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**AFNOR Certification of the VIDAS LSX method (ref. 30224)
according to EN ISO 16140 standard for the detection of
Listeria genus**

Certificate number: BIO 12/12-07/04

SUMMARY REPORT

<u>Validation date:</u>	01/07/2004
<u>Extension date:</u> (results interpretation against EN ISO 11290-1/A1)	02/12/2004
<u>Extension date:</u> (protocol evolution: extension of incubation period)	20/09/2005
<u>Extension and Renewal date:</u> (addition of environmental samples)	01/07/2008
<u>End validation date:</u>	01/07/2012

VIDAS LSX-summary 2009 v01

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1 Introduction

1.1 Validation references and scope

The VIDAS LSX method has been validated with the certificate number BIO 12/12–07/04.

1st validation: July 2004 and extension study: September 2005

- Reference protocol: EN ISO 16140:2003
- Reference method: EN ISO 11290/A1:2004 « Horizontal method for the detection of *Listeria monocytogenes* ». The diagram summarizing the method is shown in appendix A.
- Scope: meat products, dairy products and vegetables.

Extension study: July 2008

- Scope: environmental samples.

1.2 Protocol and principle of the alternative method

1.2.1 Protocol

The diagram summarising the method is shown in appendix A.

General protocol for meat products, dairy products, vegetables and environmental samples is:

- enrichment in LX broth, incubated for 16 - 22 hours at 30°C +/- 1°C,
- then inoculation of 3 mL of the LX broth in a new 6 mL LX broth bouillon, incubated for 6 to 24 hours at 30°C +/- 1°C,

Note: in the extension studies, the minimum and maximum times of incubation (6 hours and 24 hours) were studied.

- followed by a VIDAS LSX test after heating of an aliquot of the second LX broth for 15 ± 1 minutes at 95-100°C.

Simplified protocol without transfer for the environmental surface samples:

- enrichment in LX broth, incubated for 24 - 26 hours at 30°C +/- 1°C,
- followed by a VIDAS LSX test after heating of an aliquot of the second LX broth for 15 ± 1 minutes at 95-100°C.

Positive results with VIDAS LSX tests have to be confirmed by streaking the non-heated LX broth on a *Listeria* selective media (Oxford, Palcam or chromogenic media) and identification with the tests described in the reference method (including purification step).

1.2.2 Principle of the VIDAS LSX test

VIDAS LSX is an enzyme immunoassay for use on the automated VIDAS for the detection of *Listeria* antigens using the ELFA method (Enzyme Linked Fluorescent Assay).

Each test is composed of two parts:

- the Solid Phase Receptacle (SPR[®]) serves as the solid phase as well as the pipeting device. The interior of the SPR[®] is coated with anti-*Listeria* antibodies adsorbed onto its surface,
- the strip which contains all the ready-to-use reagents for the assay: washing buffer, antibodies anti-*Listeria* conjugated with alkaline phosphatase and substrate.

All of the assay steps are performed automatically by the instrument. Part of the enrichment broth is dispensed into the reagent strip. The reaction medium is cycled in and out of the SPR[®] several times.

At the end of the assay, results are automatically analyzed by the instrument. The fluorescence is measured at 450 nm and give a RFV (relative fluorescence value).

Then, the instrument calculates a test value for each sample. This value is then compared to internal references (thresholds) and each result is interpreted (positive, negative) as following:

Test value (TV) = RFV sample / RFV standard.

if TV < 0.1, the test is negative
and
if TV ≥ 0.1, the test is positive

1.3 Reference method

The validation study was carried out by reference to the EN ISO 11290-1/A1:2004 (#) standard method. The diagram summarizing the method is shown in appendix A.

1.4 Background of certification

1.4.1 1st Certification date, Renewal date and Extensions dates

The VIDAS LSX method was validated with the certificate number BIO 12/12-07/04.

- July 2004: initial certification for meat products, dairy products and vegetables
- December 2004: extension according to the new EN ISO 11290-1/A1
- September 2005: extension to increase the length of incubation period (from 6 hours to 24 hours)
- July 2008: addition of a "environmental samples" category in the application scope and renewal of the certification

1.4.2 Reference method used for the validation

EN ISO 11290-1/A1:2004 standard method: « Horizontal method for the detection of *Listeria monocytogenes* »

1.4.3 Main results obtained in the first validation study

The results obtained in the first validation study and in the different extensions are presented in this summary report (§2 and §3)

1.4.4 Report of modifications made in the alternative method, having caused or not a validation extension

The modifications of the VIDAS LSX method concerned:

- the protocol of the method, but not its principle (assays made in an extension study in 2005): initially the method was certified with a secondary enrichment for 6 hours, and this incubation period was increased to 24 hours
- the addition of a new category: environmental samples, with the use of the general protocol for all the types of samples (water, surfaces, residues, scraps) and the use of a specific protocol only for the environmental surface samples

2 Comparative study of methods

2.1 Relative accuracy, relative specificity and relative sensitivity

The aim of this study, according to the reference document ISO 16140, was to compare the performances of the VIDAS LSX method to the the reference EN ISO 11290-1/A1:2004 method on *Listeria* naturally and artificially contaminated samples and uncontaminated samples.

2.1.1 Number and nature of the samples

According to the ISO 16140 standard, a minimum of 60 products per category must be analyzed, with around 50% of positive products (at least 30 results) and 50% of negative products.

The initial validation study (July 2004) gave 190 results, obtained only with a secondary LX enrichment for 6 hours at 30°C.

The extension validation study (September 2005) gave 124 results, obtained with a secondary LX enrichment for 6 hours and for 24 hours at 30°C.

The extension validation study for the environmental samples category gave 124 results in 2008.

Each category was divided into various types and the results are displayed as follows:

1) 6 hours enrichment:

Categories	Types	Positive results*	Negative results	Total
Meat products	Raw meat	28	17	45
	Raw seasoned meat	15	3	18
	Delicatessen	10	27	37
	Total	53	47	100
Dairy products	Raw milk and raw milk cheese (cow)	40	38	78
	Raw milk and raw milk cheese (goat)	15	13	28
	Pastries	6	4	10
	Total	61	55	116
Vegetables	Raw	23	36	59
	Frozen	11	13	24
	Cooked or seasoned	12	3	15
	Total	46	52	98
Environment	Various waters	7	11	18
	Surface samples (specific protocol without transfer)	19	22	41
	Surface samples (general protocol)	28	18	46
	Residues and scraps	13	7	20
	Total	67	58	125
TOTAL	6 hours protocol All studied categories	208	190	398
TOTAL	6 hours protocol for all products EXCEPT surface samples AND surface samples with specific protocol	199	194	393

2) 24 hours enrichment

Categories	Types	Positive results*	Negative results	Total
Meat products	Raw meat	8	6	14
	Raw seasoned meat	12	3	15
	Delicatessen	4	7	11
	Total	24	16	40
Dairy products	Raw milk and raw milk cheese (cow)	16	15	31
	Raw milk and raw milk cheese (goat)	4	5	9
	Pastries	4	3	7
	Total	24	23	47
Vegetables	Raw	3	13	16
	Frozen	7	6	13
	Cooked or seasoned	5	3	8
	Total	15	22	37
Environment	Various waters	7	13	20
	Surface samples (specific protocol without transfer)	19	22	41
	Surface samples (general protocol)	28	18	46
	Residues and scraps	14	6	20
	Total	68	59	127
TOTAL	24 hours protocol All studied categories	112	98	210
TOTAL	24 hours protocol for all products EXCEPT surface samples AND surface samples with specific protocol	103	102	205

* positive results by one of the methods

2.1.2 Artificial contamination of the samples and percentage

Artificial contamination was achieved by using stressed bacterial suspensions, the stress treatment and efficiency of which have been determined according to EN ISO 16140 and AFNOR validation rules.

18 different strains were used (10 in the initial validation study and 8 in the extension studies) to obtain 82 positive results (45 in the initial validation study and 37 in the extension studies)

Finally, 39% of positive results were obtained as a result of artificial contamination for the protocol with a 6 hours secondary enrichment and 33%, for the protocol with a 24 hours secondary.

2.1.3 Results of assays

The analyses were conducted in single using the two methods.
Raw data are presented in appendix B.

The tables of the results of samples are below:

1. 6 hours secondary enrichment – All products (initial validation study + extension studies)

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 180	Positive deviation (R-/A+) PD = 13	193
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 15 *	Negative agreement (A-/R-) NA = 190 **	205
Total	195	203	398

2. 24 hours secondary enrichment – All products (extension studies)

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 98	Positive deviation (R-/A+) PD = 11	109
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 3 *	Negative agreement (A-/R-) NA = 98 ***	101
Total	101	109	210

3. All products (EXCEPT surface samples) analyzed with the 6 hours secondary enrichment protocol, plus surface samples analyzed with the specific protocol (initial validation study + extension studies)

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 175	Positive deviation (R-/A+) PD = 11	186
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 13 *	Negative agreement (A-/R-) NA = 194 **	205
Total	188	205	393

4. all products (EXCEPT surface samples) analyzed with the 24 hours secondary enrichment protocol,, plus surface samples analyzed with the specific protocol (extension studies)

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 91	Positive deviation (R-/A+) PD = 9	100
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 3 *	Negative agreement (A-/R-) NA = 102 **	105
Total	94	111	205

Legend:

A+ = positives confirmed

A- = immediate negatives **and** negatives after confirmation when presumed positive

* 0 unconfirmed VIDAS LSX positive result

** 1 unconfirmed VIDAS LSX positive result

*** 2 unconfirmed VIDAS LSX positive results

2.1.4 Calculation of relative accuracy (AC), relative specificity (SP) and relative sensitivity (SE) according to EN ISO 16140 standard

1. 6 hours secondary enrichment for all products (initial validation study + extension studies)

Category	PA	NA	ND	PD	Sum N	Relative accuracy AC (%) [100x(PA+NA)]/N	N+ PA + ND	Relative sensitivity SE (%) [100xPA]/N+	N- NA + PD	Relative specificity SP (%) [100xNA]/N-
Meat products	45	47	4	4	100	92,0	49	91,8	51	92,2
Dairy products	54	55	4	3	116	94,0	58	93,1	58	94,8
Vegetables	42	52	3	1	98	95,9	45	93,3	53	98,1
Environment	39	36	4	5	84	89,3	43	90,7	41	87,8
TOTAL	180	190	15	13	398	93,0	195	92,3	162	93,6

2. 24 hours secondary enrichment for all products (extension studies)

Category	PA	NA	ND	PD	Sum N	Relative accuracy AC (%) [100x(PA+NA)]/N	N+ PA + ND	Relative sensitivity SE (%) [100xPA]/N+	N- NA + PD	Relative specificity SP (%) [100xNA]/N-
Meat products	22	16	0	2	40	95,0	22	100	18	88,9
Dairy products	21	23	0	3	47	93,6	21	100	26	88,5
Vegetables	14	22	1	0	37	97,3	15	93,3	22	100
Environment	41	37	2	6	86	90,7	43	95,3	43	86,0
TOTAL	98	98	3	11	210	93,3	101	97,0	109	89,9

3. All products (EXCEPT surface samples) analyzed with the 6 hours secondary enrichment protocol, plus surface samples analyzed with the specific protocol (initial validation study + extension studies)

Category	PA	NA	ND	PD	Sum N	Relative accuracy AC (%) [100x(PA+NA)]/N	N+ PA + ND	Relative sensitivity SE (%) [100xPA]/N+	N- NA + PD	Relative specificity SP (%) [100xNA]/N-
Meat products	45	47	4	4	100	92,0	49	91,8	51	92,2
Dairy products	54	55	4	3	116	94,0	58	93,1	58	94,8
Vegetables	42	52	3	1	98	95,9	45	93,3	53	98,1
Environment	34	40	2	3	79	93,7	36	94,4	43	93,0
TOTAL	175	194	13	11	393	93,9	188	93,1	162	94,6

4. withal products (EXCEPT surface samples) analyzed with the 24 hours secondary enrichment protocol, plus surface samples analyzed with the specific protocol (extension studies)

Category	PA	NA	ND	PD	Sum N	Relative accuracy AC (%) [100x(PA+NA)]/N	N+ PA + ND	Relative sensitivity SE (%) [100xPA]/N+	N- NA + PD	Relative specificity SP (%) [100xNA]/N-
Meat products	22	16	0	2	40	95,0	22	100	18	88,9
Dairy products	21	23	0	3	47	93,6	21	100	26	88,5
Vegetables	14	22	1	0	37	97,3	15	93,3	22	100
Environment	34	41	2	4	81	92,6	36	94,4	45	91,1
TOTAL	91	102	3	9	205	94,1	94	96,8	111	919,9

	1)	2)	3)	4)
Relative accuracy : AC	93,0 %	93,3 %	93,9 %	94,1 %
Relative specificity : SP	93,6 %	89,9 %	94,6 %	91,9 %
Relative sensitivity : SE	92,3 %	97,0 %	93,1 %	96,8 %

The AFNOR Technical Board asks the sensitivity of the two methods to be recalculated with consideration of all the confirmed positives (this includes the additional positives of the alternative method):

	Alternative method (PA + PD) / (PA + PD + ND)	Reference method (PA + ND) / (PA + PD + ND)
1)	92,8 %	93,8 %
2)	97,3 %	90,2 %
3)	93,5 %	94,5 %
4)	97,0 %	91,3 %

2.1.5 Analysis of discrepant results

According to annex F of the EN ISO 16140 standard, the minimum number of discordances for which a statistical test must be conducted in order to compare the two methods is 6.

The statistic test was performed.

Note: the number of discordances is important because the first step of enrichment is different between both methods

When the total number of discordances is greater than 22, the McNemar test with the χ^2 distribution for one degree of freedom is used. The aim is the determination of $d = |PD - ND|$ and the comparison between d and a d value, depending on the total number of discordances and according to the EN ISO 16140 (annex F). Both methods would be considered as different if $d \geq d$ value.

Profile of protocols used	Number of discordances	d value	d	Conclusion
6 hours secondary enrichment – all products	28	15 – 13 = 2	11	Equivalence
All products (except surface samples) analyzed with the 6 hours secondary enrichment protocol, plus surface samples analyzed with the specific protocol	24	13 – 11 = 2	10	Equivalence

When the number of discordances is between 6 and 22, the aim is the determination of the M value, depending on the total number of discordances and according to the EN ISO 16140 (annex F) and the comparison between M and an m-value, as the smaller of the two values of PD and ND. Both methods would be considered as equivalent if $m > M$.

Profile of protocols used	Number of discordances	M	m	Conclusion
LX secondary enrichment: 24 hours for all studied categories	14	2	3	Equivalence
All products (except surface samples) analyzed with the 24 hours secondary enrichment protocol, plus surface samples analyzed with the specific protocol	12	2	3	Equivalence

The VIDAS LSX method can be considered equivalent to the reference method (EN ISO 11290-1/A1) for the detection of *Listeria* genus.

2.2 Relative detection level

The objective was to determine the level of contamination for which less than 50% of the responses obtained are positive and that for which more than 50% of the responses obtained are positive.

Different 'food strain matrix' couples were studied in parallel with the reference method and the VIDAS LSX method, for the four studied categories.

The artificial contaminations were realized according to EN ISO 16140 and AFNOR validation rules.

The levels of detection, calculated according to the Spearman – Kärber* method (LOD₅₀), obtained for each combination « matrix – strain » are the following:

Matrix	Strain	Relative detection level for the reference method (UFC / 25 g or 25 mL)	Relative detection level for the alternative method (UFC / 25 g or 25 mL)
Rillettes	<i>L.monocytogenes</i>	0.3 [0.2 – 0.5]	0.4 [0.2 – 0.6]
Raw milk	<i>L.ivanovii</i>	0.7 [0.6 – 0.8]	0.8 [0.7 – 0.9]
Salad	<i>L.innocua</i>	0.5 [0.3 – 0.7]	0.5 [0.4 – 0.6]
Process water	<i>L.innocua</i>	0.7 [0.4 – 1.4]	0.4 [0.2 – 0.6]

* "Hitchins A. Proposed Use of a 50 % Limit of Detection Value in Defining Uncertainty Limits in the Validation of Presence-Absence Microbial Detection Methods, Draft 10th December, 2003".

Conclusion:

The level of detection was between 0.2 and 0.9 cells per 25 grams for the VIDAS LSX method and between 0.2 and 1.4 cells per 25 grams for the reference method.

2.3 Inclusivity / exclusivity

The inclusivity and the exclusivity of the method are defined by analysis, respectively, of 50 positive strains and 30 negative strains.

2.3.1 Protocols

These assays were performed in 2004, during the initial validation study.

Protocol for inclusivity

Each of the *Listeria* strains was tested with the complete VIDAS LSX protocol.

Protocol for exclusivity

The different negative strains were inoculated in a nutrient broth at a level of about 10⁵ cells per mL. After incubation for 24 hours at 37°C, a VIDAS LSX test was performed for each strain.

2.3.2 Results and conclusion

The results are presented in appendix C.

All the 50 *Listeria* strains were detected with the VIDAS LSX method.

No cross reaction was observed with the 32 non-*Listeria* strains tested with the VIDAS LSX test.

A crossed reaction was revealing with *Pseudomonas putida* during the extension study, further to a false positive result, but the level of contamination must be very high and the colonies are non characteristic on the selective media. Other strains of *Pseudomonas putida* were tested after culture in nutrient broth and after culture in LX broth. Two strains among the eight tested gave positive results after culture in nutrient broth, but negative result after culture in LX broth.

3 Interlaboratory study

The general protocol was tested in the interlaboratory study.

3.1 Study organization

- Number of participating laboratories

14 laboratories received samples.

- Matrix used

Pasteurized milk".

- Strain used

Listeria innocua (origin « dairy products »).

- Number of samples per laboratory

2 sets of 24 samples were prepared per laboratory, one for the VIDAS LSX method and the other for the reference method. Each set of samples was divided in 3 levels of contamination, with 8 samples per level..

3.2 Control of experimental parameters

3.2.1 Contamination levels obtained after artificial contamination

The following table shows the contamination rates obtained and estimated precisions:

Level	Samples	Targeted theoretical rate (b/25ml)	Real rate (b/25ml sample)	Estimated lower contamination limit per 25ml sample	Estimated upper contamination limit per 25ml sample
Level 0 (L0)	2-4-6-8-10-12-14-16	0	0		
Low level (L1)	1-3-5-7-17-18-19-20	3	3,4	0.7	9.8
High level (L2)	9-11-13-15-21-22-23-24	30	38	27	52

3.2.2 Problems of temperature recorded during transport, temperature on reception and reception times

3.2.2.1 Analysis of temperature monitoring curves during transport

Temperatures registered by thermo button during shipment were comprised between 0°C and 8°C for all laboratories.

3.2.2.2 Temperatures on reception and reception times

The temperatures obtained are recorded in the following tables:

Laboratory	Reception Temperatures (°C)		Comments
	communicated by the laboratory	indicated by the thermo button	
A	8.0	3.6	
B	7.4	3.6	
C	4.7	4.6	
D	5.0	4.2	
E	5.8	6.9	
F	3.7	3.2	
G	1.8	0.9	Delivery at D1, but analyses at D2
H	6.5	4.9	/
I	4.9	3.4	/
J	5.8	5.5	/
K	2.9	2.9	T<0°C for 2 hours
L	5.6	4.2	/
M	3.2	5.5	/
N	6.5	6.5	/

3.2.3 Conclusion

All the laboratories realized the analyses.

3.3 Results

3.3.1 Results obtained by cooperating laboratories

The detailed results are presented in appendix D and the following tables give a synthesis of the results obtained by all the laboratories.

Among the 14 laboratories, the laboratory G received the samples at Day 1, but it informed the expert laboratory that it realized the analyses at D2. Its results are presented, in grey in the following tables, but they were not taken into account in the interpretation. However, the results are coherent with those of other laboratories.

Positive results obtained by the reference method

Laboratories	Levels of contamination					
	L0		L1		L2	
	Obtained	Nb samples	Obtained	Nb samples	Obtained	Nb samples
Lab A	0	8	8	8	8	8
Lab B	0	8	8	8	8	8
Lab C	0	8	8	8	8	8
Lab D	0	8	8	8	8	8
Lab E	1	8	8	8	8	8
Lab F	0	8	8	8	8	8
Lab G	0	8	8	8	8	8
Lab H	0	8	7	8	8	8
Lab I	0	8	8	8	8	8
Lab J	0	8	8	8	8	8
Lab K	0	8	8	8	8	8
Lab L	0	8	7	8	8	8
Lab M	0	8	8	8	8	8
Lab N	0	8	8	8	8	8

Positive results obtained by the alternative method

Laboratories	Levels of contamination					
	L0		L1		L2	
	Obtained	Nb samples	Obtained	Nb samples	Obtained	Nb samples
Lab A	0	8	8	8	8	8
Lab B	0	8	7	8	8	8
Lab C	0	8	8	8	8	8
Lab D	0	8	8	8	8	8
Lab E	1	8	8	8	8	8
Lab F	0	8	8	8	8	8
Lab G	0	8	7	8	8	8
Lab H	0	8	7	8	8	8
Lab I	0	8	8	8	8	8
Lab J	0	8	8	8	8	8
Lab K	0	8	8	8	8	8
Lab L	0	8	8	8	8	8
Lab M	0	8	8	8	8	8
Lab N	0	8	8	8	8	8

3.3.2 Comments (discordances with expected results, exclusions... for instance)

The results of the reference method and the alternative method were in agreement for 11 laboratories.

The two other laboratories found samples spiked at the low level (L1) negative with one of the methods:

- laboratory B which obtained a negative result with the alternative method,
- laboratory L which obtained a negative result with the reference method.

These results are coherent because, for a same level, 16 samples were prepared: 8 for the reference method and 8 for the alternative method. The first step of enrichment is different for the two methods.

Eventually, the results of laboratory K, for which a negative temperature during the transport occurred for 2 hours, were correct and could be interpreted. This negative temperature did not influence the results.

3.4 Calculations

The results of 13 laboratories were considered.

Note: the positive results of the alternative method were all confirmed.

3.4.1 Calculation of specificity percentage (%SP) and sensitivity percentage (%SE) for both methods

The percentages of specificity (SP) and sensitivity (SE) were calculated with the EN ISO 16140 formulas.

For level L0, it is requested that the specificity percentage (%SP) should be calculated using each of the methods:

$$SP = \{1 - (FP/N_-)\} \times 100$$

where FP, number of false positives
N₋, total number of tests L0

For levels L1 and L2, it is requested that the sensitivity percentage (%SE) should be calculated for each of the methods, compared with the number of expected positive results:

$$SE = (TP/N_+) \times 100$$

where TP, number of true positives
N₊, total number of tests L1 or L2

The results are given in the following table:

Level	Reference method		Alternative method	
	SP/SE	LCL* %	SP/SE	LCL* %
L0	SP% = 99.0	96	SP% = 99.0	96
L1	SE% = 98.1	96	SE% = 98.1	96
L2	SE% = 100	98	SE% = 100	98
L1+L2	SE% = 99.0	96	SE% = 99.0	96

* LCL: low critical value, defined in standard ISO 16140

3.4.2 Calculation of the relative precision (AC)

The relative precision is calculated using the following formula:

$$AC = \{(PA + NA) / N\} \times 100$$

where PA, number of positive agreements
NA, number of negative agreements

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 207	Positive deviation (R-/A+) PD = 1	(N+) = 208
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 1*	Negative agreement (A-/R-) NA = 103*	(N-) = 104
Total	(N+) = 208	(N-) = 104	N = 312

* 0 unconfirmed VIDAS LSX positive result

For this study, the relative accuracy is 99.4%.

3.4.3 Analysis of discordances

As defined in annex F in EN ISO 16140 standard, the minimum number of discordances beyond which a statistical test must be carried out to compare the two methods is 6. Therefore, this statistical test was not used because only two discordances were observed between the two methods.

3.5 Interpretation

3.5.1 Comparison of relative precision (AC), specificity (SP) and sensitivity (SE) values

The values obtained in the two parts of the validation study are given in the following table:

	Interlaboratory study	Comparative study Depending on the profile of protocols used			
		1)	2)	3)	4)
Relative accuracy (AC)	99.4 %	93.0 %	93.3 %	93.9 %	94.1 %
Sensitivity (SE)	99.0 %	93.6 %	89.9 %	94.6 %	91.9 %
Specificity (SP)	99.0 %	92.3 %	97.0 %	93.1 %	96.8 %

The values obtained following the interlaboratory study are higher than the values obtained during the preliminary study, explained by the fact that the interlaboratory study is realized with only one spiked matrix.

The AFNOR Technical Bureau requests the sensitivity of the two methods to be recalculated with consideration of all the confirmed positives (true positive results):

Alternative method	Reference method
$(PA + PD) / (PA + PD + ND) = 99.0 \%$	$(PA + ND) / (PA + PD + ND) = 99.0 \%$

3.5.2 Accordance (DA)

The accordance is the percentage chance of finding the same result from two identical test portions analyzed in the same laboratory under repeatability conditions, in other words a single operator using the same instrument and the same reagents within the shortest feasible time interval.

The first step to calculate the accordance is to calculate the probability that two identical samples give the same result for each of the participating laboratories, and then to determine the average of the probabilities of all laboratories.

The different tables used to deduce the accordance are given in appendix E and the accordance for each of the methods at each of the levels are given in the following table:

Level	Reference method	Alternative method
L0	DA % = 98.3 %	DA % = 98.3 %
L1	DA % = 96.6 %	DA % = 96.6 %
L2	DA % = 100 %	DA % = 100 %

3.5.3 Concordance

The concordance is the percentage chance of finding the same result for two identical samples analyzed in two different laboratories.

The objective is to calculate the percentage of all pairs giving the same results on all possible pairs of results.

Result tables used to make these calculations are given in appendix F and the concordance for each of the methods and for each of the levels are given in the following table:

Level	Reference method	Alternative method
L0	Concordance % = 98.1 %	Concordance % = 98.1 %
L1	Concordance % = 95.9 %	Concordance % = 95.9 %
L2	Concordance % = 100 %	Concordance % = 100 %

3.5.4 Odds Ratio (COR)

The concordance odds ratio is calculated using the following formula:

$$\text{COR} = \frac{\text{accordance} \times (100 - \text{concordance})}{\text{concordance} \times (100 - \text{accordance})}$$

The concordance odds ratio for each of the methods and for each of the levels is given in the following table:

Level	Alternative method	Reference method
L0	COR % = 1.15	COR % = 1.15
L1	COR % = 1.24	COR % = 1.24
L2	COR % = 1.00	COR % = 1.00

A value of 1.00 for the Odds ratio means that the degree of agreement and the agreement are equal. When the Odds ratio increases, the interlaboratory variation becomes more predominant.

4 Practicability

Practicability is studied according to the 13 criteria defined by the AFNOR technical board, comparing the EN ISO 11290 reference method to the VIDAS LSX method.

1. <i>Packaging mode of the components of the method (see package insert)</i> 2. <i>Reagent volumes (see package insert and vial packaging)</i>	The VIDAS LSX kits contain the quantity of reagent necessary for 60 analyses: - the LSX strips composed of 10 wells covered with a labeled, foil seal - the SPR® in 30 units per pouch - one vial of LSX standard (S1): 6mL - one vial of LSX positive control (C1): 6mL - one vial of negative control (C2): 6mL
3. <i>Storage conditions (see package insert)</i>	The storage temperature is between 2 to 8°C. Expiration date is shown on the box label and on the different vials.
4. <i>Modalities of use after first use (see package insert)</i>	The kit components should be stored at 2 – 8°C.
5. <i>Equipment or necessary specific premises (see package insert)</i>	Among the required equipment, - an air incubator at 30°C ± 1°C - a water bath at 95-100°C - a VIDAS system
6.	All the reagents are ready-to-use
7. <i>Ttraining of the operator</i>	For an operator trained in standard techniques of microbiology, training in the technique requires less than 1 day.

8. Real time handling - Flexibility of the technique relative to the number of samples to be analyzed

Steps	Average time for a sample (min)		Average time for 30 samples (min)	
	Standard ISO 11290-1	VIDAS LSX method	Standard ISO 11290-1	VIDAS LSX method
Preparation, weighing, dilution and stomaching	7	7	90	90
Transfer to selective broths - Half Fraser broth - LX broth	1	0 or 1	25	0 or 25
Streaking of Half Fraser and Fraser broths, on two selective media	2	/	30	/
Plates reading	2	/	20	/
VIDAS LSX test (heating and automated assay procedure)	/	5	/	10
Average total time (per sample)	12 minutes	12 or 13 minutes	5.5 minutes	3.3 or 4.2 minutes

In case of positive samples, the necessary time for isolation of the LX broth on selective media must be added to the confirmations (around 1 minute).

And the average time for the confirmation of a typical colony by reference method tests can be evaluated at around 5 minutes.

The advantage of the alternative method is particularly based on the possibility to sort negative samples from the suspicious samples and thus reducing the number of confirmations.

9. Time-to-result

Steps	Time required VIDAS LSX method	Time required ISO 11290-1 reference method
Realization of first enrichment (Half Fraser or LX)	D0	D0
Transfer to selective broths (Fraser or LX)	D1	D1
VIDAS LSX procedure	D1	/
Test result		
Obtaining negative result (if test is negative)	D1	/
Streaking of selective broths on selective media	D1	D1 and D3
Reading the plates		
Confirmation tests	D2 to D3	D2 to D5
Obtaining negative result (after streaking and negative confirmation if done, for example with a positive VIDAS LSX test)	D2 to D9	D5 to D11
Obtaining positive result		
Genus: Confirmation by reference method tests (GRAM coloration, catalase test)	D3 to D4	D5 to D6
Species: Confirmation by reference method tests (CAMP tests, haemolysis, TSBYE broth)	D8 to D9	D9 to D11
Confirmation by biochemical gallery	D4 to D5	D4 to D7

10. Type of qualification of the operator:	level identical to that necessary for the reference method
11. Steps common to the reference method	None
12. Traceability of the analysis results	A result sheet is printed with the reagents lot numbers, time, test result, and sample identification. The results can be exported to a LIMS.
13. Maintenance by the laboratory	The VIDAS user's guide explains some problems. bioMérieux offers a customer technical support for the possible problems. Different maintenance contracts are possible.

5 Conclusion

The validation study of the methods was conducted according to the reference document EN ISO 16140.

The **comparative study** allows assessing:

- the relative accuracy, the relative sensitivity and the relative specificity,
- the relative detection level,
- the inclusivity and the exclusivity.

The performances of the VIDAS LSX method are equivalent to those of the reference method EN ISO 11290-1/A1:2004. They were determined by analysis of samples distributed over four categories of products and environmental samples

Different profiles of protocols were studied:

The relative accuracy obtained was around 93% - 94%, the relative sensitivity was between 93% and 97% and the relative specificity varied from 90% to 95 %, according to the calculations required by the EN ISO 16140 standard. Because the positive samples by the alternative method are positive confirmed samples, the sensitivities were recalculated relative to all positive results and are between:

- 90% and 94.5% for the reference method,
- 93% and 97% for the alternative method.

The relative detection level of the VIDAS LSX method and of the reference method was evaluated by artificial contaminations of four different products, representative of the four categories tested.

The level of detection was between 0.2 and 0.9 cells per 25 grams for the VIDAS LSX method and between 0.2 and 1.4 cells per 25 grams for the reference method.

The inclusivity of the method is good since all the strains of *Listeria* were detected.

A crossed reaction with *Pseudomonas putida* was observed during the extension study in the accuracy study, but the level of contamination of this strain must be very high and the colonies are non characteristic on the selective media. Other strains of *Pseudomonas putida* were tested in pure cultures (exclusivity study) and they gave negative results

The 32 other non-*Listeria* strains were not detected.

The **interlaboratory study results** obtained for all of the 13 selected laboratories show that the alternative method and the reference method have comparable values of relative accuracy, specificity and sensitivity as those obtained during the preliminary study.

The variability of the alternative method (accordance, concordance, Odds ratio) is comparable with the variability of the reference method.

Set of results led to **AFNOR validation and extension of AFNOR validation** according to ISO 16140, of the VIDAS *Listeria* species Xpress (LSX) method (certificate n° BIO 12/12 – 07/04), for the detection of *Listeria* in meat products, dairy products, vegetables and environmental samples, **for a 4 years period**.

Lille, August 28th 2009



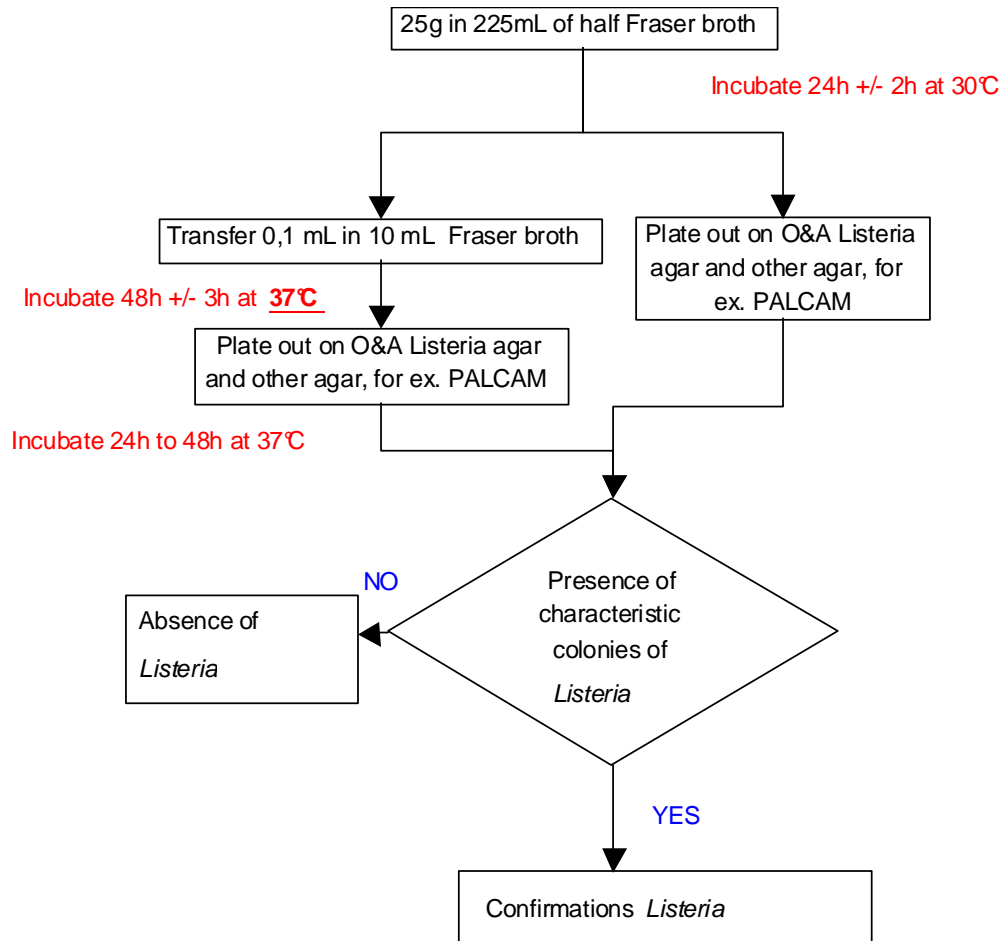
Virginie Ewe
Technical Manager

APPENDICES

APPENDIX A

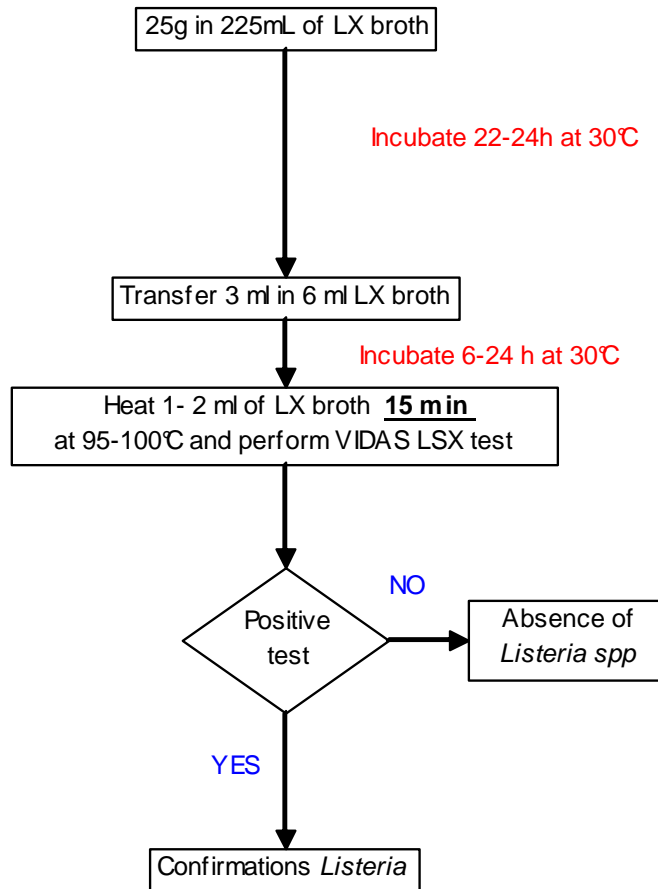
ANALYTICAL PROTOCOLS

EN ISO STANDARD 11290-1/A1: 2004 (#)



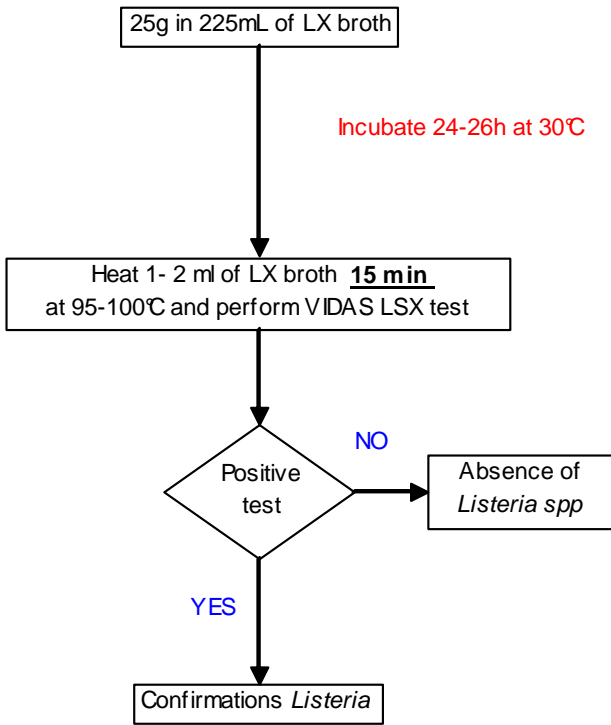
VIDAS LSX METHOD

General protocol



VIDAS LSX METHOD

Surfaces - Protocol without transfer



APPENDIX B

RELATIVE ACCURACY, RELATIVE SPECIFICITY,
RELATIVE SENSITIVITY

-

DETAILED RESULTS TABLES
FOR EACH SAMPLE CATEGORY

Legend

Total bacteria growth

∅ : no growth

L = low

M = medium

H = high

Wh = blue colonies without halo

h = blue colonies with halo

m = blue colonies with and without halo

* : presence of two types of characteristic colonies (*L.monocytogenes* + other *Listeria*)

Distribution of flora

A = pure culture of suspicious colonies

B = mix with a majority of suspicious colonies

C = mix with a minority of suspicious colonies

D = mix with rare suspicious colonies

E = absence of suspicious colonies

(x) : x characteristic colonies of *Listeria* if $x \leq 5$

a : réincubation of LX broth for 24 hours at 30°C

Initial study 6H

	MATRICES	Cat.	Sp/line a	NF EN ISO 11290-1 METHOD					VIDAS LSX METHOD							COMPARISON	
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION		IDENTIF.		FINAL RESULT 6H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	O&A	P			
2004	Mincéd beef	MP1	No	Ø	LE	Ø	Ø	/	-	29	0,00	-	/	/	/	-	=
2004	Mincéd beef	MP1	No	Ø	LE	Ø	HE	/	-	42	0,01	-	LA/Wh	LA	/	-	=
2004	Mincéd beef	MP1	No	Ø	ME	Ø	LE	/	-	25	0,00	-	/	/	/	-	=
2004	Meat	MP1	No	Ø	Ø	Ø	Ø	/	-	37	0,00	-	/	/	/	-	=
2004	Meat	MP1	No	Ø	Ø	Ø	Ø	/	-	30	0,00	-	/	/	/	-	=
2004	Meat	MP1	No	Ø	Ø	Ø	Ø	/	-	29	0,00	-	/	/	/	-	=
2004	Meat	MP1	No	Ø	Ø	Ø	Ø	/	-	77	0,02	-	/	/	/	-	=
2004	Meat	MP1	No	Ø	Ø	Ø	Ø	/	-	31	0,01	-	/	/	/	-	=
2004	Meat	MP1	No	Ø	Ø	Ø	Ø	/	-	23	0,00	-	/	/	/	-	=
2004	Meat	MP1	No	Ø	Ø	Ø	Ø	/	-	27	0,00	-	/	/	/	-	=
2004	Mincéd beef	MP1	No	Ø	LE	Ø	LE	/	-	7865	2,55	+	LA/Wh	LA	L. welshimeri	+	PS
2004	Mincéd beef	MP1	No	Ø	Ø	Ø	Ø	/	-	7977	2,58	+	HA/m	HA	L. monocytogenes	+	PS
2004	Mincéd beef	MP1	No	LA	LA	HA	HA	L. innocua	+	259	0,08	-	HA/Wh	HA	L. innocua	-	FN
2004	Meat	MP1	No	Ø	Ø	HA	HA	L. monocytogenes	+	20	0,00	-	/	/	/	-	FN
2004	Mincéd beef	MP1	No	MA	MD	HA	HA	L. monocytogenes L. welshimeri	+	4967	1,61	+	LA/m	LA	L. monocytogenes L. welshimeri	+	=
2004	Mincéd beef	MP1	No	MA	HD	HA	HA	L. innocua	+	10429	3,38	+	HA/Wh	HA	L. innocua	+	=
2004	Mincéd beef	MP1	No	MA	MD	HA	HA	L. monocytogenes L. innocua	+	7874	2,55	+	HA/m	HA	L. monocytogenes L. innocua	+	=
2004	Mincéd beef	MP1	No	LB	MD	HA	HA	L. innocua	+	7823	2,53	+	HA/m	HA	L. monocytogenes L. innocua	+	=
2004	Mincéd beef	MP1	No	LA	LD	HA	HA	L. monocytogenes L. welshimeri	+	11547	3,74	+	LA/m	LA	L. monocytogenes L. welshimeri	+	=
2004	Mincéd beef	MP1	No	LA	MD	HA	HA	L. welshimeri	+	5812	1,88	+	LA/m	LA	L. monocytogenes L. welshimeri	+	=
2004	Surface above weighing machine	MP1	No	LA	MB	HA	HA	L. monocytogenes	+	8419	2,73	+	MA/h	MA	L. monocytogenes	+	=
2004	Fish cutting table	MP1	No	LA	LA	HA	HA	L. monocytogenes	+	10046	3,25	+	HA/h	HA	L. monocytogenes L. innocua L. welshimeri	+	=
2004	Slicer	MP1	No	LA	LB	HA	HA	L. monocytogenes L. innocua	+	6906	2,24	+	HA/m	HA	L. monocytogenes L. innocua	+	=
2004	Cheese slicer	MP1	No	LA	LA	HA	HA	L. monocytogenes L. innocua	+	7409	2,40	+	HA/m	HA	L. monocytogenes L. innocua	+	=
2004	Surface of cheese knife	MP1	No	LA	LC	HA	HA	L. monocytogenes L. innocua	+	7996	2,59	+	HA/m	HA	L. monocytogenes L. innocua	+	=
2004	Swab from sausages process line	MP1	No	LA	MB	HA	HA	L. monocytogenes L. innocua L. welshimeri	+	7857	2,54	+	HA/m	HA	L. monocytogenes L. welshimeri	+	=
2004	Fish cutting table	MP1	No	LA	LB	HA	HA	L. monocytogenes L. welshimeri	+	11002	3,56	+	HA/m	HA	L. monocytogenes L. welshimeri	+	=
2004	Surface of cheese knife	MP1	No	MA	MA	HA	HA	L. innocua	+	10067	3,26	+	HA/Wh	HA	L. innocua	+	=
2004	Mincéd beef	MP1	No	LA	LC	HA	HA	L. welshimeri	+	9336	3,02	+	HA/m	HA	L. monocytogenes L. innocua L. welshimeri	+	=
2004	Mincéd beef	MP1	No	HB	HC	HA	HA	L. monocytogenes L. innocua	+	6236	2,02	+	HA/m	HA	L. monocytogenes L. innocua	+	=
2004	Mincéd beef	MP1	No	LA	LC	HA	HA	L. welshimeri	+	8289	2,68	+	HA/Wh	HA	L. welshimeri	+	=
2004	Sausage meat	MP2	No	LA	LB	HA	HC	L. innocua	+	8028	2,59	+	MA/h	MA	L. monocytogenes L. innocua	+	=
2004	Sausage meat	MP2	No	MA	MD	HA	HA	L. welshimeri	+	8396	2,70	+	HA	MA/m	L. monocytogenes L. welshimeri	+	=
2004	Meat for stuffed tomatoes	MP2	No	LE	LE	HA	HB	L. welshimeri	+	496	0,15	+	MA/Wh	MB	L. welshimeri	+	=

2004	MATRICES	Cat.	Sp/ite a	NF EN ISO 11290-1 METHOD						VIDAS LSX METHOD						COMPARISON	
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H		CONFIRMATION		IDENTIF.	FINAL RESULT 6H		
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	O&A				P
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	18	0,00	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	18	0,00	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	19	0,00	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	17	0,00	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	18	0,00	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	40	0,01	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	18	0,00	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	25	0,00	-	/	/	/	-	=
	Pâté	MP3	No	Ø	LE	Ø	Ø	/	-	25	0,00	-	/	/	/	-	=
	Sausages	MP3	No	Ø	LE	Ø	Ø	/	-	43	0,01	-	/	/	/	-	=
	Pâté	MP3	No	Ø	LE	Ø	LE	/	-	38	0,01	-	/	/	/	-	=
	Pâté	MP3	No	Ø	LE	ME	ME	/	-	32	0,01	-	/	/	/	-	=
	Pâté	MP3	No	LE	LE	Ø	Ø	/	-	66	0,02	-	/	/	/	-	=
	Pâté	MP3	No	Ø	LB	LE	ME	<i>Bacillus</i>	-	36	0,01	-	/	/	/	-	=
	Rillettes of goose	MP3	No	Ø	LE	Ø	LE	/	-	96	0,03	-	/	/	/	-	=
	Rillettes from Tours	MP3	No	Ø	LE	Ø	LE	/	-	25	0,00	-	/	/	/	-	=
	Rillettes from Le Mans	MP3	No	Ø	LE	Ø	Ø	/	-	55	0,01	-	/	/	/	-	=
	Rillettes of duck	MP3	No	Ø	LE	Ø	Ø	/	-	83	0,02	-	/	/	/	-	=
	Pâté	MP3	No	Ø	Ø	Ø	Ø	/	-	26	0,00	-	/	/	/	-	=
	Pâté	MP3	No	Ø	LE	Ø	LE	/	-	52	0,01	-	/	/	/	-	=
	Rillettes	MP3	No	Ø	Ø	Ø	Ø	/	-	8548	2.75	+	MA/h	MA	<i>L. monocytogenes</i>	+	PS
	Rillettes	MP3	No	LA	LA	HA	HA	<i>L. monocytogenes</i>	+	20	0,00	-	/	/	/	-	FN
	Pâté	MP3	No	MA	MA	HA	HA	<i>L. innocua</i>	+	28	0,00	-	/	/	/	-	FN
	Rillettes from Tours	MP3	Yes	LA	LA	HA	HB	<i>L. welshimeri</i>	+	621	0.19	+	MA/Wh	MB	<i>L. welshimeri</i>	+	=
	Pâté	MP3	Yes	LA	LA	HA	HB	<i>L. monocytogenes</i>	+	8530	2.69	+	MA/h	HA	<i>L. monocytogenes</i>	+	=
	Pâté	MP3	Yes	HA	HB	HA	HB	<i>L. monocytogenes</i>	+	7676	2.42	+	HA/h	HA	<i>L. monocytogenes</i>	+	=

Initial study 6H

2004	MATRICES	Cat.	Spike D	NF EN ISO 11290-1 METHOD					VIDAS LSX METHOD					COMPARISON			
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H		CONFIRMATION			IDENTIF.	FINAL RESULT 6H	
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	O&A				P
2004	Camembert cheese	DP1	No	LE	LE	Ø	ME	/	-	126	0.04	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	Ø	ME	LE	LE	/	-	42	0.01	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	Ø	LE	Ø	LE	/	-	34	0.01	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	Ø	ME	Ø	LE	/	-	33	0.01	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	Ø	LE	Ø	LE	/	-	61	0.01	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	LE	ME	Ø	LE	/	-	37	0.01	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	LE	ME	Ø	LE	/	-	29	0.00	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	Ø	LE	Ø	Ø	/	-	59	0.01	-	/	/	/	-	=
2004	"Vieux pâné" cheese	DP1	No	Ø	LE	Ø	Ø	/	-	30	0.00	-	/	/	/	-	=
2004	"Munster" raw milk cheese	DP1	No	Ø	ME	Ø	ME	/	-	37	0.01	-	/	/	/	-	=
2004	"Brie" cheese	DP1	No	Ø	LE	Ø	ME	/	-	27	0.00	-	/	/	/	-	=
2004	"Brie de Meaux" raw milk cheese	DP1	No	Ø	LE	Ø	ME	/	-	58	0.01	-	/	/	/	-	=
2004	Cheese	DP1	No	LE	LE	LE	LE	/	-	21	0.00	-	/	/	/	-	=
2004	Cow's milk	DP1	No	LE	LE	LE	LE	/	-	18	0.00	-	Ø	Ø	/	-	=
2004	Cow's milk	DP1	No	LE	LE	LE	LE	/	-	29	0.00	-	Ø	Ø	/	-	=
2004	Cow's milk	DP1	No	LE	LE	Ø	LE	/	-	219	0.07	-	Ø	Ø	/	-	=
2004	Cow's milk	DP1	No	LE	LE	Ø	Ø	/	-	22	0.00	-	Ø	Ø	/	-	=
2004	Cow's milk	DP1	No	Ø	LE	Ø	LE	/	-	26	0.00	-	Ø	Ø	/	-	=
2004	Goat's milk	DP1	No	LE	LE	HE	HE	/	-	23	0.00	-	Ø	LE	/	-	=
2004	Goat's milk	DP1	No	LE	LE	HE	HE	/	-	17	0.00	-	LE	LE	/	-	=
2004	Cow's milk	DP1	No	Ø	LE	Ø	Ø	/	-	22	0.00	-	Ø	Ø	/	-	=
2004	Cow's milk	DP1	No	Ø	LE	LE	ME	/	-	23	0.00	-	Ø	Ø	/	-	=
2004	Cow's milk	DP1	No	LE	LE	Ø	HE	/	-	8351	2.85	+	LA/Wh	LE	<i>L. seeligeri</i>	+	PS
2004	"St Nectaire" raw milk cheese	DP1	No	LA	LB	MA	MC	<i>L.monocytogenes</i>	+	48	0.01	-	/	/	/	-	FN
2004	"Tourée de l'aubier" cheese	DP1	No	MA	HA	HA	HA	<i>L.monocytogenes</i>	+	64	0.02	-	/	/	/	-	FN
2004	Cow's milk	DP1	No	LE	LE	LA	LC	<i>L. innocua</i>	+	20	0.00	-	Ø	Ø	/	-	FN
2004	"Morbier" raw milk cheese	DP1	No	Ø	ME	MA	MA	<i>L.monocytogenes</i>	+	335	0.10	-	/	/	/	-	FN
2004	"Cantal" cheese	DP1	Yes	LA	LB	HA	HA	<i>L.innocua</i>	+	9531	2.94	+	HA/Wh	MC	<i>L.innocua</i>	+	=
2004	"Cantal" cheese	DP1	Yes	MA	MB	HA	HA	<i>L.innocua</i>	+	9941	3.13	+	HA/Wh	HB	<i>L.innocua</i>	+	=
2004	"Cantal" cheese	DP1	Yes	MA	MB	HA	HB	<i>L.innocua</i>	+	8007	2.52	+	MA/Wh	HB	<i>L.innocua</i>	+	=
2004	"Cantal" cheese	DP1	Yes	MA	MB	HA	HC	<i>L.innocua</i>	+	8583	2.70	+	HA/Wh	HC	<i>L.innocua</i>	+	=
2004	"Cantal" cheese	DP1	Yes	MA	MB	HA	HB	<i>L.innocua</i>	+	10643	3.35	+	HA/Wh	HB	<i>L.innocua</i>	+	=
2004	"Tourée de l'aubier" cheese	DP1	No	HA	HA	HA	HA	<i>L.monocytogenes</i>	+	6451	2.08	+	HA/h	HA	<i>L.monocytogenes</i>	+	=
2004	Cow's milk	DP1	No	LC	LE	LA	LA	<i>L. innocua</i>	+	494	0.16	+	MA/Wh	MA	<i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LA	LD	HA	HB	<i>L. innocua</i>	+	8462	2.88	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LA	LC	HB	HA	<i>L. innocua</i>	+	11360	3.85	+	LA/Wh	LE	<i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LA	LE	HA	HA	<i>L. innocua</i>	+	11083	3.78	+	MA/Wh	HA	<i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LC	LD	HB	HB	<i>L. innocua</i>	+	7075	2.41	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LD	LE	HA	HD	<i>L. innocua</i>	+	8795	3.00	+	MA/Wh	MA	<i>L. innocua</i>	+	=
2004	"Chaumont" cheese	DP1	Yes	HA	HB	HA	MA	<i>L. innocua</i>	+	7902	2.93	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LA	LC	HC	HC	<i>L. innocua</i>	+	11526	3.93	+	HD/h	HC	<i>L. monocytogenes</i>	+	=
2004	Cow's milk	DP1	No	LA	LA	LA	LA	<i>L. monocytogenes</i> <i>L. innocua</i>	+	10350	3.53	+	HA/m	HA	<i>L. monocytogenes</i> <i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LA	LA	HA	HA	<i>L. monocytogenes</i> <i>L. innocua</i>	+	7606	2.59	+	LA/m	LA	<i>L. monocytogenes</i> <i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LA	LA	HA	HD	<i>L. monocytogenes</i> <i>L. innocua</i>	+	7264	2.47	+	HA/m	HA	<i>L. monocytogenes</i> <i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	HA	MD	HA	HC	<i>L. monocytogenes</i> <i>L. innocua</i>	+	6956	2.37	+	HA/m	HC	<i>L. monocytogenes</i> <i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	MD	MC	HC	HD	<i>L. monocytogenes</i> <i>L. innocua</i>	+	6904	2.35	+	HA/m	HA	<i>L. monocytogenes</i> <i>L. innocua</i>	+	=
2004	Cow's milk	DP1	No	LE	LE	LA	LC	<i>L. innocua</i>	+	7530	2.56	+	HA/m	HA	<i>L. monocytogenes</i> <i>L. innocua</i>	+	=

	MATRICES	Cat.	Spike g	NF EN ISO 11290-1 METHOD						VIDAS LSX METHOD							COMPARISON
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION		IDENTIF.	FINAL RESULT 6H	
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	O&A	P			
2004	Goat's cheese	DP2	No	LE	LE	Ø	HE	/	-	19	0.00	-	/	/	/	-	=
2004	Goat's cheese	DP2	No	Ø	LE	Ø	Ø	/	-	80	0.02	-	/	/	/	-	=
2004	Goat's milk	DP2	No	Ø	LE	Ø	LE	/	-	21	0.00	-	/	/	/	-	=
2004	Ewe's cheese	DP2	No	LE	ME	LE	LE	/	-	24	0.00	-	/	/	/	-	=
2004	Feta cheese	DP2	No	Ø	LE	Ø	Ø	/	-	36	0.01	-	/	/	/	-	=
2004	Ewe's cheese	DP2	No	LE	LE	LE	LE	/	-	17	0.00	-	/	/	/	-	=
2004	Gorgonzola cheese	DP2	No	Ø	LE	Ø	Ø	/	-	32	0.01	-	/	/	/	-	=
2004	Ewe's cheese	DP2	No	Ø	LE	Ø	Ø	/	-	4167	1.34	+	MA/h	MA	<i>L.monocytogenes</i>	+	PS
2004	Goat's cheese	DP2	No	LA	LC	HA	HA	<i>L. innocua</i>	+	2107	0.68	+	HA/Wh	HA	/	+	=
2004	Blue cheese	DP2	No	Ø	ME	MA	HA	<i>L.monocytogenes</i>	+	5161	1.66	+	MA/h	MA	<i>L.monocytogenes</i>	+	=
2004	Feta cheese	DP2	Yes	LD	LD	HA	HA	<i>L.monocytogenes</i>	+	1414	0.44	+	LC/h	MB	<i>L.monocytogenes</i>	+	=
2004	Feta cheese	DP2	Yes	LD	LD	HA	HA	<i>L.monocytogenes</i>	+	4669	1.47	+	MB/h	MB	<i>L.monocytogenes</i>	+	=
2004	Feta cheese	DP2	Yes	LD	LD	HA	HA	<i>L.monocytogenes</i>	+	5288	1.66	+	HB/h	HB	<i>L.monocytogenes</i>	+	=
2004	Feta cheese	DP2	Yes	LD	LD	HA	HA	<i>L.monocytogenes</i>	+	7471	2.35	+	HB/h	HA	<i>L.monocytogenes</i>	+	=
2004	Goat's milk	DP2	No	LA	LA	LA	LA	<i>L. innocua</i>	+	8772	2.99	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Goat's milk	DP2	No	LA	LB	HA	HB	<i>L. innocua</i>	+	8190	2.79	+	HA/Wh	MA	<i>L. innocua</i>	+	=
2004	Goat's milk	DP2	No	MA	MB	HA	HB	<i>L. innocua</i>	+	7994	2.82	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Goat's cheese	DP2	Yes	MA	MA	HA	HA	<i>L. innocua</i>	+	7995	2.96	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	"Ste Maure" goat cheese	DP2	Yes	LA	LA	LA	LA	<i>L. welshimeri</i>	+	8141	3.02	+	LA/Wh	LA	<i>L. welshimeri</i>	+	=
2004	White cheese cake	DP3	No	Ø	LE	Ø	LE	/	-	21	0.00	-	/	/	/	-	=
2004	Crème fraîche	DP3	Yes	MA	MA	HA	MA	<i>L. monocytogenes</i>	+	8668	3.21	+	HA/h	MA	<i>L. monocytogenes</i>	+	=
2004	Cheese	DP3	Yes	MA	MB	HA	MA	<i>L. monocytogenes</i>	+	7737	2.87	+	HA/h	MA	<i>L. monocytogenes</i>	+	=

Initial study 6H

	MATRICES	Cat.	Spike D	NF EN ISO 11290-1 METHOD					VIDAS LSX METHOD							COMPARISON	
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION		IDENTIF.		FINAL RESULT 6H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	O&A	P			
2004	Celery	VG1	No	Ø	LE	Ø	ME	/	-	45	0.01	-	/	/	/	-	=
2004	Fennel	VG1	No	Ø	Ø	Ø	LE	/	-	52	0.01	-	/	/	/	-	=
2004	Coco beans	VG1	No	Ø	Ø	Ø	Ø	/	-	51	0.01	-	/	/	/	-	=
2004	Radish	VG1	No	LE	HE	Ø	ME	/	-	130	0.04	-	/	/	/	-	=
2004	Endives	VG1	No	Ø	Ø	Ø	Ø	/	-	22	0.00	-	/	/	/	-	=
2004	Yellow peppers	VG1	No	Ø	Ø	Ø	Ø	/	-	26	0.00	-	/	/	/	-	=
2004	Red peppers	VG1	No	Ø	Ø	Ø	Ø	/	-	30	0.00	-	/	/	/	-	=
2004	Turnip	VG1	No	Ø	LE	Ø	Ø	/	-	132	0.04	-	/	/	/	-	=
2004	Green cabbage	VG1	No	Ø	Ø	Ø	Ø	/	-	42	0.01	-	/	/	/	-	=
2004	Eggplant	VG1	No	Ø	Ø	Ø	Ø	/	-	27	0.00	-	/	/	/	-	=
2004	Green pepper	VG1	No	Ø	Ø	Ø	Ø	/	-	21	0.00	-	/	/	/	-	=
2004	Artichoke	VG1	No	LE	LE	HE	HE	/	-	21	0.00	-	/	/	/	-	=
2004	Cucumber	VG1	No	LE	ME	HE	HE	/	-	41	0.01	-	/	/	/	-	=
2004	Salad	VG1	No	Ø	LE	Ø	Ø	/	-	61	0.01	-	/	/	/	-	=
2004	Green cabbage	VG1	No	LE	HE	HE	HE	/	-	124	0.03	-	/	/	/	-	=
2004	Leeks for vinaigrette	VG1	No	Ø	Ø	Ø	Ø	/	-	66	0.02	-	/	/	/	-	=
2004	Carrots	VG1	No	Ø	Ø	Ø	Ø	/	-	23	0.00	-	/	/	/	-	=
2004	Dark tuber	VG1	No	ME	HE	LE	ME	/	-	145	0.04	-	/	/	/	-	=
2004	Avocado	VG1	No	Ø	Ø	Ø	Ø	/	-	102	0.03	-	/	/	/	-	=
2004	Tomatoes	VG1	No	Ø	ME	Ø	Ø	/	-	26	0.00	-	/	/	/	-	=
2004	Red cabbage	VG1	No	Ø	Ø	Ø	HE	/	-	36	0.01	-	/	/	/	-	=
2004	Salad Batavia	VG1	No	ME	HE	HE	HE	/	-	24	0.00	-	/	/	/	-	=
2004	Leeks	VG1	Yes	Ø	LE	Ø	HE	/	-	30	0.00	-	/	/	/	-	=
2004	Potatoes	VG1	Yes	MA	MA	HA	HA	<i>L. monocytogenes</i>	+	11776	3.76	+	LB	LA	<i>L. seeligeri</i>	+	=
2004	Kiwi	VG1	Yes	Ø	LE	LE	LE	/	-	318	0.10	+	LA/h	LA	<i>L. seeligeri</i>	+	PS
2004	Potatoes	VG1	Yes	LB	LE	LA	LC	<i>L. monocytogenes</i>	+	59	0.02	-	LA/Wh	LE	<i>L. seeligeri</i>	-	FN
2004	Broccoli	VG1	Yes	LA	LB	HA	HA	<i>L. monocytogenes</i>	+	11706	4.34	+	MA/h	MA	<i>L. monocytogenes</i>	+	=
2004	Tomatoes	VG1	Yes	MA	MA	HA	HA	<i>L. innocua</i>	+	8063	2.99	+	HC/Wh	HA	<i>L. innocua</i>	+	=
2004	Zucchini	VG1	Yes	LA	LB	HA	HA	<i>L. monocytogenes</i>	+	7342	2.72	+	HA/h	HA	<i>L. monocytogenes</i>	+	=
2004	Banana	VG1	Yes	LA	MA	HA	HA	<i>L. monocytogenes</i>	+	7219	2.68	+	HA/h	HA	<i>L. monocytogenes</i>	+	=
2004	Red cabbage	VG1	Yes	LA	LA	HA	HA	<i>L. monocytogenes</i>	+	8819	3.27	+	MA/h	LA	<i>L. monocytogenes</i>	+	=
2004	Tomatoes	VG1	Yes	HA	HA	HA	HA	<i>L. innocua</i>	+	7116	2.64	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Zucchini	VG1	Yes	HA	HB	HA	HB	<i>L. innocua</i>	+	6920	2.57	+	MA/Wh	HA	<i>L. innocua</i>	+	=
2004	Tomatoes	VG1	Yes	MA	MA	HA	HA	<i>L. innocua</i>	+	6545	2.09	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Salad	VG1	Yes	HA	HA	HA	HA	<i>L. monocytogenes</i>	+	7613	2.82	+	HA/h	HA	<i>L. monocytogenes</i>	+	=
2004	Salad 'Scarole'	VG1	Yes	HA	HA	HA	HA	<i>L. innocua</i>	+	7791	2.89	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Salad	VG1	No	LB	LB	HA	HA	<i>L. monocytogenes</i>	+	11442	3.66	+	MA/h	LA	<i>L. monocytogenes</i>	+	=
2004	Salad	VG1	No	LA	LA	HA	HA	<i>L. monocytogenes</i>	+	7468	2.38	+	HA/h	HA	<i>L. monocytogenes</i>	+	=
2004	Salad	VG1	No	LA	LA	HA	HA	<i>L. monocytogenes</i>	+	9787	3.13	+	HA/h	MA	<i>L. monocytogenes</i>	+	=
2004	Salad	VG1	No	MA	MA	HA	HA	<i>L. monocytogenes</i>	+	7826	2.50	+	HA/h	HA	<i>L. monocytogenes</i>	+	=
2004	Salad	VG1	No	LA	LA	HA	HB	<i>L. monocytogenes</i>	+	8015	2.56	+	HA/h	HA	<i>L. monocytogenes</i>	+	=
2004	Salad	VG1	No	MA	MA	HA	HB	<i>L. innocua</i>	+	7449	2.38	+	HA/Wh	HA	<i>L. innocua</i>	+	=
2004	Salad	VG1	No	MB	MC	HA	HA	<i>L. innocua</i>	+	7903	2.52	+	HA/Wh	HA	<i>L. innocua</i>	+	=

Initial study 6H

2004	MATRICES	Cat.	Spike d	NF EN ISO 11290-1 METHOD					VIDAS LSX METHOD							COMPARISON	
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION		IDENTIF.		FINAL RESULT 6H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	O&A	P			
	Broccoli	VG2	No	LE	LE	Ø	HE	/	-	46	0.01	-	/	/	/	-	=
	Green beans	VG2	No	Ø	LE	Ø	Ø	/	-	25	0.00	-	/	/	/	-	=
	Zucchini	VG2	No	LE	LE	LE	HE	/	-	29	0.00	-	/	/	/	-	=
	White mushrooms	VG2	No	Ø	LE	Ø	Ø	/	-	34	0.01	-	/	/	/	-	=
	Cabbage flower	VG2	Yes	Ø	LE	Ø	Ø	/	-	71	0.02	-	/	/	/	-	=
	Bruxelles sprouts	VG2	Yes	Ø	LE	LE	HE	/	-	110	0.03	-	/	/	/	-	=
	Sliced onions	VG2	Yes	Ø	Ø	Ø	Ø	/	-	25	0.00	-	/	/	/	-	=
	Artichokes hearts	VG2	Yes	MA	MA	HA	HA	<i>L. monocytogenes</i>	+	8163	3.03	+	HA/h	HA	<i>L. monocytogenes</i>	+	=
	Broccoli and zucchinis	VG2	Yes	LA	LA	HA	HB	<i>L. monocytogenes</i>	+	7420	2.75	+	MC/h	MC	<i>L. monocytogenes</i>	+	=
	Sliced onions	VG2	Yes	MA	MA	HA	HA	<i>L. innocua</i>	+	7788	2.49	+	HA/Wh	HA	<i>L. innocua</i>	+	=
	Peas	VG2	Yes	MA	MD	HA	HD	<i>L. monocytogenes</i>	+	7132	2.64	+	HA/h	MA	<i>L. monocytogenes</i>	+	=
	Pancakes of potatoes	VG3	Yes	LA	LB	HA	HB	<i>L. monocytogenes</i>	+	7232	2.68	+	MA/h	MA	<i>L. monocytogenes</i>	+	=
	Celery purée	VG3	Yes	LA	LA	HA	HA	<i>L. welshimeri</i>	+	7424	2.75	+	MA/Wh	LA	<i>L. welshimeri</i>	+	=
	Vegetables puree	VG3	Yes	MA	MB	HA	HB	<i>L. innocua</i>	+	6966	2.58	+	MC/Wh	MB	<i>L. innocua</i>	+	=
	Carrots puree	VG3	Yes	MA	MD	HA	HC	<i>L. monocytogenes</i>	+	7031	2.61	+	MA/h	MA	<i>L. monocytogenes</i>	+	=
	Broccolis puree	VG3	Yes	LA	LA	MA	HD	<i>L. monocytogenes</i>	+	7222	2.68	+	MA/h	MD	<i>L. monocytogenes</i>	+	=
	Mashed potatoes	VG3	Yes	LA	MC	HB	HC	<i>L. welshimeri</i>	+	7038	2.61	+	MC/Wh	MC	<i>L. welshimeri</i>	+	=
	Leeks pellets	VG3	Yes	MA	MA	HA	HB	<i>L. seeligeri</i>	+	6841	2.54	+	MA/Wh	MA	<i>L. seeligeri</i>	+	=

CODE	MATRICES	Cat.	Spiked	NF EN ISO 11290-1 (#) METHOD					VIDAS LSX METHOD														COMPARISON		
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION 6H ENRICHMENT			VIDAS LSX 24H			CONFIRMATION 24H ENRICHMENT			IDENTIF.		FINAL RESULT 6H	FINAL RESULT 24H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	PAL	OAA	RLM	RFV LSX 24H	TV	TEST RESULT	PAL	OAA	RLM				
D1	Chicken kebab	MP1	No	+LA*	+LA*	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	7345	3.37	+	+MA	+MA*	+MA*	7209	3.31	+	+HA	+HA*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	+	=
D2	Chicken wings	MP1	No	+MA*	+MA*	+HA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6791	3.12	+	+HA	+HA*	+HA*	6728	3.09	+	+HA*	+HA*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
D7	Minced beef	MP1	No	Ø	Ø	Ø	Ø	/	-	39	0.01	-	/	/	/	1328	0.61	+	+LB	+LB	+LA	<i>L.monocytogenes</i>	-	+	= 6H & PS 24H
E2	Minced beef	MP1	No	+LA	+LA(2)	+MA	+MA	<i>L.monocytogenes</i>	+	10063	4.90	+	+HA	+MA	+MA	6733	3.04	+	+HA	+MB	/	<i>L.monocytogenes</i>	+	+	=
E3	Minced beef	MP1	No	+LA	+LA	+MA	+MA	<i>L.monocytogenes</i>	+	8037	3.69	+	+MA	+MA	+MA	7118	3.21	+	+HA	+MA	/	<i>L.monocytogenes</i>	+	+	=
E7	Minced beef	MP1	No	Ø	Ø	+HA	+HA	<i>L.monocytogenes</i>	+	7621	3.50	+	+HA	+MA	+HA	6302	2.84	+	+HA	+MA	/	<i>L.monocytogenes</i>	+	+	=
E10	Beef meat	MP1	No	+LA	+LA	+MA	+MA	<i>L.welshimeri</i>	+	8908	4.09	+	+MA	+MA	+MA	6618	2.99	+	+HA	+HA	/	<i>L.welshimeri</i>	+	+	=
E12	Lamb meat	MP1	No	Ø	Ø	Ø	-LE	/	-	24	0.01	-	/	/	/	26	0.01	-	/	/	/	/	-	-	=
C23	Beef heart	MP1	No	+MA	+MB	+MA	+MA	<i>L.monocytogenes</i>	+	10157	4.73	+	+MA	+MA	+MA	7313	3.4	+	+HA	+MA	/	<i>L.monocytogenes</i>	+	+	=
F1	Beef meat	MP1	No	Ø	Ø	Ø	Ø	/	-	41	0.02	-	/	/	/	48	0.02	-	/	/	/	/	-	-	=
F3	Horse meat	MP1	No	Ø	Ø	Ø	Ø	/	-	25	0.01	-	/	/	/	105	0.04	-	/	/	/	/	-	-	=
F4	Pork chops	MP1	No	Ø	Ø	Ø	Ø	/	-	39	0.01	-	/	/	/	164	0.07	-	/	/	/	/	-	-	=
F5	Beef meat	MP1	No	Ø	Ø	Ø	Ø	/	-	30	0.01	-	/	/	/	37	0.01	-	/	/	/	/	-	-	=
F6	Beef meat	MP1	No	Ø	Ø	Ø	Ø	/	-	38	0.01	-	/	/	/	51	0.02	-	/	/	/	/	-	-	=
A2	Bolognaise minced meat	MP2	No	-LE	Ø	-HE	Ø	/	-	46	0.02	-	/	/	/	54	0.02	-	/	/	/	/	-	-	=
A4	Bolognaise minced meat	MP2	No	Ø	Ø	-LE	Ø	/	-	46	0.02	-	/	/	/	41	0.01	-	/	/	/	/	-	-	=
B30	Sausages	MP2	No	+HA	+HA	+HA*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6236	2.83	+	+HA*	+MA*	+MA*	7231	3.28	+	+HA*	+HB*	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
C19	Chipolatas	MP2	No	-LE	-LE	Ø	Ø	/	-	8236	3.83	+	+MA	+MA	+MA	6286	2.92	+	+HA	+HB	/	<i>L.monocytogenes</i> <i>L.welshimeri</i>	+	+	PS
D3	Merguez	MP2	No	+MA*	+MB*	+HA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	6757	3.10	+	+HA	+HA*	+HA*	6840	3.14	+	+HA	+HB*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	+	=
D4	Merguez	MP2	No	Ø	Ø	+MA	+MA	<i>L.monocytogenes</i>	+	755	0.34	+	+LA	+LA	+LA	9458	4.35	+	+MA*	+MB*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
D6	Surface above weighing machine	MP2	No	Ø	Ø	+HC	+MB	<i>L.monocytogenes</i>	+	6278	2.88	+	+HA	+MA	+HA	6870	3.16	+	+HA	+HA	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
D9	Fish cutting table	MP2	No	+LA*	+LA*	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	5896	2.71	+	+MA	+MB*	+MA*	10882	5.00	+	+MA*	+MB*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
D11	Slicer	MP2	No	+LA	+LA	+HA	+HA	<i>L.monocytogenes</i>	+	6570	3.02	+	+HA	+HA	+HA	6492	2.98	+	+MA	+HB	+HA	<i>L.monocytogenes</i>	+	+	=
E9	Cheese slicer	MP2	No	+LA	+LB	+LB	+MA*	<i>L.monocytogenes</i> <i>L.welshimeri</i> <i>L.innocua</i>	+	7627	3.50	+	+HA	+HA*	+HA*	6983	3.15	+	+MA*	+MA*	/	<i>L.monocytogenes</i> <i>L.welshimeri</i> <i>L.innocua</i>	+	+	=
E11	Surface of cheese knife	MP2	No	+LA*	+LA*	+HA	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6743	3.10	+	+HA	+HA	+HA*	6649	3.00	+	+HA	+MA*	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
F2	Swab from sausages process line	MP2	No	-LE	Ø	-LE	Ø	/	-	49	0.02	-	/	/	/	140	0.06	-	/	/	/	/	-	-	=
F7	Fish cutting table	MP2	No	+MA*	+MA*	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6474	3.25	+	+HA	+MA*	+MA*	6430	2.9	+	+HA	+MB*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
F8	Surface of cheese knife	MP2	No	+MB	+LA	+HA	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	6438	3.23	+	+HA	+HA	+HB	6537	2.95	+	+HA	+HA	+HB	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	+	=
G4	Texas pork chop for barbecue	MP2	No	+MA*	+MA*	+HA*	+MA*	<i>L.monocytogenes</i>	+	6801	3.07	+	+MA	+MA*	+HA*	6563	3.29	+	+MA*	+MB	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
C26	Pâté	MP3	No	Ø	Ø	Ø	Ø	/	-	35	0.01	-	/	/	/	59	0.02	-	/	/	/	/	-	-	=
D5	Bacon	MP3	No	+MA*	+MA*	+HA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i> <i>L.welshimeri</i>	+	7114	3.27	+	+HA	+HA	+HA	6792	3.12	+	+HA	+HB	+HA*	<i>L.monocytogenes</i> <i>L.welshimeri</i>	+	+	=
D8	Ham	MP3	No	+MA	+MA	+MA	+MA	<i>L.welshimeri</i>	+	6645	3.05	+	+HA	+MA	+HA	6596	3.03	+	+HA	+MA	+HA	<i>L.welshimeri</i>	+	+	=
D10	Cooked minced meat	MP3	No	+LA(4)	+LA*(2)	+HA*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	8446	3.88	+	+HA	+HA	+HA	7183	3.3	+	+MA	+HA	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
E5	Pâté	MP3	No	Ø	-LE	Ø	Ø	/	-	33	0.01	-	/	/	/	30	0.01	-	/	/	/	/	-	-	=
E6	Strasbourg sausage	MP3	No	-LE	Ø	-LE	Ø	/	-	42	0.01	-	/	/	/	30	0.01	-	/	/	/	/	-	-	=
E8	Pâté	MP3	No	Ø	-LE	Ø	-ME	/	-	61	0.03	-	Ø	-LE	Ø	49	0.02	-	/	/	/	/	-	-	=
F9	Pâté	MP3	No	Ø	Ø	Ø	Ø	/	-	38	0.01	-	/	/	/	47	0.02	-	/	/	/	/	-	-	=
F10	Ham	MP3	No	Ø	Ø	Ø	-LE	/	-	49	0.02	-	/	/	/	63	0.02	-	/	/	/	/	-	-	=
F11	Pâté	MP3	No	Ø	Ø	-ME	-LE	/	-	34	0.01	-	/	/	/	70	0.03	-	/	/	/	/	-	-	=
G3	Ham	MP3	No	+MA	+MA	+HA	+HA	<i>L.monocytogenes</i>	+	6804	3.07	+	+MA	+MA	+MA	6209	3.11	+	+MA	+MA	/	<i>L.monocytogenes</i>	+	+	=

CODE	MATRICES	Cat.	Spiked	NF EN ISO 11290-1 (#) METHOD						VIDAS LSX METHOD													COMPARISON		
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION 6H ENRICHMENT			VIDAS LSX 24H			CONFIRMATION 24H ENRICHMENT			IDENTIF.		FINAL RESULT 6H	FINAL RESULT 24H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	PAL	OAA	RLM	RFV LSX 24H	TV	TEST RESULT	PAL	OAA	RLM				
B2	"Maroilles" cheese	DP1	No	+LB	+LA	+HB	+MA	<i>L.monocytogenes</i>	+	6154	2.79	+	+HB	+MA	+HA	6425	2.92	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
B4	"Maroilles" raw milk cheese	DP1	No	+LA	+LA	+HA	+HA	<i>L.monocytogenes</i>	+	6719	3.05	+	+HA	+MA	+MA	7148	3.25	+	+MA	+MA	/	<i>L.monocytogenes</i>	+	+	=
B6	"Maroilles" cheese	DP1	No	+LB	+LB	+HA	+HA	<i>L.monocytogenes</i>	+	7204	3.27	+	-ME	+HA	+HA	7093	3.22	+	+HB	+HA	/	<i>L.monocytogenes</i>	+	+	=
B17	"Maroilles" cheese	DP1	No	-LE	-LE	-ME	Ø	/	-	36	0.01	-	/	/	/	48	0.02	-	/	/	/	/	-	-	=
B18	"Epoisses" cheese	DP1	No	+MA	+MB	+HA	+HA	<i>L.monocytogenes</i>	+	7463	3.39	+	+HA	+HA	+HA	7426	3.37	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
B19	"Maroilles" cheese	DP1	No	+LA	+LA	+HA	+HB	<i>L.monocytogenes</i>	+	9669	4.39	+	+MA	+MB	+MA	4506	2.05	+	+HA	+MB	/	<i>L.monocytogenes</i>	+	+	=
B21	Raw milk cheese	DP1	No	+LA	+LB	+HA	+HB	<i>L.monocytogenes</i> <i>L.innocua</i>	+	8125	3.69	+	+MA	+MA	+MA	4883	2.22	+	+MA	+HA	/	<i>L.monocytogenes</i>	+	+	=
B22	Raw milk cheese	DP1	No	+LA	+MC	+HA	+HA	<i>L.monocytogenes</i>	+	10826	4.92	+	+MA*	+MA*	+MA*	5104	2.32	+	+HA	+HA	/	<i>L.monocytogenes</i> <i>L.seeligeri</i>	+	+	=
B23	"Maroilles" cheese	DP1	No	+LA	+LA	+HA	+HA	<i>L.monocytogenes</i>	+	9173	4.17	+	+MD	+MA	+MA	5450	2.47	+	+HA	+MA	/	<i>L.monocytogenes</i>	+	+	=
B24	"St Germain" cheese	DP1	No	+LB	+LA	+HB	+HA	<i>L.monocytogenes</i>	+	11954	5.43	+	+MA	+MA	+MA	5700	2.59	+	+HB	+HA	/	<i>L.monocytogenes</i>	+	+	=
C7	Raw milk cheese	DP1	No	Ø	Ø	Ø	Ø	/	-	21	0.00	-	/	/	/	7289	3.39	+	+HB	+LB	/	<i>L.seeligeri</i>	-	+	= 6H & PS 24H
C8	"Epoisses" cheese	DP1	No	+LA	+LA	+HA	+MB	<i>L.monocytogenes</i>	+	7085	3.30	+	+HA	+HA	+HA	6670	3.1	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
C18	"Cambrai" cheese	DP1	No	+MA	+HA	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6984	3.25	+	+MA	+MA*	+MA*	7768	3.61	+	+MA*	+MA*	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
C22	"Epoisses" cheese	DP1	No	Ø	Ø	Ø	Ø	/	-	28	0.01	-	/	/	/	32	0.01	-	/	/	/	/	-	-	=
C24	"Picodon" cheese	DP1	No	Ø	Ø	Ø	-LE	/	-	28	0.01	-	/	/	/	36	0.01	-	/	/	/	/	-	-	=
C25	"Maroilles" cheese	DP1	No	Ø	-LE	Ø	Ø	/	-	25	0.01	-	/	/	/	27	0.01	-	/	/	/	/	-	-	=
D12	"Coulommiers" cheese	DP1	No	Ø	Ø	Ø	Ø	/	-	40	0.01	-	/	/	/	51	0.02	-	/	/	/	/	-	-	=
D13	"Maroilles" cheese	DP1	No	Ø	Ø	Ø	Ø	/	-	23	0.01	-	/	/	/	27	0.01	-	/	/	/	/	-	-	=
D14	"Munster" cheese	DP1	No	Ø	-ME	Ø	Ø	/	-	63	0.02	-	/	/	/	110	0.05	-	/	/	/	/	-	-	=
D15	Camembert cheese	DP1	No	Ø	-LE	Ø	-ME	/	-	34	0.01	-	/	/	/	28	0.01	-	/	/	/	/	-	-	=
D16	"Reblochon" cheese	DP1	No	Ø	-LE	Ø	Ø	/	-	32	0.01	-	/	/	/	30	0.01	-	/	/	/	/	-	-	=
D17	"Reblochon" cheese	DP1	No	Ø	-ME	Ø	-ME	/	-	54	0.02	-	/	/	/	30	0.01	-	/	/	/	/	-	-	=
D18	"Neufchâtel" cheese	DP1	No	-ME	-ME	-ME	Ø	/	-	30	0.01	-	/	/	/	62	0.02	-	/	/	/	/	-	-	=
D19	Cheese from Langres	DP1	No	Ø	Ø	Ø	Ø	/	-	31	0.01	-	/	/	/	34	0.01	-	/	/	/	/	-	-	=
G1	"Morbier" cheese	DP1	No	+MA	+MB	+HB	+HB	<i>L.monocytogenes</i>	+	6853	3.09	+	+MA	+MA	+MA	5998	3.01	+	+MA	+HA	/	<i>L.monocytogenes</i>	+	+	=
G2	"Morbier" cheese	DP1	No	Ø	-ME	Ø	Ø	/	-	34	0.01	-	/	/	/	30	0.01	-	/	/	/	/	-	-	=
H5	"Reblochon" cheese	DP1	Yes	+LA	+LB	+HA	+HA	<i>L.innocua</i>	+	7976	2.64	+	+MA	+LA	+MA	6925	2.29	+	+HB	+MA	/	<i>L.innocua</i>	+	+	=
H6	"Reblochon" cheese	DP1	Yes	Ø	-LE	Ø	-LE	/	-	50	0.01	-	/	/	/	40	0.01	-	/	/	/	/	-	-	=
H1	Grated Gruyère	DP1	Yes	Ø	Ø	Ø	-ME	/	-	7073	2.34	+	+HB	+HA	+HA	5937	1.98	+	+HB	+HA	/	<i>L.innocua</i>	+	+	= PS
H2	"Vieux pâné" cheese	DP1	Yes	Ø	+LA(1)	+MA	+MA	<i>L.innocua</i>	+	10317	3.41	+	+MA	+MA	+MA	6871	2.27	+	+HB	+HB	/	<i>L.innocua</i>	+	+	=
H4	"Brie" cheese	DP1	Yes	Ø	-ME	Ø	-LE	/	-	41	0.01	-	/	/	/	53	0.01	-	/	/	/	/	-	-	=
B8	"Roquefort" cheese	DP2	No	+LA(4)	+LA	-ME	+LB(1)	<i>L.monocytogenes</i>	+	1199	0.54	+	+LA*	+LA*	+LA*	6173	2.8	+	+HA*	+HA*	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
B10	"Roquefort" cheese	DP2	No	Ø	Ø	Ø	Ø	/	-	26	0.01	-	/	/	/	26	0.01	-	/	/	/	/	-	-	=
B15	Goat's cheese	DP2	No	Ø	-LE	Ø	-LE	/	-	61	0.02	-	/	/	/	29	0.01	-	/	/	/	/	-	-	=
B16	Ewe's cheese	DP2	No	Ø	+LB	-LE	-LE	<i>L.seeligeri</i>	+	6816	3.10	+	+HA	+HA	+HA	6874	3.12	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
C9	Goat's cheese	DP2	No	+MA	+MB	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	5831	2.71	+	+HA	+MA	+HA	6725	3.13	+	+HB	+HA	/	<i>L.monocytogenes</i>	+	+	=
C10	Goat's cheese	DP2	No	Ø	-LE	Ø	Ø	/	-	40	0.01	-	/	/	/	35	0.01	-	/	/	/	/	-	-	=
C11	Goat's cheese	DP2	No	-LE	-LE	Ø	Ø	/	-	64	0.02	-	/	/	/	977	0.45	+	+LB	+LB	/	<i>L.monocytogenes</i>	-	+	= 6H & PS 24H
D20	Goat's cheese	DP2	No	Ø	-LE	Ø	-ME	/	-	61	0.02	-	/	/	/	33	0.01	-	/	/	/	/	-	-	=
H3	Ewe's cheese	DP2	Yes	-LE	-LE	-LE	-ME	/	-	42	0.01	-	/	/	/	198	0.06	-	/	/	/	/	-	-	=
B5	Chocolate profiteroles	DP3	No	+LA	+LA	+HA	+HA	<i>L.monocytogenes</i>	+	6695	3.04	+	+HA*	+MA*	+MA*	6885	3.13	+	+HA*	+HA*	/	<i>L.monocytogenes</i>	+	+	=
B9	Chocolate profiteroles	DP3	No	+MA	+MA	+HA*	+HA*	<i>L.monocytogenes</i>	+	6613	3.00	+	+HA	+HA*	+HA*	6450	2.93	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
B11	Strawberries tart	DP3	No	Ø	-LE	Ø	-LE	/	-	579	0.26	+	Ø	Ø	Ø	35	0.01	-	-LE	Ø	/	-	-	-	= (FP 6H)
B29	Strawberries tart	DP3	No	Ø	Ø	-LE	-LE	/	-	38	0.01	-	/	/	/	44	0.02	-	/	/	/	/	-	-	=
C12	Whipped cream	DP3	No	+MA	+HA	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6642	3.09	+	+HA	+MA*	+HA*	6978	3.25	+	+HA	+HA	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
C13	Cream pastry	DP3	No	+LA	+LB	Ø	-ME	<i>L.grayi</i>	+	460	0.21	+	+LA	+MA	+MA	10881	5.07	+	+LB	+MB	/	<i>L.grayi</i>	+	+	=
E4	Chocolate cakes	DP3	No	Ø	Ø	-ME	-LE	/	-	35	0.01	-	/	/	/	36	0.01	-	/	/	/	/	-	-	=

CODE	MATRICES	Cat.	Spiked	NF EN ISO 11290-1 (#) METHOD						VIDAS LSX METHOD														COMPARISON	
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION 6H ENRICHMENT			VIDAS LSX 24H			CONFIRMATION 24H ENRICHMENT			IDENTIF.	FINAL RESULT 6H		FINAL RESULT 24H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	PAL	OAA	RLM	RFV LSX 24H	TV	TEST RESULT	PAL	OAA	RLM				
A14	Vegetables for couscous	VG1	No	+LB	+LB	+HA	+MB	<i>L.innocua</i>	+	11656	5.30	+	+HA	+MB	+MB	5967	2.71	+	+HA	+MB	+HB	<i>L.seeligeri</i>	+	+	=
A15	Vegetables for couscous	VG1	No	+LA	+LC	+HA	+MB	<i>L.innocua</i>	+	75	0.03	-	-LE	-LE	-LE	117	0.05	-	-LE	-ME	-LE	∅	-	-	FN
B25	Salad	VG1	No	+LA(1)	+LA(2)	+HB	+HA	<i>L.monocytogenes</i>	+	432	0.19	+	+LB	+LB	+LA	5787	2.63	+	+HA	+LB	/	<i>L.monocytogenes</i>	+	+	=
B26	Red cabbage	VG1	No	∅	∅	∅	∅	/	-	82	0.03	-	/	/	/	58	0.02	-	/	/	/	/	-	-	=
B27	Grated celery	VG1	No	∅	∅	∅	∅	/	-	45	0.02	-	/	/	/	45	0.02	-	/	/	/	/	-	-	=
E1	Mixed salad	VG1	No	∅	-LE	-LE	-LE	/	-	44	0.02	-	/	/	/	49	0.02	-	/	/	/	/	-	-	=
E13	Raw vegetables	VG1	No	∅	-LE	∅	-ME	/	-	36	0.01	-	/	/	/	31	0.01	-	/	/	/	/	-	-	=
E14	Grated celery	VG1	No	∅	∅	∅	-LE	/	-	43	0.01	-	/	/	/	57	0.02	-	/	/	/	/	-	-	=
E15	Grated carrots	VG1	No	∅	∅	∅	∅	/	-	33	0.01	-	/	/	/	39	0.01	-	/	/	/	/	-	-	=
E16	Grated carrots	VG1	No	∅	∅	∅	∅	/	-	32	0.01	-	/	/	/	37	0.01	-	/	/	/	/	-	-	=
E17	Raw mushrooms	VG1	No	∅	∅	∅	-ME	/	-	97	0.04	-	/	/	/	5133	2.32	+	∅	-ME	/	<i>Pseudomonas putida</i>	-	-	= (FP 24H)
E18	Red cabbage	VG1	No	∅	∅	∅	∅	/	-	46	0.02	-	/	/	/	164	0.07	-	/	/	/	/	-	-	=
E19	Red cabbage	VG1	No	∅	∅	∅	∅	/	-	56	0.02	-	/	/	/	69	0.03	-	/	/	/	/	-	-	=
F13	Salad	VG1	No	-LE	∅	-LE	∅	/	-	38	0.01	-	/	/	/	43	0.01	-	/	/	/	/	-	-	=
F14	Mixed salad	VG1	No	-LE	-LE	-ME	-ME	/	-	38	0.01	-	/	/	/	44	0.01	-	/	/	/	/	-	-	=
F17	Grated carrots and celery	VG1	No	∅	-LE	∅	-LE	/	-	53	0.02	-	/	/	/	59	0.02	-	/	/	/	/	-	-	=
A13	Fried potatoes	VG2	No	+MA*	+MA*	+HA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	7114	3.23	+	+HA	+HA	+HA	5883	2.67	+	+HA	+HA	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
B7	Frozen broccoli	VG2	No	+LA	+LA	+HA	+MA	<i>L.monocytogenes</i>	+	6612	3.00	+	+MA	+MA	+MA	5984	2.72	+	+HA	+MA	/	<i>L.monocytogenes</i>	+	+	=
B12	Frozen fries	VG2	No	+LA	+LB	+HA	+HA	<i>L.monocytogenes</i>	+	7239	3.29	+	+HA	+MA	+HA	7440	3.38	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
B20	Frozen fried potatoes	VG2	No	+LB	+LA	+HB	+HA	<i>L.monocytogenes</i>	+	6511	2.96	+	-HE	+MA	+HA	4607	2.09	+	+HD	+MA	/	<i>L.monocytogenes</i>	+	+	=
C1	Frozen fried potatoes	VG2	No	-LE	+LA	∅	∅	<i>L.grayi</i>	+	6750	3.14	+	+HA	+HA	+HA	5847	2.72	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
C4	Frozen broccoli	VG2	No	∅	∅	∅	∅	/	-	48	0.01	-	/	/	/	56	0.02	-	/	/	/	/	-	-	=
C5	Frozen fries	VG2	No	+MA	+MB	+MB	+MB	<i>L.monocytogenes</i>	+	92	0.04	-	/	/	/	7068	3.29	+	+HA	+HA	/	<i>L.monocytogenes</i>	-	+	FN 6H & = 24H
C6	Potatoes and onions	VG2	No	∅	∅	∅	∅	/	-	48	0.02	-	∅	-LE	∅	38	0.01	-	∅	-ME	/	/	-	-	=
C20	Frozen fries	VG2	No	-LE	-LE	∅	-LE	/	-	51	0.02	-	/	/	/	66	0.03	-	/	/	/	/	-	-	=
C21	Frozen fries	VG2	No	∅	∅	∅	∅	/	-	43	0.02	-	/	/	/	42	0.01	-	/	/	/	/	-	-	=
E21	Green beans	VG2	No	+LA	+LA	+HA	+HA	<i>L.innocua</i>	+	3255	1.47	+	+MA	+MA	+MB	5799	2.62	+	+HA	+HA	/	<i>L.innocua</i>	+	+	=
F15	Frozen fries	VG2	No	∅	-LE	∅	-LE	/	-	43	0.02	-	/	/	/	39	0.01	-	/	/	/	/	-	-	=
F16	Frozen fries	VG2	No	∅	-LE	∅	-ME	/	-	71	0.03	-	/	/	/	31	0.01	-	/	/	/	/	-	-	=
B1	Rice salad	VG3	No	+MA	+MA	+HA	+MA	<i>L.monocytogenes</i>	+	5842	2.65	+	+HA	+MA	+HA	6154	2.79	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
B3	Mixed vegetables panful	VG3	No	∅	∅	∅	∅	/	-	32	0.01	-	/	/	/	32	0.01	-	/	/	/	/	-	-	=
B13	Tagliatelles	VG3	No	+MA	+MA	+HA	+MA	<i>L.monocytogenes</i>	+	5843	2.65	+	+HA	+MA	+HA	6095	2.77	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
B14	Tagliatelles	VG3	No	+MA	+MA	+MA	+HA	<i>L.monocytogenes</i>	+	6222	2.83	+	+HA	+HA	+HA	6465	2.94	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
C2	Pasta	VG3	No	+LA	∅	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	8260	3.84	+	+MA	+MA	+MA	6027	2.8	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
C3	Spinaches with cream	VG3	No	+LA	+LA	+MA	+MA	<i>L.monocytogenes</i>	+	3623	1.68	+	+MA	+MA	+LA	6460	3.01	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=
E22	Mashed carrots	VG3	No	∅	∅	-ME	∅	/	-	109	0.04	-	/	/	/	141	0.06	-	/	/	/	/	-	-	=
F12	Cooked broccolis	VG3	No	∅	∅	∅	∅	/	-	48	0.02	-	/	/	/	47	0.02	-	/	/	/	/	-	-	=

CODE	MATRICES	Cat.	Spiked	NF EN ISO 11290-1 (#) METHOD						VIDAS LSX METHOD													COMPARISON		
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION 6H ENRICHMENT			VIDAS LSX 24H			CONFIRMATION 24H ENRICHMENT			IDENTIF.		FINAL RESULT 6H	FINAL RESULT 24H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	PAL	OAA	RLM	RFV LSX 24H	TV	TEST RESULT	PAL	OAA	RLM				
A16	Water from vegetables rinse	EN1	No	Ø	-LE	-LE	-LE	/	-	58	0.02	-	/	/	/	129	0.05	-	/	/	/	/	-	-	=
F18	Water from butcherie siphon	EN1	No	+LA	+LA	+HA	+MA*	<i>L.monocytogenes</i>	+	11428	5.73	+	+MA	+MA	+MA	5765	2.60	+	+HA	+MA	+HA	<i>L.monocytogenes</i>	+	+	=
G19	Waste waters	EN1	No	Ø	Ø	Ø	Ø	/	-	30	0.01	-	/	/	/	32	0.01	-	/	/	/	/	-	-	=
G20	Stagnant water	EN1	No	Ø	Ø	Ø	Ø	/	-	35	0.01	-	/	/	/	83	0.04	-	/	/	/	/	-	-	=
G21	Water from washing machine	EN1	No	+LA	+LA*	+HA	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	5976	2.7	+	+MA	+MA*	+MA*	6633	3.32	+	+MA	+MA*	/	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
G22	Rinse water	EN1	No	Ø	Ø	Ø	Ø	/	-	30	0.01	-	/	/	/	55	0.01	-	/	/	/	/	-	-	=
G23	Process water	EN1	No	Ø	Ø	Ø	-LE	/	-	31	0.01	-	/	/	/	48	0.01	-	/	/	/	/	-	-	=
H7	Rinse water	EN1	Yes	Ø	Ø	Ø	Ø	/	-	6724	2.22	+	+HA	+MA	+HA	6536	2.16	+	+HA	+HA	/	<i>L.seeligeri</i>	+	+	PS
H8	Rinsing bath	EN1	Yes	Ø	Ø	+LC	+MA	<i>L.seeligeri</i>	+	1764	0.58	+	Ø	+LA	Ø	6698	2.22	+	+HB	+HA	/	<i>L.seeligeri</i>	+(OAA)	+	=
H9	Vegetables washing bath	EN1	Yes	Ø	Ø	Ø	Ø	/	-	33	0.01	-	/	/	/	31	0.01	-	/	/	/	/	-	-	=
H10	Residual water	EN1	Yes	Ø	Ø	Ø	Ø	/	-	33	0.01	-	/	/	/	33	0.01	-	/	/	/	/	-	-	=
H11	Rinse water	EN1	Yes	Ø	Ø	Ø	-LE	/	-						68	0.02	-	/	/	/	/			=	
H12	Stagnant water	EN1	Yes	Ø	Ø	Ø	Ø	/	-						43	0.01	-	/	/	/	/			=	
H13	Rinse water	EN1	Yes	Ø	Ø	Ø	-LE	/	-	2920	0.96	+	Ø	+LA	+LB	5850	1.93	+	+HA	+HA	/	<i>L.innocua</i> <i>L.seeligeri</i>	+	+	PS
J10	Residual water	EN1	No	-LE	-LE	-ME	-ME	/	-	32	0.01	-	Ø	-ME	Ø	44	0.01	-	/	/	/	/	-	-	=
J11	Residual water	EN1	No	Ø	Ø	Ø	Ø	/	-	31	0.01	-	Ø	Ø	Ø	30	0.01	-	/	/	/	/	-	-	=
J12	Water from washing machine	EN1	No	Ø	Ø	Ø	Ø	/	-	26	0.00	-	Ø	Ø	Ø	32	0.01	-	/	/	/	/	-	-	=
J13	Water from washing machine	EN1	No	Ø	Ø	Ø	Ø	/	-	31	0.01	-	Ø	-ME	Ø	60	0.02	-	/	/	/	/	-	-	=
O18	Rinse tank	EN1	Yes	+LA	+LA	+MA	+MB	<i>L.innocua</i>	+	5737	1.9	+	+MB	+MB	+MA	7635	2.78	+	+HA	+MB	+HA	<i>L.innocua</i>	+	+	=
O20	Water from cooling tower	EN1	Yes	+LA	+LA	+MA	+MA	<i>L.monocytogenes</i>	+	6194	2.06	+	+HA	+MA	+HA	4704	1.71	+	+HA	+HA	+HA	<i>L.monocytogenes</i>	+	+	=

CODE	MATRICES	Cat.	Spiked	NF EN ISO 11290-1 (#) METHOD								VIDAS LSX METHOD												COMPARISON	
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX 6H			CONFIRMATION 6H ENRICHIMENT			VIDAS LSX 24H			CONFIRMATION 24H ENRICHIMENT			IDENTIF.	FINAL RESULT 6H		FINAL RESULT 24H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	PAL	OAA	RLM	RFV LSX 24H	TV	TEST RESULT	PAL	OAA	RLM				
B28	Surface weighing workstation	EN2	No	Ø	Ø	+HA	+HA	<i>L.monocytogenes</i>	+	9737	4.42	+	+MA	+MA	+MA	6481	2.94	+	+MA	+MA	/	<i>L.monocytogenes</i>	+	+	=
C16	Fish cutting table	EN2	No	Ø	Ø	Ø	-LE	/	-	24	0.01	-	/	/	/	65	0.03	-	/	/	/	/	-	-	=
C17	Slicer surface	EN2	No	Ø	Ø	Ø	-LE	/	-	27	0.01	-	/	/	/	76	0.03	-	/	/	/	/	-	-	=
D21	Cheese slicer surface	EN2	No	Ø	Ø	Ø	Ø	/	-	32	0.01	-	/	/	/	53	0.02	-	/	/	/	/	-	-	=
D22	Surface of cheese knife	EN2	No	Ø	Ø	Ø	Ø	/	-	27	0.01	-	/	/	/	30	0.01	-	/	/	/	/	-	-	=
D23	Swab from sausages process line	EN2	No	+HA	+HA	+MA	+MA	<i>L.monocytogenes</i>	+	6099	2.8	+	+HA	+MA	+HA	6041	2.77	+	+HA	+HA	+HA	<i>L.monocytogenes</i>	+	+	=
D24	Fish cutting table	EN2	No	-LE	-LE	-ME	-ME	/	-	32	0.01	-	/	/	/	47	0.02	-	/	/	/	/	-	-	=
F19	Surface of butchery knife	EN2	No	Ø	Ø	Ø	-LE	/	-	27	0.01	-	/	/	/	31	0.01	-	/	/	/	/	-	-	=
F20	Meat preparation pan	EN2	No	Ø	Ø	Ø	-LE	/	-	33	0.01	-	/	/	/	34	0.01	-	/	/	/	/	-	-	=
F21	Slicer surface	EN2	No	Ø	Ø	Ø	-LE	/	-	27	0.01	-	/	/	/	34	0.01	-	/	/	/	/	-	-	=
F22	Slicer surface	EN2	No	Ø	Ø	Ø	-LE	/	-	61	0.03	-	/	/	/	72	0.03	-	/	/	/	/	-	-	=
F23	Surface of delicatessen knife	EN2	No	Ø	Ø	Ø	-LE	/	-	34	0.01	-	/	/	/	30	0.01	-	/	/	/	/	-	-	=
F24	Spit roasting surface	EN2	No	Ø	Ø	Ø	-LE	/	-	33	0.01	-	/	/	/	32	0.01	-	/	/	/	/	-	-	=
F25	Delicatessen slicer surface	EN2	No	+HA	+MA	+MA*	+MA*	<i>L.innocua</i>	+	31	0.01	-	Ø	Ø	Ø	33	0.01	-	Ø	Ø	Ø	-	-	-	FN
G24	Swab from channel floor	EN2	No	Ø	Ø	Ø	-LE	/	-	32	0.01	-	/	/	/	38	0.01	-	/	/	/	/	-	-	=
G25	Surface of cheese knife	EN2	No	+LA	+LB	+HA	+HA	<i>L.monocytogenes</i>	+	6366	2.87	+	+HA	+MA	+HB	6171	2.21	+	+MA	+HA	/	<i>L.monocytogenes</i>	+	+	=
G26	Cheese cutting table	EN2	No	Ø	-LE	Ø	Ø	/	-	31	0.01	-	/	/	/	31	0.01	-	/	/	/	/	-	-	=
G27	Surface of delicatessen knife	EN2	No	Ø	-LE	-LE	-LE	/	-	7871	3.55	+	+HA	+MA	+HA	6523	2.34	+	+HA	+MA	/	<i>L.welshimeri</i>	+	+	PS
G28	Floor of fish cutting room	EN2	No	+MA	+MB	+HA	+MB	<i>L.monocytogenes</i>	+	6563	2.96	+	+MA	+MA	+LB	6423	2.3	+	+MB	+MA	/	<i>L.monocytogenes</i>	+	+	=
H15	Floor of storage room	EN2	Yes	Ø	-LE	+LC	+MB	<i>L.seeligeri</i>	+	7338	2.43	+	+LB	+LB	+LB	8738	2.89	+	+LB	+HD	/	<i>L.seeligeri</i>	+	+	=
H16	Surface of dirty lift	EN2	Yes	-LE	-LE	+HA	+HA	<i>L.innocua</i>	+	6681	2.21	+	+MA	+MA	+MA	5836	1.95	+	+HA	+HB	/	<i>L.innocua</i>	+	+	=
J1	Stainless steel table from pastries preparation	EN2	Yes	Ø	Ø	-ME	-ME	/	-	10944	3.53	+	+MA	+MB	+MB	5983	2.12	+	+HA	+HB	+HA	<i>L.innocua</i>	+	+	PS
J2	Butchery slicer surface	EN2	Yes	Ø	Ø	+MA	+MA	<i>L.innocua</i>	+	196	0.06	-	+LA	+LA	+LA	6073	2.15	+	+HA	+HA	+HA	<i>L.innocua</i>	-	+	FN 6H & = 24H
J3	Cheese cutting table	EN2	Yes	+LA	+LB	+MA*	+MB	<i>L.monocytogenes</i>	+	7544	2.43	+	+MB	+MA	+MB*	6164	2.18	+	+HA*	+MA*	+HA*	<i>L.monocytogenes</i>	+	+	=
J4	Surface of cheese knife	EN2	Yes	+LA	+LA	+MA	+MA	<i>L.innocua</i>	+	3927	1.26	+	+MA	+MB	+MB	6387	2.26	+	+HA	+HA	+HB	<i>L.innocua</i>	+	+	=
J5	Surface of butchery knife	EN2	Yes	+LA(3)	+LA	+MA	+MA	<i>L.innocua</i>	+	173	0.05	-	+LA	+LA	+LA	6423	2.27	+	+HA	+HA	+HA	<i>L.innocua</i>	-	+	FN 6H & = 24H
J6	Thawing chamber for pastries	EN2	Yes	+LA(2)	-LE	+MA	+MA	<i>L.innocua</i>	+	97778	3.15	+	+MA	+MB	+MA	6677	2.36	+	+HA	+HA	+HB	<i>L.innocua</i>	+	+	=
J7	Surface of cheese knife	EN2	No	+HA*	+MA*	+MA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6469	2.08	+	+HA	+MA*	+HB*	5778	2.05	+	+HA	+HA	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
J8	Butchery floor	EN2	Yes	Ø	Ø	Ø	Ø	/	-	119	0.03	-	Ø	Ø	Ø	32	0.01	-	/	/	/	/	-	-	=
J9	Cutting table surface in butchery	EN2	Yes	Ø	Ø	-LE	Ø	/	-	32	0.01	-	Ø	Ø	Ø	38	0.01	-	/	/	/	/	-	-	=
J30	Cutting table surface in butchery	EN2	Yes	Ø	Ø	-LE	-ME	/	-	26	0.00	-	-LE	-ME	-ME	24	0.00	-	/	/	/	/	-	-	=
O1	Surface Pastries retail outlet	EN2	No	+LA	+LA*	+HA	+HA	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6857	2.28	+	+HA	+MA*	+HA*	6677	2.43	+	+HA	+MA	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
O3	Surface of delicatessen knife	EN2	No	+LB	-ME	+HB	+MB	<i>L.monocytogenes</i>	+	117	0.03	-	Ø	Ø	Ø	73	0.02	-	Ø	Ø	Ø	/	-	-	FN
O4	Thawing chamber for meats	EN2	No	+LA	+LA*	+HA*	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6873	2.28	+	+HA	+HA*	+HA*	7157	2.60	+	+HA	+HA	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
O5	Swab from fries processing line	EN2	No	+MA	+MA	+HA*	+MA*	<i>L.monocytogenes</i>	+	6933	2.3	+	+HA	+HA	+HA*	7217	2.62	+	+HA	+MA*	+HA*	<i>L.monocytogenes</i>	+	+	=
O11	Cooling room surface	EN2	Yes	+MA	+MA*	+HB	+MB*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6641	2.2	+	+HA	+MA*	+HA*	7522	2.73	+	+HA	+MA*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
O12	Thawing chamber	EN2	Yes	+MA	+MA*	+HA	+MA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6459	2.14	+	+HA	+MA*	+HA*	7777	2.83	+	+HA	+MA*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=
O13	Stainless steel shelves surface	EN2	Yes	+LA	+LA	+MA	+MA	<i>L.monocytogenes</i>	+	5898	1.96	+	+HA	+MA	+HA	6294	2.29	+	+MA	+MA	+HA	<i>L.monocytogenes</i>	+	+	=
O16	Delicatessen slicer surface	EN2	Yes	-LE	-LE	-LE	-LE	/	-	1616	0.53	+	-LE	-LE	-LE	1378	0.50	+	Ø	-LE	-LE	Ø	-	-	FP
O17	Cold room for cheese	EN2	Yes	Ø	-LE	Ø	-ME	/	-	59	0.01	-	Ø	-HE	Ø	70	0.02	-	/	/	/	/	-	-	=
O19	Trolley	EN2	Yes	+MA	+LA	+HA	+HA	<i>L.innocua</i>	+	6052	2.01	+	+HA	+MA	+MA	4585	1.66	+	+HA	+HA	+HA	<i>L.innocua</i>	+	+	=
P9	Surface	EN2	No	+HA	+MB	+HB	+HB	<i>L.monocytogenes</i>	+	5894	1.34	+	+HB	+HB	+HB	5894	1.99	+	+HA	+MB*	/	<i>L.monocytogenes</i>	+	+	=
P15	Stainless steel table in delicatessen retail outlet	EN2	Yes	+HB	+MA	+HB	+MA	<i>L.innocua</i>	+	6004	1.99	+	+HA	+HA	+HB	6628	2.20	+	+MA	+MB	/	<i>L.innocua</i>	+	+	=
P16	Sink in manufacturing plant	EN2	Yes	+MA	+HB	+MA	+HB	<i>L.innocua</i>	+	6168	2.05	+	+HA	+HB	+HA	6616	2.20	+	+MA	+MB	/	<i>L.innocua</i>	+	+	=
P17	Swab floor - wall junction	EN2	Yes	+HA	+MB*	+HA*	+MB*	<i>L.innocua</i> <i>L.ivanovii</i>	+	6112	2.03	+	+MA	+MB	+HA*	6689	2.22	+	+HA	+MB	/	<i>L.innocua</i> <i>L.ivanovii</i>	+	+	=
P18	Trolley	EN2	Yes	+HA	+MB	+HA	+MB	<i>L.ivanovii</i>	+	5999	1.99	+	+HA	+HB	+HA	6640	2.20	+	+HA	+HC	/	<i>L.ivanovii</i>	+	+	=

CODE	MATRICES	Cat.	Spiked	NF EN ISO 11290-1 (#) METHOD							VIDAS LSX METHOD													COMPARISON		
				FRASER 1/2		FRASER		CONFIRMATION			VIDAS LSX 6H			CONFIRMATION 6H ENRICHMENT			VIDAS LSX 24H			CONFIRMATION 24H ENRICHMENT			IDENTIF.		FINAL RESULT 6H	FINAL RESULT 24H
				P1	OA1	P2	OA2	IDENTIF.	RESULT	RFV LSX 6H	TV	TEST RESULT	PAL	OAA	RLM	RFV LSX 24H	TV	TEST RESULT	PAL	OAA	RLM					
C14	Scraps in production line	EN3	No	+MA	+MA	+MB	+MB	<i>L.monocytogenes</i>	+	344	0.16	+	+LA	+LA	+LA	6084	2.83	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=	
C15	Scraps from dirty tank	EN3	No	+MA	+MA	+HA	+MA	<i>L.monocytogenes</i>	+	6162	2.87	+	+HA	+MA	+HA	6281	2.92	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	=	
H14	Scraps from filter machine	EN3	Yes	+LA	+LA	+HA	+HA	<i>L.seeligeri</i>	+	5965	1.97	+	+HA	+HA*	+HA	6035	2.00	+	+HA	+HB	/	<i>L.seeligeri</i>	+	+	=	
I29	Scraps from cheese retail outlet	EN3	No	Ø	-LE	-LE	-ME	/	-	33	0.01	-	Ø	-ME	-ME	40	0.01	-	/	/	/	/	-	-	=	
I30	Scraps from cheese retail outlet	EN3	No	Ø	Ø	Ø	Ø	/	-	33	0.01	-	Ø	Ø	Ø	35	0.01	-	/	/	/	/	-	-	=	
I31	Scraps from production room	EN3	No	Ø	Ø	-LE	Ø	/	-	32	0.01	-	Ø	Ø	Ø	31	0.01	-	/	/	/	/	-	-	=	
I32	Sawdust bones	EN3	No	Ø	Ø	Ø	Ø	/	-	207	0.06	-	Ø	-LE	-LE	347	0.11	+	+LA	+LA	/	<i>L.welshimeri</i> <i>L.innocua</i>	-	+	= 6H & PS 24H	
I43	Scraps from retail outlet	EN3	No	Ø	Ø	Ø	Ø	/	-	6049	1.95	+	+MA	+MA	+HB	6010	1.93	+	+HA	+HA	/	<i>L.monocytogenes</i>	+	+	PS	
O2	Scraps from fish retail outlet	EN3	No	Ø	Ø	Ø	Ø	/	-	72	0.02	-	Ø	Ø	Ø	104	0.03	-	Ø	Ø	Ø	/	-	-	=	
O6	Scraps from fries storage	EN3	No	+MA	+MB	+HA*	+MB*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6838	2.27	+	+HA	+MB	+MA	7473	2.72	+	+HA	+MB	+MA	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=	
O7	Scraps from meat cutting table	EN3	No	+MA	+MA	+MA*	+MA*	<i>L.monocytogenes</i>	+	6596	2.19	+	+HA	+HA	+HA	6261	2.28	+	+HA	+MA	+HA	<i>L.monocytogenes</i>	+	+	=	
O8	Scraps production line	EN3	No	+MA	+MA	+MA	+MB	<i>L.monocytogenes</i>	+	6544	2.17	+	+MA	+HA	+HA	6396	2.32	+	+HA	+MA	+HA	<i>L.monocytogenes</i>	+	+	=	
O9	Scraps from meat cutting room	EN3	No	+MA	+MA	+MA	+MA	<i>L.monocytogenes</i>	+	6565	2.18	+	+HA	+MA	+HA	6764	2.46	+	+HB	+MB	+HA	<i>L.monocytogenes</i>	+	+	=	
O10	Scraps from cutting room table	EN3	Yes	+MA	+MB*	+MB	+MB*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	6644	2.21	+	+MB	+MB*	+MA*	7073	2.57	+	+HB	+MB*	+HA*	<i>L.monocytogenes</i> <i>L.innocua</i>	+	+	=	
O14	Scraps from sink	EN3	Yes	+MA	+MB	+MA	+LB	<i>L.monocytogenes</i>	+	10029	3.33	+	+LA	-ME	+LA	11064	4.02	+	+LA	-ME	+LA	<i>L.monocytogenes</i>	+	+	=	
O15	Scraps from dirty tank	EN3	Yes	+MA	+MB	+MA	+LB	<i>L.monocytogenes</i>	+	6105	2.03	+	+MA	-ME	+MA	6948	2.53	+	+HA	+MB	+HA	<i>L.monocytogenes</i>	+	+	=	
P10	Scraps from delicatessen retail outlet	EN3	No	-LE	-LE	-ME	-ME	/	-	63	0.02	-	-ME	-ME	-ME	65	0.02	-	-ME	-LE	/	/	-	-	=	
P11	Scraps from delicatessen retail outlet	EN3	No	Ø	+LB	Ø	Ø	<i>L.monocytogenes</i>	+	6279	2.08	+	Ø	+MA	+LA	6107	2.03	+	+LA	+MA	/	<i>L.monocytogenes</i>	+	+	=	
P12	Scraps from fish weighing workstation	EN3	No	Ø	+LB	+MA	+MA*	<i>L.monocytogenes</i>	+	5884	1.95	+	+HA	+HA	+HA	6131	2.00	+	+LA	+HB	/	<i>L.monocytogenes</i>	+	+	=	
P14	Scraps from cheese retail outlet	EN3	No	Ø	-LE	Ø	-LE	/	-	100	0.03	-	Ø	Ø	Ø	165	0.05	-	Ø	Ø	/	/	-	-	=	

CODE	MATRICES	Cat.	Spiked	NF EN ISO 11290-1 (#) METHOD						VIDAS LSX METHOD							COMPARISON	
				FRASER 1/2		FRASER		CONFIRMATION		VIDAS LSX			CONFIRMATION 24H ENRICHIMENT			IDENTIF.		FINAL RESULT
				P1	OA1	P2	OA2	IDENTIF.	RESULTAT	RFV LSX 24H	TV	TEST RESULT	PAL	OAA	RLM			
O28	Surface windows	EN2	Yes	+MA	+LB	+HB	+MB	<i>L.innocua</i>	+	6834	2.26	+	+MA	+LB	+MB	<i>L.innocua</i>	+	=
O29	Delicatessen tank	EN2	Yes	+MA	+MA	+MA	+MA	<i>L.innocua</i>	+	10930	3.62	+	+MA	+MA	+MA	<i>L.innocua</i>	+	=
O30	Siphon	EN2	No	Ø	Ø	Ø	Ø	/	-	102	0.03	-	/	/	/	/	-	=
O31	Siphon	EN2	No	Ø	-LE	-ME	-LE	/	-	126	0.04	-	/	/	/	/	-	=
O32	Swab floor - wall	EN2	No	-LE	-LE	-LE	-LE	/	-	72	0.02	-	/	/	/	/	-	=
O33	Cutting table	EN2	No	-ME	+MB?/-LE	-ME	-ME	<i>Bacillus</i>	-	79	0.02	-	/	/	/	/	-	=
O34	Stainless steel table in delicatessen retail outlet	EN2	No	-LE	-LE	Ø	Ø	/	-	103	0.03	-	/	/	/	/	-	=
O35	Cooking table	EN2	No	Ø	Ø	Ø	Ø	/	-	32	0.01	-	/	/	/	/	-	=
O36	Swab opens limps	EN2	No	Ø	Ø	Ø	Ø	/	-	32	0.01	-	/	/	/	/	-	=
O37	Siphon sink Vegetables production line	EN2	No	Ø	Ø	Ø	Ø	/	-	30	0.00	-	/	/	/	/	-	=
O38	Dirty plate	EN2	No	Ø	Ø	Ø	Ø	/	-	41	0.01	-	/	/	/	/	-	=
P22	Preparation table	EN2	No	-ME	-LE	Ø	Ø	/	-	118	0.03	-	/	/	/	/	-	=
P23	Cutting table for fish	EN2	No	-ME	-LE	Ø	Ø	/	-	66	0.02	-	/	/	/	/	-	=
P24	Gutter in gradind production line	EN2	No	-LE	-LE	Ø	Ø	/	-	207	0.06	-	/	/	/	/	-	=
P25	Slicer	EN2	No	-LE	-LE	Ø	-ME	/	-	96	0.03	-	/	/	/	/	-	=
P26	Cutting table	EN2	No	+MA	+MA	+HA	+MA	<i>L.monocytogenes</i>	+	9192	3.04	+	+MB	+MA	+MB	<i>L.monocytogenes</i>	+	=
R13	Floor in packaging room	EN2	No	-ME	Ø	-ME	Ø	/	-	117	0.03	-	/	/	/	/	-	=
R14	Packaging machine in butchery retail outlet	EN2	No	Ø	Ø	Ø	Ø	/	-	56	0.01	-	/	/	/	/	-	=
R15	Meat grinder in butchery retail outlet	EN2	No	+MA	+MA	+MB	+MB	<i>L.monocytogenes</i>	+	49	0.01	-	Ø	-LE	Ø	/	-	FN
R16	Workstation	EN2	No	-LE	+MB?/-ME	-LE	-LE	<i>Bacillus</i>	-	139	0.04	-	/	/	/	/	-	=
R17	Surface Sandwiches preparation	EN2	No	Ø	Ø	-LE	-LE	/	-	75	0.02	-	/	/	/	/	-	=
R18	Cold room shelves	EN2	Yes	+MA	+MA	+MA	+MA	<i>L.innocua</i>	+	11493	3.80	+	+HB	+MA	+MB	<i>L.innocua</i>	+	=
R19	Cold room floor	EN2	Yes	+MB	+MB	+MB	+MB	<i>L.innocua</i>	+	11272	3.73	+	+MB	+LB	+MB	<i>L.innocua</i>	+	=
R20	Dustbin lid	EN2	Yes	+MA	+MA	+MB	+MA	<i>L.innocua</i>	+	11517	3.81	+	+MC	+LB	+MA	<i>L.innocua</i>	+	=
S7	Whisk before cleaning	EN2	No	+MA	+MA	+MA	+HA	<i>L.innocua</i>	+	7577	2.54	+	+HA	+MA	+HA	<i>L.innocua</i>	+	=
S8	Filleting fish	EN2	No	Ø	Ø/-LE	Ø	Ø	/	-	134	0.04	-	/	/	/	/	-	=
S9	Waste tank	EN2	No	Ø	-ME	Ø	-LE	/	-	125	0.04	-	/	/	/	/	-	=
S10	Meat grinder in butchery retail outlet	EN2	No	Ø	Ø	Ø	-LE	/	-	56	0.01	-	/	/	/	/	-	=
S11	Plat	EN2	No	-ME	Ø	-ME	-LE	/	-	103	0.03	-	/	/	/	/	-	=
S12	Floor under production line	EN2	Yes	+LB	+LB	+MB	+MB	<i>L.monocytogenes</i>	+	8748	2.93	+	+MD	+MC	+MB	<i>L.monocytogenes</i>	+	=
S13	Cart surface	EN2	Yes	+MB	+LB	+MA	+MB	<i>L.monocytogenes</i>	+	7083	2.37	+	+MC	+MB	+MB	<i>L.monocytogenes</i>	+	=
S14	Siphon sink workshop	EN2	Yes	+MA	+LB	+MB	+MB	<i>L.monocytogenes</i>	+	10571	3.54	+	+MB	+MB	+MB	<i>L.monocytogenes</i>	+	=
S15	Waste cart	EN2	Yes	+MC	+MB	+MB	+MB	<i>L.monocytogenes</i>	+	3240	1.08	+	+MD	+MD	+MC	<i>L.monocytogenes</i>	+	=
T5	Weighing tray catering stand	EN2	No	-LE	Ø/-LE	-ME	-ME	/	-	51	0.01	-	-LE	-LE	-LE	/	-	=
T6	Cutting plate	EN2	No	+MA	+LA	+MB	+HB	<i>L.innocua</i>	+	68	0.02	-	-LE	-LE	-LE	/	-	FN
T7	Production line	EN2	No	+MA	+MA	+MA	+MA	<i>L.innocua</i>	+	7932	2.65	+	+MA	+MA	+MA	<i>L.innocua</i>	+	=
T8	Cold room floor	EN2	No	+LB	+MA	+MA	+MB	<i>L.innocua</i>	+	8174	2.74	+	+MA	+MA	+MA	<i>L.innocua</i>	+	=
U2	Workplan in retail outlet	EN2	No	+MA	+LA	+MB	+MA	<i>L.innocua</i>	+	10137	3.10	+	+MA	+LA		<i>L.innocua</i>	+	=
U3	Cutting plate	EN2	No	Ø	+LA(3)	+HA	+MA	<i>L.monocytogenes</i>	+	8744	2.67	+	+MA	+MA		<i>L.monocytogenes</i>	+	=
U4	Dirty knife	EN2	No	+HA	+MA	+HB	+MB	<i>L.innocua</i>	+	7946	2.43	+	+HA	+MA		<i>L.innocua</i>	+	=
U5	Floor before washing	EN2	No	+MA	+MA	+MA	+MA	<i>L.monocytogenes</i>	+	11675	3.57	+	+MA	+MA		<i>L.monocytogenes</i>	+	=

APPENDIX C

INCLUSIVITY / EXCLUSIVITY

INCLUSIVITY

Strains of *Listeria*

Strain	Origin	RFV	TV	Final result
<i>Listeria monocytogenes</i>	Beef minced meat	7606	2.59	Positive
<i>Listeria welshimeri</i>	Beef minced meat	7560	2.58	Positive
<i>Listeria innocua</i>	Beef minced meat	7710	2.63	Positive
<i>Listeria innocua</i>	Beef minced meat	7539	2.57	Positive
<i>Listeria monocytogenes</i>	Beef minced meat	7560	2.58	Positive
<i>Listeria welshimeri</i>	Beef minced meat	7637	2.60	Positive
<i>Listeria welshimeri</i>	Beef minced meat	7823	2.66	Positive
<i>Listeria innocua</i>	Beef minced meat	7917	2.70	Positive
<i>Listeria welshimeri</i>	Beef minced meat	7821	2.66	Positive
<i>Listeria welshimeri</i>	Beef minced meat	7904	2.69	Positive
<i>Listeria innocua</i>	Beef minced meat	7981	2.72	Positive
<i>Listeria innocua</i>	Meat product	7842	2.67	Positive
<i>Listeria monocytogenes</i>	Meat product	6819	2.32	Positive
<i>Listeria welshimeri</i>	Meat product	6912	2.35	Positive
<i>Listeria monocytogenes</i>	Meat product	6777	2.31	Positive
<i>Listeria innocua</i>	Meat product	6932	2.36	Positive
<i>Listeria welshimeri</i>	Meat product	6808	2.32	Positive
<i>Listeria monocytogenes</i>	Meat product	6709	2.28	Positive
<i>Listeria innocua</i>	Meat product	6742	2.30	Positive
<i>Listeria monocytogenes</i>	Meat product	6875	2.34	Positive
<i>Listeria welshimeri</i>	Meat product	6947	2.37	Positive
<i>Listeria innocua</i>	Meat product	6960	2.37	Positive
<i>Listeria welshimeri</i>	Meat product	6833	2.33	Positive
<i>Listeria monocytogenes</i>	Meat product	7046	2.40	Positive
<i>Listeria innocua</i>	Beef minced meat	6841	2.33	Positive
<i>Listeria monocytogenes</i>	Beef minced meat	6923	2.36	Positive
<i>Listeria seeligeri</i>	Cheese "Reblochon"	6701	2.28	Positive
<i>Listeria seeligeri</i>	Surface sample	6866	2.34	Positive
<i>Listeria seeligeri</i>	Fennel	6860	2.34	Positive
<i>Listeria seeligeri</i>	Fennel	6578	2.24	Positive
<i>Listeria innocua</i>	Beef minced meat	7392	2.52	Positive
<i>Listeria monocytogenes</i>	Beef minced meat	7669	2.61	Positive
<i>Listeria monocytogenes</i>	Beef minced meat	7625	2.60	Positive
<i>Listeria welshimeri</i>	Beef minced meat	7745	2.64	Positive
<i>Listeria monocytogenes</i>	Meat product	7737	2.64	Positive
<i>Listeria innocua</i>	Meat product	7596	2.59	Positive
<i>Listeria monocytogenes</i>	Beef minced meat	7747	2.64	Positive
<i>Listeria innocua</i>	Beef minced meat	7700	2.62	Positive
<i>Listeria monocytogenes</i>	Beef minced meat	7668	2.61	Positive
<i>Listeria innocua</i>	Beef minced meat	8011	2.73	Positive
<i>Listeria monocytogenes</i>	Beef minced meat	8008	2.73	Positive
<i>Listeria monocytogenes</i>	Meat product	8032	2.74	Positive
<i>Listeria seeligeri</i>	Collection	6857	2.34	Positive
<i>Listeria ivanovii</i>	Collection	6894	2.35	Positive
<i>Listeria grayi</i>	Collection CIP/KHI103213	7735	2.63	Positive
<i>Listeria monocytogenes</i>	Collection	6760	2.30	Positive
<i>Listeria innocua</i>	Beef minced meat	6746	2.30	Positive
<i>Listeria ivanovii</i>	Goat's milk	6743	2.30	Positive
<i>Listeria ivanovii</i>	Goat's milk	6647	2.26	Positive
<i>Listeria monocytogenes</i>	Rillettes	6928	2.36	Positive

EXCLUSIVITY

Non *Listeria* strains

Initial study:

Strain	Origin	RFV	TV	Final result
<i>Salmonella typhimurium</i>	Pâté	20	0.00	Negative
<i>Bacillus cereus</i>	Taboulé	20	0.00	Negative
<i>Bacillus mycoides</i>	Germinated seeds	21	0.00	Negative
<i>Bacillus cereus</i>	Collection	61	0.02	Negative
<i>Enterococcus faecium</i>	Collection	21	0.00	Negative
<i>Escherichia coli</i>	Collection	30	0.01	Negative
<i>Rhodococcus equi</i>	Collection	27	0.00	Negative
<i>Salmonella indiana</i>	Duck breast	22	0.00	Negative
<i>Escherichia coli</i> O157 H7	Collection	21	0.00	Negative
<i>Salmonella anatum</i>	Collection	32	0.01	Negative
<i>Leuconostoc lactis</i>	Collection	20	0.00	Negative
<i>Brochothrix campestris</i>	Collection	20	0.00	Negative
<i>Lactobacillus plantarum</i>	Collection	22	0.00	Negative
<i>Enterococcus faecium</i>	Milk	20	0.00	Negative
<i>Enterococcus faecium</i>	Milk	21	0.00	Negative
<i>Enterococcus faecium</i>	Milk	19	0.00	Negative
<i>Staphylococcus intermedius</i>	Milk	21	0.00	Negative
<i>Staphylococcus haemolyticus</i>	Milk	31	0.01	Negative
<i>Staphylococcus aureus</i>	Egg products	199	0.06	Negative
<i>Escherichia coli</i>	Milk	20	0.00	Negative
<i>Staphylococcus intermedius</i>	Goat's milk	20	0.00	Negative
<i>Staphylococcus haemolyticus</i>	Milk	22	0.00	Negative
<i>Staphylococcus aureus</i>	Goat's milk	280	0.09	Negative
<i>Rhodococcus equi</i>	Milk	21	0.00	Negative
<i>Candida sp</i>	Milk	23	0.00	Negative
<i>Lactobacillus sp</i>	Milk	21	0.00	Negative
<i>Enterobacter sp</i>	Milk	42	0.01	Negative
<i>Enterobacter cloacae</i>	Egg products	45	0.01	Negative
<i>Enterobacter cloacae</i>	Egg products	48	0.01	Negative
<i>Pantoea sp</i>	Milk	23	0.00	Negative
<i>Staphylococcus aureus</i>	Goat's milk	92	0.03	Negative
<i>Staphylococcus aureus</i>	Goat's milk	86	0.03	Negative

Extension study:

Strain reference <i>Pseudomonas putida</i>		Incubation 24h at 30°C		Incubation 48h at 30°C	
		TV	RES	TV	RES
PS91	After culture in LX broth	0,11	+	2,66	+
	After culture in nutrient broth	0,02	-	0,02	-
	After culture in LX broth	0,02	-	0,02	-
PS90	After culture in nutrient broth	0,02	-	0,02	-
	After culture in LX broth	0,02	-	0,02	-
PS34	After culture in nutrient broth	0,02	-	0,02	-
	After culture in LX broth	0,01	-	0,02	-
PS96	After culture in nutrient broth	0,02	-	0,03	-
	After culture in LX broth	0,02	-	0,02	-
PS88	After culture in nutrient broth	0,01	-	0,02	-
	After culture in LX broth	0,02	-	0,01	-
PS89	After culture in nutrient broth	0,02	-	0,02	-
	After culture in LX broth	0,02	-	0,01	-
PS85	After culture in nutrient broth	0,02	-	0,03	-
	After culture in LX broth	0,02	-	0,02	-
PS87	After culture in nutrient broth	0,09	-	0,22	+
	After culture in LX broth	0,02	-	0,03	-
	After culture in nutrient broth, and then in LX broth			0,02	-

APPENDIX D

INTERLABORATORY STUDY

-

DETAILED RESULTS OF
PARTICIPANT LABORATORIES

Laboratory A

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	8146	2.50	+	+	+	=
2	-	-	-	-	-	=	25	0.00	-	-	-	=
3	+	+	+	+	+	=	8126	2.50	+	+	+	=
4	-	-	-	-	-	=	26	0.00	-	-	-	=
5	+	+	+	+	+	=	8180	2.51	+	+	+	=
6	-	-	-	-	-	=	39	0.01	-	-	-	=
7	+	+	+	+	+	=	7826	2.40	+	+	+	=
8	-	-	-	-	-	=	31	0.00	-	-	-	=
9	+	+	+	+	+	=	7678	2.36	+	+	+	=
10	-	-	-	-	-	=	29	0.00	-	-	-	=
11	+	+	+	+	+	=	7895	2.42	+	+	+	=
12	-	-	-	-	-	=	25	0.00	-	-	-	=
13	+	+	+	+	+	=	7731	2.37	+	+	+	=
14	-	-	-	-	-	=	31	0.00	-	-	-	=
15	+	+	+	+	+	=	7613	2.34	+	+	+	=
16	-	-	-	-	-	=	27	0.00	-	-	-	=
17	+	+	+	+	+	=	7973	2.45	+	+	+	=
18	+	+	+	+	+	=	8043	2.47	+	+	+	=
19	+	+	+	+	+	=	7928	2.44	+	+	+	=
20	+	+	+	+	+	=	8206	2.52	+	+	+	=
21	+	+	+	+	+	=	8251	2.53	+	+	+	=
22	+	+	+	+	+	=	8342	2.56	+	+	+	=
23	+	+	+	+	+	=	7926	2.43	+	+	+	=
24	+	+	+	+	+	=	7918	2.43	+	+	+	=
Total flora of milk (UFC/ml):					20							

Laboratory B

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	7336	2.22	+	+	+	=
2	-	-	-	-	-	=	27	0.00	-	-	-	=
3	+	+	+	+	+	=	6426	1.95	+	+	+	=
4	-	-	-	-	-	=	42	0.01	-	-	-	=
5	+	+	+	+	+	=	6431	1.95	+	+	+	=
6	-	-	-	-	-	=	41	0.01	-	-	-	=
7	+	+	+	+	+	=	6555	1.99	+	+	+	=
8	-	-	-	-	-	=	32	0.00	-	-	-	=
9	+	+	+	+	+	=	6951	2.11	+	+	+	=
10	-	-	-	-	-	=	78	0.02	-	-	-	=
11	+	+	+	+	+	=	6896	2.09	+	+	+	=
12	-	-	-	-	-	=	59	0.01	-	-	-	=
13	+	+	+	+	+	=	6845	2.08	+	+	+	=
14	-	-	-	-	-	=	81	0.02	-	-	-	=
15	+	+	+	+	+	=	7115	2.16	+	+	+	=
16	-	-	-	-	-	=	89	0.00	-	-	-	=
17	+	+	+	+	+	=	7001	2.12	+	+	+	=
18	+	+	+	+	+	=	7107	2.16	+	+	+	=
19	+	+	+	+	+	=	7069	2.14	+	+	+	=
20	+	+	+	+	+	=	28	0.00	-	-	-	#
21	+	+	+	+	+	=	6680	2.03	+	+	+	=
22	+	+	+	+	+	=	6665	2.02	+	+	+	=
23	+	+	+	+	+	=	6632	2.01	+	+	+	=
24	+	+	+	+	+	=	6647	2.02	+	+	+	=
Total flora of milk (UFC/ml):					30							

Laboratory C

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	7116	2.71	+	+	+	=
2	-	-	-	-	-	=	26	0.00	-	-	-	=
3	+	+	+	+	+	=	7382	2.81	+	+	+	=
4	-	-	-	-	-	=	27	0.01	-	-	-	=
5	+	+	+	+	+	=	7296	2.77	+	+	+	=
6	-	-	-	-	-	=	29	0.01	-	-	-	=
7	+	+	+	+	+	=	7438	2.83	+	+	+	=
8	-	-	-	-	-	=	31	0.01	-	-	-	=
9	+	+	+	+	+	=	7666	2.92	+	+	+	=
10	-	-	-	-	-	=	30	0.01	-	-	-	=
11	+	+	+	+	+	=	7730	2.94	+	+	+	=
12	-	-	-	-	-	=	32	0.01	-	-	-	=
13	+	+	+	+	+	=	6908	2.63	+	+	+	=
14	-	-	-	-	-	=	31	0.01	-	-	-	=
15	+	+	+	+	+	=	7427	2.82	+	+	+	=
16	-	-	-	-	-	=	27	0.01	-	-	-	=
17	+	+	+	+	+	=	7531	2.86	+	+	+	=
18	+	+	+	+	+	=	7261	2.76	+	+	+	=
19	+	+	+	+	+	=	8742	3.33	+	+	+	=
20	+	+	+	+	+	=	8909	3.39	+	+	+	=
21	+	+	+	+	+	=	8569	3.26	+	+	+	=
22	+	+	+	+	+	=	8222	3.13	+	+	+	=
23	+	+	+	+	+	=	8051	3.06	+	+	+	=
24	+	+	+	+	+	=	7599	2.89	+	+	+	=
Total flora of milk (UFC/ml):					20							

Laboratory D

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	Résult	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	6477	2.06	+	+	+	=
2	-	-	-	-	-	=	33	0.01	-	-	-	=
3	+	+	+	+	+	=	6894	2.19	+	+	+	=
4	-	-	-	-	-	=	25	0.00	-	-	-	=
5	+	+	+	+	+	=	6809	2.16	+	+	+	=
6	-	-	-	-	-	=	82	0.02	-	-	-	=
7	+	+	+	+	+	=	6650	2.11	+	+	+	=
8	-	-	-	-	-	=	37	0.01	-	-	-	=
9	+	+	+	+	+	=	6689	2.12	+	+	+	=
10	-	-	-	-	-	=	31	0.00	-	-	-	=
11	+	+	+	+	+	=	6595	2.09	+	+	+	=
12	-	-	-	-	-	=	26	0.00	-	-	-	=
13	+	+	+	+	+	=	6386	2.03	+	+	+	=
14	-	-	-	-	-	=	30	0.00	-	-	-	=
15	+	+	+	+	+	=	6683	2.12	+	+	+	=
16	-	-	-	-	-	=	22	0.00	-	-	-	=
17	+	+	+	+	+	=	6496	2.06	+	+	+	=
18	+	+	+	+	+	=	6386	2.03	+	+	+	=
19	+	+	+	+	+	=	6356	2.02	+	+	+	=
20	+	+	+	+	+	=	6108	1.94	+	+	+	=
21	+	+	+	+	+	=	6819	2.17	+	+	+	=
22	+	+	+	+	+	=	6600	2.10	+	+	+	=
23	+	+	+	+	+	=	6616	2.10	+	+	+	=
24	+	+	+	+	+	=	6606	2.10	+	+	+	=
Total flora of milk (UFC/ml):					20							

Laboratory E

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	Résult	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	6699	2.06	+	+	+	=
2	-	-	-	-	-	=	29	0.00	-	-	-	=
3	+	+	+	+	+	=	6244	1.92	+	+	+	=
4	-	-	-	-	-	=	34	0.01	-	-	-	=
5	+	+	+	+	+	=	5973	1.84	+	+	+	=
6	-	-	-	-	-	=	27	0.00	-	-	-	=
7	+	+	+	+	+	=	6210	1.91	+	+	+	=
8	-	-	-	-	-	=	29	0.00	-	-	-	=
9	+	+	+	+	+	=	6436	1.98	+	+	+	=
10	-	-	-	-	-	=	26	0.00	-	-	-	=
11	+	+	+	+	+	=	6387	1.97	+	+	+	=
12	-	-	-	-	-	=	24	0.00	-	-	-	=
13	+	+	+	+	+	=	6337	1.95	+	+	+	=
14	+	+	-	-	+	#	6412	2.32	+	+	+	#
15	+	+	+	+	+	=	7312	2.25	+	+	+	=
16	-	-	-	-	-	=	34	0.01	-	-	-	=
17	+	+	+	+	+	=	7304	2.25	+	+	+	=
18	+	+	+	+	+	=	7278	2.24	+	+	+	=
19	+	+	+	+	+	=	7282	2.24	+	+	+	=
20	+	+	+	+	+	=	7076	2.18	+	+	+	=
21	+	+	+	+	+	=	6161	1.90	+	+	+	=
22	+	+	+	+	+	=	6077	1.87	+	+	+	=
23	+	+	+	+	+	=	6087	1.87	+	+	+	=
24	+	+	+	+	+	=	6100	1.88	+	+	+	=
Total flora of milk (UFC/ml):					10							

Laboratory F

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	Résult	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	7031	2.32	+	+	+	=
2	-	-	-	-	-	=	34	0.01	-	-	-	=
3	+	+	+	+	+	=	7437	2.45	+	+	+	=
4	-	-	-	-	-	=	28	0.00	-	-	-	=
5	+	+	+	+	+	=	7266	2.40	+	+	+	=
6	-	-	-	-	-	=	34	0.01	-	-	-	=
7	+	+	+	+	+	=	6084	2.01	+	+	+	=
8	-	-	-	-	-	=	29	0.00	-	-	-	=
9	+	+	+	+	+	=	6318	2.08	+	+	+	=
10	-	-	-	-	-	=	46	0.01	-	-	-	=
11	+	+	+	+	+	=	6409	2.11	+	+	+	=
12	-	-	-	-	-	=	36	0.01	-	-	-	=
13	+	+	+	+	+	=	6467	2.13	+	+	+	=
14	-	-	-	-	-	=	41	0.01	-	-	-	=
15	+	+	+	+	+	=	6777	2.24	+	+	+	=
16	-	-	-	-	-	=	29	0.00	-	-	-	=
17	+	+	+	+	+	=	6998	2.31	+	+	+	=
18	+	+	+	+	+	=	6848	2.26	+	+	+	=
19	+	+	+	+	+	=	6207	2.05	+	+	+	=
20	+	+	+	+	+	=	6367	2.10	+	+	+	=
21	+	+	+	+	+	=	6709	2.21	+	+	+	=
22	+	+	+	+	+	=	6482	2.14	+	+	+	=
23	+	+	+	+	+	=	6410	2.11	+	+	+	=
24	+	+	+	+	+	=	6236	2.06	+	+	+	=
Total flora of milk (UFC/ml):					<1							

Laboratory G J+2

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	6027	1.98	+	+	+	=
2	-	-	-	-	-	=	22	0,00	-	-	-	=
3	+	+	+	+	+	=	5979	1.97	+	+	+	=
4	-	-	-	-	-	=	49	0.01	-	-	-	=
5	+	+	+	+	+	=	5968	1.96	+	+	+	=
6	-	-	-	-	-	=	29	0,00	-	-	-	=
7	+	+	+	+	+	=	6058	1.99	+	+	+	=
8	-	-	-	-	-	=	21	0,00	-	-	-	=
9	+	+	+	+	+	=	6121	2.01	+	+	+	=
10	-	-	-	-	-	=	21	0,00	-	-	-	=
11	+	+	+	+	+	=	5891	1.94	+	+	+	=
12	-	-	-	-	-	=	23	0,00	-	-	-	=
13	+	+	+	+	+	=	6487	2.16	+	+	+	=
14	-	-	-	-	-	=	39	0.01	-	-	-	=
15	+	+	+	+	+	=	6515	2.17	+	+	+	=
16	-	-	-	-	-	=	28	0,00	-	-	-	=
17	+	+	+	+	+	=	6548	2.18	+	+	+	=
18	+	+	+	+	+	=	6497	2.17	+	+	+	=
19	+	+	+	+	+	=	43	0.01	-	-	-	=
20	+	+	+	+	+	=	6130	2.04	+	+	+	=
21	+	+	+	+	+	=	6003	2,00	+	+	+	=
22	+	+	+	+	+	=	5976	1.99	+	+	+	=
23	+	+	+	+	+	=	5997	2,00	+	+	+	=
24	+	+	+	+	+	=	6013	2,00	+	+	+	=
Total flora of milk (UFC/ml):					300							

Laboratory H

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	6053	1.77	+	+	+	=
2	-	-	-	-	-	=	31	0,00	-	-	-	=
3	+	+	+	+	+	=	6235	1.82	+	+	+	=
4	-	-	-	-	-	=	48	0.01	-	-	-	=
5	-	-	-	-	-	#	39	0.01	-	-	-	#
6	-	-	-	-	-	=	27	0,00	-	-	-	=
7	+	+	+	+	+	=	5820	1.7	+	+	+	=
8	-	-	-	-	-	=	30	0,00	-	-	-	=
9	+	+	+	+	+	=	5941	1.73	+	+	+	=
10	-	-	-	-	-	=	34	0,00	-	-	-	=
11	+	+	+	+	+	=	6082	1.77	+	+	+	=
12	-	-	-	-	-	=	37	0.01	-	-	-	=
13	+	+	+	+	+	=	6013	1.75	+	+	+	=
14	-	-	-	-	-	=	35	0.01	-	-	-	=
15	+	+	+	+	+	=	6114	1.78	+	+	+	=
16	-	-	-	-	-	=	298	0,08	-	-	-	=
17	+	+	+	+	+	=	6095	1.78	+	+	+	=
18	+	+	+	+	+	=	6227	1.82	+	+	+	=
19	+	+	+	+	+	=	5903	1.72	+	+	+	=
20	+	+	+	+	+	=	6009	1.75	+	+	+	=
21	+	+	+	+	+	=	6026	1.76	+	+	+	=
22	+	+	+	+	+	=	6076	1.77	+	+	+	=
23	+	+	+	+	+	=	6142	1.79	+	+	+	=
24	+	+	+	+	+	=	6233	1.82	+	+	+	=
Total flora of milk (UFC/ml):					<1							

Laboratory I

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	6023	1.94	+	+	+	=
2	-	-	-	-	-	=	92	0.02	-	-	-	=
3	+	+	+	+	+	=	6167	1.99	+	+	+	=
4	-	-	-	-	-	=	35	0.01	-	-	-	=
5	+	+	+	+	+	=	6225	2.01	+	+	+	=
6	-	-	-	-	-	=	37	0.01	-	-	-	=
7	+	+	+	+	+	=	5767	1.86	+	+	+	=
8	-	-	-	-	-	=	35	0.01	-	-	-	=
9	+	+	+	+	+	=	5688	1.83	+	+	+	=
10	-	-	-	-	-	=	50	0.01	-	-	-	=
11	+	+	+	+	+	=	5746	1.85	+	+	+	=
12	-	-	-	-	-	=	40	0.01	-	-	-	=
13	+	+	+	+	+	=	6117	2.05	+	+	+	=
14	-	-	-	-	-	=	24	0,00	-	-	-	=
15	+	+	+	+	+	=	6196	2.08	+	+	+	=
16	-	-	-	-	-	=	46	0.01	-	-	-	=
17	+	+	+	+	+	=	6194	2.08	+	+	+	=
18	+	+	+	+	+	=	6229	2.09	+	+	+	=
19	+	+	+	+	+	=	6565	2.2	+	+	+	=
20	+	+	+	+	+	=	6511	2.18	+	+	+	=
21	+	+	+	+	+	=	6454	2.16	+	+	+	=
22	+	+	+	+	+	=	6373	2.14	+	+	+	=
23	+	+	+	+	+	=	6506	2.18	+	+	+	=
24	+	+	+	+	+	=	6516	2.18	+	+	+	=
Total flora of milk (UFC/ml):					14							

Laboratory J

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	Résult	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	8547	3.09	+	+	+	=
2	-	-	-	-	-	=	35	0.01	-	-	-	=
3	+	+	+	+	+	=	8892	3.22	+	+	+	=
4	-	-	-	-	-	=	31	0.01	-	-	-	=
5	+	+	+	+	+	=	8393	3.04	+	+	+	=
6	-	-	-	-	-	=	33	0.01	-	-	-	=
7	+	+	+	+	+	=	8944	3.24	+	+	+	=
8	-	-	-	-	-	=	31	0.01	-	-	-	=
9	+	+	+	+	+	=	9227	3.34	+	+	+	=
10	-	-	-	-	-	=	54	0.01	-	-	-	=
11	+	+	+	+	+	=	8803	3.19	+	+	+	=
12	-	-	-	-	-	=	37	0.01	-	-	-	=
13	+	+	+	+	+	=	7659	2.77	+	+	+	=
14	-	-	-	-	-	=	70	0.02	-	-	-	=
15	+	+	+	+	+	=	8092	2.93	+	+	+	=
16	-	-	-	-	-	=	45	0.01	-	-	-	=
17	+	+	+	+	+	=	8053	2.91	+	+	+	=
18	+	+	+	+	+	=	8039	2.91	+	+	+	=
19	+	+	+	+	+	=	7664	2.77	+	+	+	=
20	+	+	+	+	+	=	7864	2.85	+	+	+	=
21	+	+	+	+	+	=	8109	2.94	+	+	+	=
22	+	+	+	+	+	=	7968	2.88	+	+	+	=
23	+	+	+	+	+	=	7818	2.83	+	+	+	=
24	+	+	+	+	+	=	7937	2.87	+	+	+	=
Total flora of milk (UFC/ml):					10							

Laboratory K

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	Résult	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	6625	2.28	+	+	+	=
2	-	-	-	-	-	=	85	0.02	-	-	-	=
3	+	+	+	+	+	=	6758	2.32	+	+	+	=
4	-	-	-	-	-	=	49	0.01	-	-	-	=
5	+	+	+	+	+	=	6981	2.40	+	+	+	=
6	-	-	-	-	-	=	45	0.01	-	-	-	=
7	+	+	+	+	+	=	6843	2.35	+	+	+	=
8	-	-	-	-	-	=	43	0.01	-	-	-	=
9	+	+	+	+	+	=	6750	2.33	+	+	+	=
10	-	-	-	-	-	=	137	0.04	-	-	-	=
11	+	+	+	+	+	=	6876	2.36	+	+	+	=
12	-	-	-	-	-	=	39	0.01	-	-	-	=
13	+	+	+	+	+	=	6821	2.38	+	+	+	=
14	-	-	-	-	-	=	44	0.001	-	-	-	=
15	+	+	+	+	+	=	6887	2.37	+	+	+	=
16	-	-	-	-	-	=	65	0.02	-	-	-	=
17	+	+	+	+	+	=	6885	2.37	+	+	+	=
18	+	+	+	+	+	=	6449	2.28	+	+	+	=
19	+	+	+	+	+	=	7853	2.71	+	+	+	=
20	+	+	+	+	+	=	7701	2.65	+	+	+	=
21	+	+	+	+	+	=	7677	2.64	+	+	+	=
22	+	+	+	+	+	=	7350	2.53	+	+	+	=
23	+	+	+	+	+	=	7044	2.42	+	+	+	=
24	+	+	+	+	+	=	7033	2.42	+	+	+	=
Total flora of milk (UFC/ml):					40							

Laboratory L

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	Résult	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	7073	2.62	+	+	+	=
2	-	-	-	-	-	=	22	0.00	-	-	-	=
3	+	+	+	+	+	=	6937	2.57	+	+	+	=
4	-	-	-	-	-	=	22	0.00	-	-	-	=
5	+	+	+	+	+	=	6808	2.52	+	+	+	=
6	-	-	-	-	-	=	24	0.00	-	-	-	=
7	+	+	+	+	+	=	6980	2.59	+	+	+	=
8	-	-	-	-	-	=	28	0.01	-	-	-	=
9	+	+	+	+	+	=	6954	2.58	+	+	+	=
10	-	-	-	-	-	=	24	0.00	-	-	-	=
11	+	+	+	+	+	=	6887	2.55	+	+	+	=
12	-	-	-	-	-	=	21	0.00	-	-	-	=
13	+	+	+	+	+	=	6841	2.54	+	+	+	=
14	-	-	-	-	-	=	25	0.00	-	-	-	=
15	+	+	+	+	+	=	6587	2.44	+	+	+	=
16	-	-	-	-	-	=	20	0.00	-	-	-	=
17	+	+	+	+	+	=	6723	2.49	+	+	+	=
18	-	-	-	-	-	#	6419	2.38	+	+	+	=
19	+	+	+	+	+	=	6887	2.55	+	+	+	=
20	+	+	+	+	+	=	6699	2.48	+	+	+	=
21	+	+	+	+	+	=	6664	2.47	+	+	+	=
22	+	+	+	+	+	=	6923	2.57	+	+	+	=
23	+	+	+	+	+	=	6669	2.47	+	+	+	=
24	+	+	+	+	+	=	6593	2.44	+	+	+	=
Total flora of milk (UFC/ml):					10							

Laboratory M

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	5083	1.61	+	+	+	=
2	-	-	-	-	-	=	39	0.01	-	-	-	=
3	+	+	+	+	+	=	6927	2.20	+	+	+	=
4	-	-	-	-	-	=	33	0.01	-	-	-	=
5	+	+	+	+	+	=	6965	2.21	+	+	+	=
6	-	-	-	-	-	=	107	0.03	-	-	-	=
7	+	+	+	+	+	=	6832	2.17	+	+	+	=
8	-	-	-	-	-	=	116	0.03	-	-	-	=
9	+	+	+	+	+	=	7148	2.27	+	+	+	=
10	-	-	-	-	-	=	31	0.00	-	-	-	=
11	+	+	+	+	+	=	7684	2.44	+	+	+	=
12	-	-	-	-	-	=	42	0.01	-	-	-	=
13	+	+	+	+	+	=	7605	2.41	+	+	+	=
14	-	-	-	-	-	=	36	0.01	-	-	-	=
15	+	+	+	+	+	=	7468	2.37	+	+	+	=
16	-	-	-	-	-	=	37	0.01	-	-	-	=
17	+	+	+	+	+	=	7886	2.50	+	+	+	=
18	+	+	+	+	+	=	8289	2.63	+	+	+	=
19	+	+	+	+	+	=	8538	2.71	+	+	+	=
20	+	+	+	+	+	=	8998	2.86	+	+	+	=
21	+	+	+	+	+	=	6623	2.10	+	+	+	=
22	+	+	+	+	+	=	6590	2.09	+	+	+	=
23	+	+	+	+	+	=	6530	2.07	+	+	+	=
24	+	+	+	+	+	=	6587	2.09	+	+	+	=

Total flora of milk (UFC/ml): 200

Laboratory N

Code sample	Reference method ISO 11290-1					Comparison / expected results	Alternative method VIDAS LSX					Comparison / expected results
	Fraser 1/2		Fraser		Result		LSX test		Test result	Confirmation	R�sultat	
	OAA	PALCAM	OAA	PALCAM			RFV	TV				
1	+	+	+	+	+	=	6370	2.01	+	+	+	=
2	-	-	-	-	-	=	24	0.00	-	-	-	=
3	+	+	+	+	+	=	6462	2.04	+	+	+	=
4	-	-	-	-	-	=	109	0.03	-	-	-	=
5	+	+	+	+	+	=	6707	2.11	+	+	+	=
6	-	-	-	-	-	=	25	0.00	-	-	-	=
7	+	+	+	+	+	=	6469	2.04	+	+	+	=
8	-	-	-	-	-	=	27	0.00	-	-	-	=
9	+	+	+	+	+	=	6343	2.00	+	+	+	=
10	-	-	-	-	-	=	24	0.00	-	-	-	=
11	+	+	+	+	+	=	6351	2.00	+	+	+	=
12	-	-	-	-	-	=	74	0.02	-	-	-	=
13	+	+	+	+	+	=	6926	2.18	+	+	+	=
14	-	-	-	-	-	=	24	0.00	-	-	-	=
15	+	+	+	+	+	=	6904	2.17	+	+	+	=
16	-	-	-	-	-	=	36	0.01	-	-	-	=
17	+	+	+	+	+	=	7012	2.21	+	+	+	=
18	+	+	+	+	+	=	7186	2.26	+	+	+	=
19	+	+	+	+	+	=	6980	2.20	+	+	+	=
20	+	+	+	+	+	=	7258	2.29	+	+	+	=
21	+	+	+	+	+	=	7220	2.27	+	+	+	=
22	+	+	+	+	+	=	7478	2.36	+	+	+	=
23	+	+	+	+	+	=	7513	2.37	+	+	+	=
24	+	+	+	+	+	=	7626	2.40	+	+	+	=

Total flora of milk (UFC/ml): <1

APPENDIX E
INTERLABORATORY STUDY
-
ACCORDANCE

ALTERNATIVE METHOD

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Probability of negatives	Probability of negative pairs	Probability of positives	Probability of positive pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory C	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory N	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							0,98
Accordance:							98,3%

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negatives pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory C	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory N	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							0,97
Accordance:							96,6%

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negatives pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory C	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory N	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							1,00
Accordance:							100%

REFERENCE METHOD

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Probability of negatives	Probability of negative pairs	Probability of positives	Probability of positive pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory C	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory N	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							0,98
Accordance:							98,3%

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negatives pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory C	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	7	0,88	0,77	0,13	0,02	0,78
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory N	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							0,97
Accordance:							96,6%

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positive pairs	Probability of negatives	Probability of negatives pairs	Probability of identical result pairs
Laboratory A	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory B	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory C	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory D	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory E	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory F	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory H	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory I	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory J	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory K	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory L	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory M	8	8	1,00	1,00	0,00	0,00	1,00
Laboratory N	8	8	1,00	1,00	0,00	0,00	1,00
Mean:							1,00
Accordance:							100%

APPENDIX F

INTERLABORATORY STUDY - CONCORDANCE

ALTERNATIVE METHOD

Number of laboratories 13
 Number of positives per laboratory 8

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	760	768
Laboratory B	8	8	760	768
Laboratory C	8	8	760	768
Laboratory D	8	8	760	768
Laboratory E	8	7	672	768
Laboratory F	8	8	760	768
Laboratory H	8	8	760	768
Laboratory I	8	8	760	768
Laboratory J	8	8	760	768
Laboratory K	8	8	760	768
Laboratory L	8	8	760	768
Laboratory M	8	8	760	768
Laboratory N	8	8	760	768
Total			9792	9984
Concordance	98,08%			

Number of laboratories 13
 Number of positives per laboratory 8

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	752	768
Laboratory B	8	7	650	768
Laboratory C	8	8	752	768
Laboratory D	8	8	752	768
Laboratory E	8	8	752	768
Laboratory F	8	8	752	768
Laboratory H	8	7	650	768
Laboratory I	8	8	752	768
Laboratory J	8	8	752	768
Laboratory K	8	8	752	768
Laboratory L	8	8	752	768
Laboratory M	8	8	752	768
Laboratory N	8	8	752	768
Total			9572	9984
Concordance	95,87%			

Number of laboratories 13
 Number of positives per laboratory 8

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	768	768
Laboratory B	8	8	768	768
Laboratory C	8	8	768	768
Laboratory D	8	8	768	768
Laboratory E	8	8	768	768
Laboratory F	8	8	768	768
Laboratory H	8	8	768	768
Laboratory I	8	8	768	768
Laboratory J	8	8	768	768
Laboratory K	8	8	768	768
Laboratory L	8	8	768	768
Laboratory M	8	8	768	768
Laboratory N	8	8	768	768
Total			9984	9984
Concordance	100,00%			

REFERENCE METHOD

Number of laboratories 13
 Number of positives per laboratory 8

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	760	768
Laboratory B	8	8	760	768
Laboratory C	8	8	760	768
Laboratory D	8	8	760	768
Laboratory E	8	7	672	768
Laboratory F	8	8	760	768
Laboratory H	8	8	760	768
Laboratory I	8	8	760	768
Laboratory J	8	8	760	768
Laboratory K	8	8	760	768
Laboratory L	8	8	760	768
Laboratory M	8	8	760	768
Laboratory N	8	8	760	768
Total			9792	9984
Concordance	98,08%			

Number of laboratories 13
 Number of positives per laboratory 8

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	752	768
Laboratory B	8	8	752	768
Laboratory C	8	8	752	768
Laboratory D	8	8	752	768
Laboratory E	8	8	752	768
Laboratory F	8	8	752	768
Laboratory H	8	7	650	768
Laboratory I	8	8	752	768
Laboratory J	8	8	752	768
Laboratory K	8	8	752	768
Laboratory L	8	7	650	768
Laboratory M	8	8	752	768
Laboratory N	8	8	752	768
Total			9572	9984
Concordance	95,87%			

Number of laboratories 13
 Number of positives per laboratory 8

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
Laboratory A	8	8	768	768
Laboratory B	8	8	768	768
Laboratory C	8	8	768	768
Laboratory D	8	8	768	768
Laboratory E	8	8	768	768
Laboratory F	8	8	768	768
Laboratory H	8	8	768	768
Laboratory I	8	8	768	768
Laboratory J	8	8	768	768
Laboratory K	8	8	768	768
Laboratory L	8	8	768	768
Laboratory M	8	8	768	768
Laboratory N	8	8	768	768
Total			9984	9984
Concordance	100,00%			