-	-	-	-	-	-	-	2.63	0	2.62	0	0	0					
8742	5	3.65	3.71	-	-	-	-	-	-	4.32	<1	<1	-	-	-	4.2	3.86	4.08	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
8756	4.91	3.85	3.86	-	-	-	4.34	2.8	2.52	3.58	<1	<1	4.5	<1	<1	4.19	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
8766	4.99	3.81	3.78	-	-	-	4.3	0	0	4.13	0	0	4.38	0	0	4.23	3.78	3.59	-	-	-	0	2.32	2.52	-	-	-	-	0	2.4	2.6	0	2.15	2.45					
8829	5	4.04	3.95	-	-	-	-	-	-	-	-	-	4.2	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.62	2.65	0	2.07	2.11					
8891	4.9	3.69	3.8	-	-	-	4.51	<1	<1	3.97	<1	<1	5	<1	3.45	4.05	3.68	3.64	-	-	-	-	-	-	-	-	-	-	<1	2.66	2.61	<1	2.25	2.32					
8909	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
8955	5.04	3.86	3.86	-	-	-	-	-	-	4.11	<1	<1	4.15	<1	<1	4.32	3.75	3.74	4.66	2.15	2.3	<1	2.41	2.54	<1	2.49	2.41	5.08	3.9	3.89	4.6	<1	<1	<1	2.7	2.76			
9002	4.96	3.89	3.89	4.34	0	0	4.63	<1	<1	3.9	<1	<1	3.88	<1,7	<1,7	4.2	3.74	3.76	4.11	<1	<1	<1	2.41	2.54	<1	2.42	2.4	-	0	2.68	2.63	0	2.2	2.23					
9003	4.9	3.89	3.91	-	-	-	4.57	-	-	4.1	0	0	-	-	-	4.25	3.58	3.62	-	-	-	-	-	-	-	-	-	-	0	2.66	2.59	0	1.87	1.89					
9025	5.07	3.83	3.92	-	-	-	4.89	2.81	2.51	-	-	-	-	-	-	-	-	-	-	-	-	0	2.32	2.66	-	-	-	0	2.94	2.23	0	2.28	2.29						
9034	5	3.9	3.9	4.4	2.1	1.7	4.6	0	0	3.9	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
9078	5.06	2.89	3.75	-	-	-	4.45	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
9217	6.91	5.38	5.23	-	-	-	5.97	4.1	4.18	0	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
9408	5.04	3.91	3.79	-	-	-	4.58	<1	<1	4.13	<1	<1	4.36	<1	<1	4.3	3.76	3.6	-	-	-	<0	2.2	2.32	<0	2.2	2.32	5.04	3.89	3.67	4.53	<1	<1	<0	2.65	2.72			
9429	5.06	3.82	3.76	-	-	-	-	-	-	-	-	-	4.56	<1	<1	4.41	3.81	3.69	-	-	-	<1	2.57	2.41	<1	2.43	2.34	-	<1	2.72	2.76	<1	2.32	1.9					
9436	5.03	3.84	3.78	4.32	1.73	<1	4.12	<1	<1	3.84	<1	<1	4.68	<1	<1	4.32	3.76	3.66	4.68	<1	<1	<1	2.36	2.37	<1	2.44	2.58	-	<1	2.82	2.8	<1	2.24	2.6					
9441	-	-	-	-	-	-	-	-	-	-	-	-	4.65	<1	<1	-	-	-	-	-	-	0	2.4	2.4	0	2.51	2.56	5.04	3.52	3.69	4.6	<1	<1	0	2.59	2.71			
9453	5.01	3.67	3.63	-	-	-	4.45	<1	<1	-	-	-	4.26	<1	<1	4.34	3.78	3.73	-	-	-	-	-	-	-	-	-	-	<1	2.71	2.68	<1	2.31	2.03					
9512	4.79	3.46	3.67	-	-	-	3.65	<1	<1	-	-	-	-	-	-	-	-	-	4.39	2.38	2.67	-	-	-	-	-	-	<1	2.46	2.45	<1	1.6	1.69						
9559	4.99	3.89	3.86	-	-	-	4.59	0	0	4.04	0	0	4.46	0	0	4.32	3.54	3.56	0	2.3	2	-	-	-	-	-	-	0	2.62	2.62	0	1.6	1.48						
9662	5	3.7	3.64	-	-	-	4.57	0	0	2.94	0	0	4.29	2.8	3.3	4.31	3.3	3.14	-	-	-	0	-	0	2.4	2.57	5.02	3.7	3.8	4.5	0	0	-	-	-				
9747	4.79	2.25	3.71	-	-	-	4.51	3.18	2.91	-	-	-	4.34	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.57	2.7	0	2.04	2.08					
9783	5.03																																						

Appendix 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Preumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	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
Max	6.91	5.38	5.23	5.04	4.59	3.78	5.97	4.10	4.18	5.04	0	1.90	5.15	3.28	3.78	4.69	4.49	4.08	4.85	3.70	3.79	4.56	2.68	2.78	4.56	2.62	2.66	5.11	4.93	4.04	4.66	0	0	4.63	3.71	3.74	2.63	3.15	3.31
Med	5.00	3.85	3.88	4.46	3.13	3.10	4.56	0	0	4.04	0	0	4.31	0	0	4.30	3.74	3.70	4.43	0	0	0	2.40	2.41	0	2.44	2.48	5.04	3.86	3.78	4.53	0	0	0	2.65	2.63	0	2.15	2.16
m_{PT}	4.987	3.849	3.870	4.576	2.991	2.922	4.533	-	-	3.974	-	-	4.317	-	-	4.286	3.717	3.696	4.455	-	-	-	2.344	2.390	-	2.394	2.395	3.831	3.766	4.518	-	-	-	2.631	2.629	-	2.123	2.128	
s_{PT}	0.143	0.129	0.139	0.354	0.703	0.777	0.138	-	-	0.256	-	-	0.290	-	-	0.117	0.089	0.106	0.203	-	-	-	0.229	0.203	-	0.149	0.203	0.150	0.154	0.103	-	-	-	0.108	0.110	-	0.331	0.297	
u_{PT}	0.015	0.013	0.014	0.102	0.220	0.260	0.015	-	-	0.033	-	-	0.037	-	-	0.016	0.012	0.015	0.041	-	-	-	0.043	0.037	-	0.026	0.035	-	0.041	0.042	0.031	-	-	-	0.012	0.012	-	0.038	0.034
CV (%)	3	3	4	8	23	27	3	-	-	6	-	-	7	-	-	3	2	3	5	-	-	-	10	8	-	6	8	-	4	4	2	-	-	-	4	4	-	16	14
u_{rel,mPT}	0.2	0.3	0.3	1.8	5.9	7.1	0.3	-	-	0.7	-	-	0.7	-	-	0.3	0.3	0.3	0.7	-	-	-	1.5	1.3	-	0.9	1.2	-	0.9	0.9	0.6	-	-	-	0.4	0.4	-	1.4	1.3
F+	0	0	0	0	0	0	0	49	50	0	0	2	0	2	5	0	0	0	0	15	15	1	0	0	1	0	0	-	0	0	0	0	0	5	0	0	2	0	0
F-	0	0	0	1	4	6	0	0	0	3	0	0	0	0	0	1	8	7	6	0	0	0	2	1	0	1	1	-	0	0	1	0	0	0	2	0	0	6	5
<	10	5	2	0	0	0	5	0	0	6	0	0	4	0	0	5	5	3	2	0	0	0	2	3	0	4	4	-	2	1	1	0	0	0	7	7	0	2	2
>	3	2	2	0	0	0	2	0	0	1	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	-	1	0	0	0	0	0	4	3	0	1	1
Lower	4.56	3.46	3.45	3.51	0.88	0.59	4.12	0	0	3.21	0	0	3.45	0	0	3.93	3.45	3.38	3.85	0	0	0	1.66	1.78	0	1.95	1.79	3.28	3.38	3.30	4.21	0	0	0	2.31	2.30	0	1.13	1.24
Upper	5.41	4.24	4.29	5.64	5.10	5.25	4.95	0	0	4.74	0	0	5.19	0	0	4.64	3.98	4.01	5.06	0	0	0	3.03	3.00	0	2.84	3.00	5.11	4.28	4.23	4.83	0	0	0	2.95	2.96	0	3.11	3.02

N = number of reported results

n = results without annotation

Min = lowest reported result

Max = highest reported result

Med = median value

m_{PT} = assigned value

s_{PT} = standard deviation

u_{PT} = measurement uncertainty

F+ = false positive

F- = false negative

< = low outlier

> = high outlier

Lower = lowest accepted value

Upper = highest accepted value

False positive or false negative

Outside the acceptance limits

Results "larger than" are not evaluated

The parameter is not evaluated

The result not evaluated

u_{PT} > 0,3 s_{PT} and/or > 20 % outliers and/or fewer than 12 evaluated results

Appendix 2. Z-scores of all participants

Lab no.	Aerobic microorganisms 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Preumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds			
	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	0.021	1.018	0.721				1.140			-0.096	0	0	0.285	0	0																		0	0.267	0.924	0	0.476	0.445		
1237	-4.000	-4.000	-4.000	-2.953			-4.000			-4.000	0	0				-4.000	-4.000	-4.000	-4.000		0	-4.000	-4.000	0	-4.000	-4.000	-4.000	-4.000	0	0	0	-4.000	-4.000	0	-3.394	-3.193				
1545	1.003	0.085	0.288				0.269	0	0	0.491	0	0	0.078	0	0	-0.479	-1.762	-0.147	-0.320	0	0	0	0.815	1.235	0	0.912	1.208	0	0	0	-1.680	-2.720	0	0.688	0.412					
1594	0.863	-0.148	-0.867				0.559	0	0	0.413	0	0	0.319	0	0	-0.907		-0.053	1.949	0	0	0	-2.726	-2.761	0	0.912	0.961	0	0	0	0.082	-0.625	0	1.171	0.445					
1970	0.372	-1.547	-1.227	-0.357			0.269	0	0	0.100	0	0	0.100	0	0	0.289	1.615	-0.147	1.505	0	0	0	-0.015	0.100	0	-0.768	1.109	0.194	0.285	-0.078	0	0	0	1.194	1.561	0	0.930	1.928		
2000	-1.311	-1.158	-1.227				1.212	0		-1.074	0	0	-0.750	0	0	0.119	-1.311					0	0.247	0.544									0	-0.289	-0.260	0	0.839	0.917		
2035										0.882	0	0	-2.820	0	0											0	0.711	0.518						0	0.638	-0.260	0	0.234	0.580	
2058	-3.135	-4.000	0.937				0.414			0.100	0	0	-0.750	0	0				-0.123	0	0			1.925									0	-1.865	-1.080	0	-0.824	-0.767		
2064	-0.189	0.008	-0.217				1.357	0	0				-0.612	0	0																		0	-0.382	-0.443	0	-0.733	-0.262		
2221	0.863	-0.847	-1.011				0.777			-2.286	0	0	1.009	0	0	0.887	0.152	1.075	0.420	0	0	0	1.471	1.531	0	-0.902	-0.517					0	-0.197	0.924	0	1.413	1.995			
2317	-0.119	-0.770	-1.372				0.704			0.335	0	0	-0.026	0	0	0.375	-0.186	-1.088				0	-2.551	-4.000	0	-4.000	-3.869					0	0.730	1.015	0	0.627	0.782			
2324	0.302	-0.770	-0.867				-0.892	0	0				0.664	0	0	-0.565	0.377	0.041														0	0.174	0.650	0	-1.278	-1.138			
2344	-0.540	-2.169	-0.578				-0.529	0	0	-1.230	0	0	-0.578	0	0	0.546	0.039	0.417				0		-2.663	0	-1.750						0	-0.443	0		0.580				
2375	0.372	0.008	0.216				-0.166																										0	-0.104	0.559	0	1.171	0.546		
2386	0.372	1.096	1.515				1.140			0.530	0	0	-1.854	0	0	1.485	0.602	0.511				0	-0.715	-1.380							0	-0.289	-1.809	0	-0.129	-0.060				
2402	2.196	-0.070	0.288				-0.094	0	0	-0.526	0	0																				0	0.082	0.650	0	0.385	0.412			
2443	0.512	-0.381	0.721				1.212																										0	2.028	1.835	0		-0.430		
2459	-4.000	0.940	1.515																													0	-4.000	-1.536	0					
2659	0.863	0.008	2.236				-0.094			0.256	0	0																					0	0.174	-0.260	0	-0.582	-0.498		
2720	-0.329	0.085	0.144				-0.674	0					-0.647	0	0																	0	-0.104	-4.000	0	-0.038	1.490			
2745	0.652	0.707	0.432				-0.094	0	0	0.452	0	0	-0.474	0	0	0.033						0	0.728	0.643							0	0.638	0.013	0	1.081	0.715				
2794	-0.119	-0.536	-0.361																																					
2805	-2.153	-1.003	-0.794				0.487			-3.694	0	0																												
2810	0.302	1.484	0.577																																0	0.267	0.013	0	-1.247	-0.262
2812	1.073	0.552	-0.289																															0	-0.104	-0.807	0	-1.066	-0.296	
2920	0.652	-0.536	-0.650				0.124	0	0	0.452	0	0																												
2941	-0.540	0.474	-0.578				-0.457			1.000	0	0	-0.233	0	0	0.375	0.827	0.793	-0.616			0	0.711	0.813							0	0.174	0.650	0	-0.975	-1.778				
3031	0.372	-0.226	-1.155				-0.094			-0.761	0	0				1.656	-0.524	-1.558										0.194	-0.040	0.604	0	0								
3055																																								
3159	1.214	1.717	0.216				0.487	0	0	0.296	0	0	-0.198	0	0	1.229	0.264	0.041	-0.912	0	0																			
3243	0.302	0.552	1.587				-0.239	0	0																															
3305	-0.470	0.396	0.072				0.704	0	0	0.530	0	0	0.561	0	0	0.460	0.602	0.041	0.716	0	0	0	1.121	0.593	0	0.576	0.715	-0.274	-0.365	-0.663	0	0	0	0.730	0.286	0	0.234	-0.969		
3415	-0.189	-0.459	-1.083				-0.384	0	0	0.022	0	0	-0.716	0	0	1.400	0.489	0.887				0	0.160	0.347	0	0.039	-1.207					0	1.472	0.013	0	-0.038	-0.161			
3457	0.091	0.319	3.030				0.196			0.217	0	0				-2.871	0.602	1.922	-1.060			0	-1.371	-1.331								0	0.730	-0.443	0	0.083	-3.529			
3515	1.985	2.417	1.948				0.922	0	0	1.273	0	0	1.423	0	0	0.033	-4.000	-4.000	0.913	0	0																			
3543	0.372	-0.536	1.515				-2.561						-1.130	0	0		-0.974	-1.088				0																		
3587	-1.171	-1.003	-1.083				-0.166			0.374	0	0	-1.026	0	0	-0.821	0.039	0.229				0																		
3831	-0.750	-0.925	-0.506							2.486	0																													
3878	0.624	-0.124	-0.939				-0.101			-3.397	0		0.364	0	0	-2.094	-0.400	-0.881																						
3965																																								
4050	-0.329	-0.925	0.144				0.051	0	0				-3.269	0	0																									
4064	-0.049	-0.381	-0.289				0.487	0	0																															
4100	0.372	0.008	0.216	-0.470			0.269	0	0	-1.426	0	0	0.871	0	0							0	0.553	0.741	0	0.980	0.419													
4171	-0.961	0.629	0.432				0.342			-1.387	0	0	0.388	0	0																									
4246	-0.540	1.329	1.515				0.995			0.178	0	0				0.033																								
4288	-4.000	0.319	-0.217				-0.602	0	0	0.022	0	0	2.734	0	0	0.375	-0.749	-1.464				0	-1.108	-0.689	0	-2.852	-1.700													
4339	0.863	0.552	0.505				-0.166	0	0	0.413	0	0	0.561	0	0	-0.907	4.000	-2.310	1.209			0	0.509	0.741	0	1.181	0.468	0.929	0.740	0.214	0	0	0	-1.587	0.286	0	0.234	0.715		
4400	-3.626	3.505	-4.000				-4.000	0	0	-0.800	0	0	-4.000	0	0																									
4418	-4.000	0.085	-2.021	-1.514	0.240	0.718	-4.000	0	0	0.608	0	0				-4.000	-4.000	-1.088																						
4449	0.652	1.484	1.731				-0.384	0	0				-3.062	0	0																									
4557	1.003	0.785	1.																																					

Appendix 2. Z-scores of all participants

Lab no.	Aerobic microorganisms 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Preumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	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
7825	0.793	2.883	1.587				0.849			0	0								0.124												0	-0.845	-0.169	0	-1.489	-0.363			
7876	0.442	0.863	0.360				-0.820	0	0	0.843	0	0	-0.267	0	0	-0.736	0.827	0.981			0	-0.453	-0.245							0	0.823	0.377	0	1.383	0.580				
7877	1.214	1.640	1.803	-0.639	0.211	-0.041	1.212						2.872	0	0															0	0.082	2.746							
7882	0.021	0.474	0.577				0.777			0.921	0	0	-0.854	0	0	0.289	0.714	-0.618	-0.370	0	0	0	-4.000	-4.000	0	-4.000	-4.000		0	1.009	0.377	0	1.595	0.378					
7930	0.302	0.008	-0.794				1.140	0	0	0.374	0	0	-0.233	0	0	-0.309	0.602	1.828			0	1.209	0.939				1.129	0.610	-0.176	0	0	0	0.360	0.013	0	0.113	-0.801		
7940	-0.891	0.707	0.072				1.140																																
7962																																							
7975	-4.000	0.085	0.577				-4.000	0	0							-4.000	-1.762	-2.593															0	-0.289	-1.262	0	-0.310	0.075	
8066										-0.448	0	0	-1.785	0	0	1.229			-0.764	0	0	0	-1.240	-1.183			-0.875	0.025	-2.710	0	0								
8068	0.372	-0.148	-0.794				-1.400	0	0	0.882	0	0	-0.957	0	0	-0.907	0.714	0.887			0	1.078	-0.344	0	-1.911	-1.060						0	-0.567	-0.807	0	-1.036	-1.171		
8105	0.863	1.407	0.793				0.765	0	0							-1.761	-0.636	0.793														0	-4.000	-4.000	0	1.323	1.658		
8228	-2.153	-0.770	-0.794	0.885	0.823	0.795	-2.271	0	0																														
8252	0.372	0.863	0.937							0.413	0	0	-0.405	0	0	-0.223	0.264	-0.806																					
8260	-0.400	0.319	0.288				-0.021	0	0							-0.223	-0.411	0.229			0	-0.496	-0.097	0	-0.701	0.074							0	0.638	-0.807	0	0.537	0.344	
8313	-0.961	-0.148	0.288				-0.892	0	0							-0.907	-0.974	0.041															0	-1.865	0.742	0	0.537	-0.060	
8397	0.372	2.106	1.587				-0.529	0	0	0.960	0	0	0.561	0	0	0.375	1.615	0.793	1.801	0	0																		
8430	3.037	0.085	0.937				-0.747			-3.108	0	0				0.546	0.152	-0.147																					
8435	0.512	-0.692	1.226				0.995	0	0	0.648	0	0	0.733	0	0	-0.309	-0.411	-0.900									0.261	0.610											
8506	0.863	1.484	0.505				-1.763	0	0	-1.387	0	0	0.906	0	0																								
8523	0.302	0.552	0.649	1.280	0.553	0.499	1.503			-1.426	0	0				-0.223	0.377	0.887																					
8528	3.598	0.163	-0.506				0.487	0	0							-0.440	0	0																					
8568	-0.049	1.329	0.072				0.995			-0.487	0	0	2.665	0	0																								
8626	1.073	-0.381	4.000				0.342	0	0	0.256	0	0																											
8628																																							
8657	-0.049	-0.303	-0.434				-1.473	0	0																														
8734	-0.049	0.940	1.010				-0.674																																
8742	0.091	-1.547	-1.155							1.352	0	0				-0.736	1.615	3.615																					
8756	-0.540	0.008	-0.073				-1.400			-1.543	0	0	0.630	0	0	-0.821																							
8766	0.021	-0.303	-0.650				-1.690	0	0	0.608	0	0	0.216	0	0	-0.479	0.714	-0.994			0	-0.103	0.643																
8829	0.091	1.484	0.577													-0.405	0	0																					
8891	-0.610	-1.236	-0.506				-0.166	0	0	-0.017	0	0	2.355	0	0	-2.017	-0.411	-0.523																					
8909																																							
8955	0.372	0.085	-0.073							0.530	0	0	-0.578	0	0	0.289	0.377	0.417	1.012			0	0.291	0.741	0	0.644	0.074	0.461	0.805	0.799	0	0	0	0.638	1.197	0	-0.129	-0.060	
9002	-0.189	0.319	0.144	-0.667			0.704	0	0	-0.291	0	0	-1.509	0	0	-0.736	0.264	0.605	-1.702	0	0																		
9003	-0.610	0.319	0.288				0.269			0.491	0	0				-0.309	-1.536	-0.712																					
9025	0.582	-0.148	0.360				2.591																																
9034	0.091	0.396	0.216	-0.498	-1.269	-1.573	0.487	0	0	-0.291	0	0																											
9078	0.512	-4.000	-0.867				-0.602	0	0																														
9217	4.000	4.000	4.000				4.000																																
9408	0.372	0.474	-0.578				0.342	0	0	0.608	0	0	0.147	0	0	0.119	0.489	-0.900																					
9429	0.512	-0.226	-0.794							0.837	0	0	1.058	1.052	-0.053																								
9436	0.302	-0.070	-0.650	-0.724	-1.795		-2.997	0	0	-0.526	0	0	1.251	0	0	0.289	0.489	-0.335	1.110	0	0	0	0.072	-0.097	0	0.307	0.912												
9441																																							
9453	0.162	-1.391	-1.733				-0.602	0	0																														
9512	-1.382	-3.023	-1.444				-4.000	0	0																														
9559	0.021	0.319	-0.073				0.414	0	0	0.256	0	0	0.492	0	0	0.289	-1.987	-1.276																					
9662	0.091	-1.158	-1.660				0.269	0	0	-4.000	0	0	-0.095	0	0	0.204	-4.000	-4.000																					
9747	-1.382	-4.000	-1.155				-0.166									0.078	0	0																					
9783	0.302	0.940	0.072																																				
9886				0.715	-0.642	0.100																																	
9890	-4.000	-1.236	-0.289				0.559	0	0	-0.213	0	0	1.216	0	0	-0.052	-2.324	-1.088																					
9903	0.091	-0.226	0.288				-1.037	0	0	0.804	0	0	0.009	0	0	0.631	1.165	0.793																					
9950	0.863	0.163	0.216				-0.457	0	0																														

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

Appendix 2. Z-scores of all participants

Lab no.	Aerobic microorganisms 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Preumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	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
	The result is not evaluated																																						

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

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

In a PT, identical test material is analysed by a number of participants. After reporting of results by the participants, the organiser evaluates the results and compiles them in a report.

The Swedish Food Agency's PT program offers

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

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

The Swedish Food Agency's reference material

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

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