

CODE BOOK

Книга кодов



for / для MIKROLATEST®

ENTEROtest 16

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Introduction

The codebook for ENTEROtest 16 is designed to identify bacteria using the MIKRO-LA-TEST ENTEROtest 16 test kit. The identification, ie interpretation of the result, can be done in three ways:

1. **manually** - by comparing the result with the data in the differentiation table
2. **using an identification program** (eg ErbaExpert)
3. **using this codebook**

All of the mentioned identification methods are based on the data of the identification matrix (frequency matrix, etc.), ie table containing taxa, tests and percentages of positive reactions of particular tests for each taxon. The taxon may be:

- genus - *Morganella* sp.
- species - *Morganella morganii*
- subspecies - *Morganella morganii* ssp. *morganii*

The codebook contains the identification results using the ENTEROtest 16 set ordered according to the value of the so-called profile code. Sorting results by the value of the profile code allows for easy and fast search. The identification quality evaluation for each profile code is based on the calculation of the probability of the result from the identification matrix data; the evaluation is detailed below.

Creating a profile code

For easier identification, it is advisable to convert the obtained results of each test (+/-) into a numerical profile (octal code). Tests are first divided into groups:

ONP	H2S	LYS	IND	ORN	URE	PHE	ESL	SCI	MAL	INO	ADO	CEL	SUC	SOR	TRE	MAN	
1			2			3			4			5			6		

The test groups are created in accordance with the sequence of tests in the strip. Three tests are included in all groups.

In each created group, there are assigned values 1, 2, and 4 to the particular tests according to the following scheme:

ONP	H2S	LYS	IND	ORN	URE	PHE	ESL	SCI	MAL	INO	ADO	CEL	SUC	SOR	TRE	MAN	
1	2	4	1	2	4	1	2	4	1	2	4	1	2	4	1	2	

When creating a profile code for a specific result, proceed as follows:

- positive tests are assigned 1, 2 or 4 values
- negative tests are always assigned a zero value
- the values assigned to the tests are added in each test group
- the resulting group of numbers represents the **profile code**

ONP	H2S	LYS	IND	ORN	URE	PHE	ESL	SCI	MAL	INO	ADO	CEL	SUC	SOR	TRE	MAN	
+	-	-	+	+	+	-	-	+	+	+	-	-	+	+	+	-	
1	0	0	1	2	4	0	0	4	1	2	0	0	2	4	1	0	
1			7			4			3			6			1		

In this example, a profile **174361** was created.

The results are organized in the codebook according to the value of the profile code in ascending order.

Using the codebook

The following information is provided for each profile code in the codebook:

- Profile code.
- Identification score and T-index values. They are listed for each taxon:

Identification score – the taxon with the highest value is ranked first; the identification score indicates the probability of occurrence of a given result for that taxon, related to the probability of occurrence of the result for all other taxa.

Identification score ≥ 99 ... the strain is excellently distinguished

Identification score ≥ 95 ... the strain is very good distinguished

Identification score ≥ 90 ... the strain is distinguished

Identification score < 90 ... the strain is not sufficiently distinguished

T-index – an indication of the extent to which the result corresponds to the most typical result for that taxon; an entirely typical result corresponds to a T-index value equal to 1. The value may lie in the range from 0 to 1 and is inversely proportional to the number of atypical tests.

T-index $\geq 0,75$... typical strain

T-index $\geq 0,50$... less typical strain

T-index $\geq 0,25$... atypical strain

T-index $< 0,25$... completely atypical strain

- **List of atypical characters (tests)** - the list of all atypical characters (listed below) is valid only for the first taxon; the percentage of positive reactions is given for every atypical test.
- **List of additional tests** – if taxa are insufficiently differentiated, additional tests allow for more accurate identification. Additional tests show percentages of positive reactions.

If the profile code in the diagnostic list is not listed, it is a very atypical result, or it is a taxon that is not included in the identification matrix.

List of taxa used to create a codebook

Citrobacter amalonaticus
Citrobacter braakii
Citrobacter farmeri
Citrobacter freundii
Citrobacter koseri
Citrobacter sedlakii
Citrobacter werkmanii
Citrobacter youngae
Cronobacter sakazakii
Edwardsiella tarda
Enterobacter aerogenes
Enterobacter cloacae subsp. *cloacae*
Escherichia coli
Escherichia fergusonii
Escherichia hermannii
Escherichia vulneris
Hafnia alvei
Klebsiella oxytoca
Klebsiella pneumoniae subsp. *ozaenae*
Klebsiella pneumoniae subsp. *pneumoniae*
Klebsiella pneumoniae subsp. *rhinoscleromatis*
Kluyvera ascorbata
Leclercia adecarboxylata
Morganella morganii subsp. *morganii*
Morganella morganii subsp. *sibonii*
Pantoea agglomerans
Proteus mirabilis
Proteus penneri
Proteus vulgaris
Providencia alcalifaciens
Providencia rettgeri
Providencia stuartii
Salmonella bongori
Salmonella enterica subsp. *arizonae*
Salmonella enterica subsp. *diarizonae*
Salmonella enterica subsp. *enterica*
Salmonella enterica subsp. *houtenae*
Salmonella enterica subsp. *salamae*
Salmonella serovar *enteritidis*
Salmonella serovar *paratyphi*
Salmonella serovar *typhi*
Serratia ficaria
Serratia marcescens
Serratia odorifera biovar 1
Serratia odorifera biovar 2
Serratia rubidaea
Shigella boydii (group C)
Shigella dysenteriae (group A)
Shigella flexneri (group B)
Shigella sonnei
Yersinia enterocolitica ssp. *enterocolitica*
Yersinia kristensenii
Yersinia pseudotuberculosis

Yersinia rohdei

Yokenella regensburgei

List of tests used to create a codebook

Basic set of tests

ONP	β -galactosidase (ONPG)
H ₂ S	hydrogen sulfide production
LYS	lysine decarboxylase
IND	indole production
ORN	ornithine decarboxylase
URE	urea hydrolysis
PHE	phenylalanine deaminase
ESL	aesculine hydrolysis
SCI	citrate utilization
MAL	malonate utilization
INO	acid from myo-inositol
ADO	acid from adonitol
CEL	acid from cellobiose
SUC	acid from saccharose
SOR	acid from sorbitol
TRE	acid from trehalose
MAN	acid from mannitol

Additional (distinguishing) tests

OXI	oxidase (Kovács)
VPT	acetoin production
PYR	pyrrolidonyl arylamidase
YEP	yellow pigment production

Введение

Кодовая книга для ЭНТЕРОтест 16 предназначена для идентификации бактерий с использованием тестового набора MIKRO-LA-TEST ЭНТЕРОтест 16. Идентификация, т.е. интерпретация результата, может быть выполнена тремя способами:

- 1. вручную - путем сравнения результата с данными в таблице дифференцирования
- 2. с использованием программы идентификации (например, ErbaExpert)
- 3. используя эту кодовую книгу

Все упомянутые методы идентификации основаны на данных матрицы идентификации (частотной матрицы), то есть таблицы, содержащей таксоны, тесты и проценты положительных реакций конкретных тестов для каждого таксона. Таксоном может быть:

- род - *Morganella sp.*
- вид - *Morganella morganii*
- подвид - *Morganella morganii ssp. Morganii*

Кодовая книга содержит результаты идентификации с использованием набора ЭНТЕРОтест 16, упорядоченного в соответствии со значением так называемых кодов профиля. Сортировка результатов по значению кода профиля позволяет легко и быстро искать. Оценка качества идентификации для каждого кода профиля основана на вычислении вероятности результата из данных матрицы идентификации; оценка приведена ниже.

Создание кода профиля:

Для более точной идентификации целесообразно преобразовать полученные результаты каждого теста (+/-) в числовой профиль (восьмеричный код). Тесты сначала делятся на группы:

ONP	H2S	LYS	IND	ORN	URE	PHE	ESL	SCI	MAL	INO	ADO	CEL	SUC	SOR	TRE	MAN	
1			2			3			4			5			6		

Теперь получаем 5 групп по три и в одной группе два теста. В каждой группе только каждому положительному тесту даются числовые значения 1, 2 и 4:

первый тест тройки - 1

второй тест тройки - 2

третий тест тройки - 4

всем отрицательным результатам дается значение 0

ONP	H2S	LYS	IND	ORN	URE	PHE	ESL	SCI	MAL	INO	ADO	CEL	SUC	SOR	TRE	MAN	
1	2	4	1	2	4	1	2	4	1	2	4	1	2	4	1	2	

При создании кода профиля для конкретного результата необходимо выполнить следующие действия:

- положительным испытаниям присваиваются 1, 2 или 4 значения
- отрицательным испытаниям всегда присваивается нулевое значение
- полученные значения суммируются в каждой тестовой группе
- итоговая группа чисел представляет собой **код профиля**

ONP	H2S	LYS	IND	ORN	URE	PHE	ESL	SCI	MAL	INO	ADO	CEL	SUC	SOR	TRE	MAN	
+	-	-	+	+	+	-	-	+	+	+	-	-	+	+	+	-	
1	0	0	1	2	4	0	0	4	1	2	0	0	2	4	1	0	
1			7			4			3			6			1		

В этом примере был создан профиль **174301**.

Результаты располагаются в кодовой книге в соответствии со значением кода профиля в порядке возрастания.

ИСПОЛЬЗОВАНИЕ ИНДЕКСА ЧИСЛОВЫХ ПРОФИЛЕЙ

Найдите числовой профиль в индексе; профили систематизированы в регистре в порядке возрастания величин чисел.

Профиль сопровождается следующей информацией:

- значения 2-х индексов для каждого таксона:
 - а) процент идентификации (% id) – показатель, оценивающий насколько близко полученный профиль соответствует идентифицированному таксону по сравнению с другими таксонами, включенными в банк данных; таксоны систематизированы в соответствии с их величинами % id.
 - б) Т индекс (Tin) – показывает насколько близко профиль соответствует большинству типичных реакций данного таксона. Его величина варьирует от 0 до 1 и обратно пропорциональна количеству атипичных тестов.
- перечень атипичных тестов (T. against) для первого из перечисленных таксонов с указанием процента положительных реакций, заложенных в базу данных;
- перечень дополнительных тестов – если таксоны не достаточно хорошо идентифицируются с помощью ЭНТЕРОтест 16; дополнительные тесты приводятся с процентом положительных реакций, заложенных в базу данных;
- пояснения в случае, если качество идентификации выходит за рамки вышеперечисленных показателей;
- оценка качества идентификации, исходя из значений %id и T-index:

Процент идентификации

%id >= 99 – таксон отлично отличается от других таксонов

%id >= 95 - таксон очень хорошо отличается от других таксонов

%id >= 90 - таксон удовлетворительно отличается от других таксонов

%id < 90 - таксон неудовлетворительно отличается от других таксонов

Т-индекс

Т-индекс >= 0.75- типичный штамм

Т-индекс >= 0.50- менее типичный штамм

Т-индекс >= 0.25- атипичный штамм

Т-индекс < 0.25- полностью атипичный штамм

Т-индекс	%id	качество идентификации
>= 0.75	>= 0.99	ОТЛИЧНАЯ ИДЕНТИФИКАЦИЯ
>= 0.50	>= 0.95	ОЧЕНЬ ХОРОШАЯ ИДЕНТИФИКАЦИЯ
>= 0.25	>= 0.90	ХОРОШАЯ ИДЕНТИФИКАЦИЯ для первого таксона
>= 0	>= 0.90	ПРИЕМЛИМАЯ ИДЕНТИФИКАЦИЯ для первого таксона
	< 0.90	НИЗКОЕ РАЗЛИЧИЕ - выбранные таксоны относятся к разным родам ИДЕНТИФИКАЦИЯ ДО РОДА - выбраны более одного таксона того же рода ИДЕНТИФИКАЦИЯ ДО ВИДА - выбраны более чем один вид и подвида в одном образце

В случае, если профиль не найден в индексе профилей, то возможно:

- профиль является совсем атипичным и частота его встречаемости очень низкая
- профиль относится к таксону, который не включен в базу данных.

Список таксонов, используемых для создания кодовой книги

Citrobacter amalonaticus
Citrobacter braakii
Citrobacter farmeri
Citrobacter freundii
Citrobacter koseri
Citrobacter sedlakii
Citrobacter werkmanii
Citrobacter youngae
Cronobacter sakazakii
Edwardsiella tarda
Enterobacter aerogenes
Enterobacter cloacae subsp. *cloacae*
Escherichia coli
Escherichia fergusonii
Escherichia hermannii
Escherichia vulneris
Hafnia alvei
Klebsiella oxytoca
Klebsiella pneumoniae subsp. *ozaenae*
Klebsiella pneumoniae subsp. *pneumoniae*
Klebsiella pneumoniae subsp. *rhinoscleromatis*
Kluyvera ascorbata
Leclercia adecarboxylata
Morganella morganii subsp. *morganii*
Morganella morganii subsp. *sibonii*
Pantoea agglomerans
Proteus mirabilis
Proteus penneri
Proteus vulgaris
Providencia alcalifaciens
Providencia rettgeri
Providencia stuartii
Salmonella bongori
Salmonella enterica subsp. *arizonae*
Salmonella enterica subsp. *diarizonae*
Salmonella enterica subsp. *enterica*
Salmonella enterica subsp. *houtenae*
Salmonella enterica subsp. *salamae*
Salmonella serovar *enteritidis*
Salmonella serovar *paratyphi*
Salmonella serovar *typhi*
Serratia ficaria
Serratia marcescens
Serratia odorifera biovar 1
Serratia odorifera biovar 2
Serratia rubidaea
Shigella boydii (group C)
Shigella dysenteriae (group A)
Shigella flexneri (group B)
Shigella sonnei
Yersinia enterocolitica ssp. *enterocolitica*
Yersinia kristensenii
Yersinia pseudotuberculosis
Yersinia rohdei
Yokenella regensburgei

Список тестов, используемых для создания кода профиля

Базовый набор тестов

ONP	β-галактозидаза
H ₂ S	Сероводород
LYS	Лизин
IND	Индол
ORN	Орнитин
URE	Уреаза
PHE	Фенилаланин
ESL	Эскулин
SCI	Цитрат Симмонса
MAL	Малонат
INO	Инозит
ADO	Адонит
CEL	Целлобиоза
SUC	Сахароза
SOR	Сорбитол
TRE	Трегалоза
MAN	Маннитол

Дополнительные (отличительные) тесты

OXI	Оксидаза
VPT	Ацетоин
PYR	Образование пирролидонилариламидазы
YEP	производство желтого пигмента

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
000000	Identification to the genus				000000
<i>Shigella dysenteriae</i> (group A)	77.98	0.80	TRE 90		
<i>Shigella flexneri</i> (group B)	16.95	0.67			
<i>Shigella boydii</i> (group C)	5.06	0.53			
000001	Good identification				000001
<i>Shigella dysenteriae</i> (group A)	91.65	1.00			
<i>Shigella flexneri</i> (group B)	4.49	0.74			
<i>Shigella boydii</i> (group C)	3.75	0.69			
000002	Identification to the genus				000002
<i>Shigella flexneri</i> (group B)	66.17	0.94			
<i>Shigella boydii</i> (group C)	33.62	0.85			
<i>Shigella dysenteriae</i> (group A)	0.16	0.39			
000003	Identification to the genus				000003
<i>Shigella boydii</i> (group C)	57.87	1.00			
<i>Shigella flexneri</i> (group B)	40.81	1.00			
<i>Shigella dysenteriae</i> (group A)	0.44	0.59			
000010	Identification to the genus				000010
<i>Shigella dysenteriae</i> (group A)	77.99	0.39	CEL 1		
<i>Shigella flexneri</i> (group B)	16.95	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	5.06	0.12			
000011	Good identification				000011
<i>Shigella dysenteriae</i> (group A)	91.61	0.59	CEL 1		
<i>Shigella flexneri</i> (group B)	4.49	0.33			
<i>Shigella boydii</i> (group C)	3.74	0.28			
000012	Identification to the genus				000012
<i>Shigella flexneri</i> (group B)	66.14	0.53	CEL 1		
<i>Shigella boydii</i> (group C)	33.60	0.43			
<i>Shigella dysenteriae</i> (group A)	0.16	-.02			
000013	Low discrimination				000013
<i>Shigella boydii</i> (group C)	53.60	0.59	CEL 1		
<i>Shigella flexneri</i> (group B)	37.79	0.59			
<i>Escherichia vulneris</i>	2.77	0.28			
000020	Low discrimination				000020
<i>Shigella dysenteriae</i> (group A)	70.83	0.39	SUC 1		
<i>Shigella flexneri</i> (group B)	15.40	0.26	TRE 90		
<i>Proteus penneri</i>	8.20	0.16			
000021	Identification to the genus				000021
<i>Shigella dysenteriae</i> (group A)	89.23	0.59	SUC 1		
<i>Shigella flexneri</i> (group B)	4.38	0.33			
<i>Shigella boydii</i> (group C)	3.65	0.28			
000022	Identification to the genus				000022

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella flexneri</i> (group B)	65.44	0.53	SUC 1		
<i>Shigella boydii</i> (group C)	33.25	0.43			
<i>Yersinia rohdei</i>	0.95	0.18			
000023	Low discrimination				000023
<i>Shigella boydii</i> (group C)	44.35	0.59	SUC 1		
<i>Shigella flexneri</i> (group B)	31.28	0.59			
<i>Yersinia rohdei</i>	22.19	0.59			
000033	Low discrimination				000033
<i>Yersinia rohdei</i>	84.42	0.49	SOR 99		
<i>Shigella boydii</i> (group C)	5.11	0.18			
<i>Shigella flexneri</i> (group B)	3.61	0.18			
000040	Identification to the genus				000040
<i>Shigella dysenteriae</i> (group A)	75.63	0.73	TRE 90		
<i>Shigella flexneri</i> (group B)	15.67	0.59			
<i>Shigella boydii</i> (group C)	8.64	0.51			
000041	Identification to the genus				000041
<i>Shigella dysenteriae</i> (group A)	89.02	0.92			
<i>Shigella boydii</i> (group C)	6.40	0.66			
<i>Shigella flexneri</i> (group B)	4.16	0.66			
000042	Identification to the genus				000042
<i>Shigella flexneri</i> (group B)	51.14	0.86			
<i>Shigella boydii</i> (group C)	47.99	0.82			
<i>Salmonella</i> serovar paratyphi	0.46	0.33			
000043	Low discrimination				000043
<i>Shigella boydii</i> (group C)	63.60	0.98			
<i>Shigella flexneri</i> (group B)	24.28	0.92			
<i>Salmonella</i> serovar paratyphi	10.69	0.74			
000051	Low discrimination				000051
<i>Shigella dysenteriae</i> (group A)	84.05	0.51	CEL 1		
<i>Shigella boydii</i> (group C)	6.05	0.25			
<i>Shigella flexneri</i> (group B)	3.93	0.25			
000052	Low discrimination				000052
<i>Shigella flexneri</i> (group B)	47.41	0.45	CEL 1		
<i>Shigella boydii</i> (group C)	44.49	0.41			
<i>Yersinia kristensenii</i>	3.46	0.19			
000053	Low discrimination				000053
<i>Yersinia kristensenii</i>	30.39	0.60	ORN 92		
<i>Shigella boydii</i> (group C)	22.36	0.56			
<i>Salmonella</i> serovar paratyphi	19.58	0.47			
000061	Low discrimination				000061
<i>Yersinia rohdei</i>	56.94	0.59	MAN 99		
<i>Shigella dysenteriae</i> (group A)	36.92	0.51			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella boydii</i> (group C)	2.66	0.25			
000062	Low discrimination				000062
<i>Yersinia rohdei</i>	63.23	0.59	TRE 99		
<i>Shigella flexneri</i> (group B)	17.93	0.45			
<i>Shigella boydii</i> (group C)	16.82	0.41			
000063	Very good identification				000063
<i>Yersinia rohdei</i>	96.19	1.00			
<i>Shigella boydii</i> (group C)	1.47	0.56			
<i>Citrobacter freundii</i>	1.06	0.67			
000071	Acceptable identification				000071
<i>Yersinia rohdei</i>	94.89	0.49	MAN 99		
<i>Citrobacter freundii</i>	2.46	0.23			
<i>Shigella dysenteriae</i> (group A)	1.86	0.10			
000072	Good identification				000072
<i>Yersinia rohdei</i>	95.16	0.49	TRE 99		
<i>Citrobacter freundii</i>	2.47	0.23			
<i>Shigella flexneri</i> (group B)	0.82	0.04			
000073	Very good identification				000073
<i>Yersinia rohdei</i>	96.60	0.90			
<i>Citrobacter freundii</i>	2.50	0.64			
<i>Citrobacter youngae</i>	0.37	0.45			
000100	Identification to the genus				000100
<i>Shigella dysenteriae</i> (group A)	77.99	0.39	MAL 1		
<i>Shigella flexneri</i> (group B)	16.95	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	5.06	0.12			
000101	Good identification				000101
<i>Shigella dysenteriae</i> (group A)	91.67	0.59	MAL 1		
<i>Shigella flexneri</i> (group B)	4.50	0.33			
<i>Shigella boydii</i> (group C)	3.75	0.28			
000102	Identification to the genus				000102
<i>Shigella flexneri</i> (group B)	66.20	0.53	MAL 1		
<i>Shigella boydii</i> (group C)	33.64	0.43			
<i>Shigella dysenteriae</i> (group A)	0.16	-0.2			
000103	Identification to the genus				000103
<i>Shigella boydii</i> (group C)	57.68	0.59	MAL 1		
<i>Shigella flexneri</i> (group B)	40.68	0.59			
<i>Shigella dysenteriae</i> (group A)	0.44	0.18			
000113	Acceptable identification				000113
<i>Escherichia vulneris</i>	94.13	0.43	ONP 99		
<i>Shigella boydii</i> (group C)	3.25	0.18			
<i>Shigella flexneri</i> (group B)	2.29	0.18			
000141	Identification to the genus				000141

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella dysenteriae</i> (group A)	89.08	0.51	MAL 1		
<i>Shigella boydii</i> (group C)	6.41	0.25			
<i>Shigella flexneri</i> (group B)	4.16	0.25			
000142	Identification to the genus				000142
<i>Shigella flexneri</i> (group B)	51.25	0.45	MAL 1		
<i>Shigella boydii</i> (group C)	48.10	0.41			
<i>Salmonella</i> serovar paratyphi	0.46	-.09			
000143	Low discrimination				000143
<i>Shigella boydii</i> (group C)	62.62	0.56	MAL 1		
<i>Shigella flexneri</i> (group B)	23.91	0.51			
<i>Salmonella</i> serovar paratyphi	10.52	0.33			
000163	Low discrimination				000163
<i>Yersinia rohdei</i>	88.43	0.59	MAL 1		
<i>Citrobacter freundii</i>	8.37	0.45			
<i>Shigella boydii</i> (group C)	1.35	0.15			
000173	Low discrimination				000173
<i>Yersinia rohdei</i>	58.50	0.49	MAL 1		
<i>Klebsiella pneumoniae</i> subsp. rhinoscleromatis	27.30	0.33			
<i>Citrobacter freundii</i>	13.05	0.43			
000200	Identification to the genus				000200
<i>Shigella dysenteriae</i> (group A)	77.99	0.39	INO 1		
<i>Shigella flexneri</i> (group B)	16.95	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	5.06	0.12			
000201	Good identification				000201
<i>Shigella dysenteriae</i> (group A)	91.06	0.59	INO 1		
<i>Shigella flexneri</i> (group B)	4.47	0.33			
<i>Shigella boydii</i> (group C)	3.72	0.28			
000202	Identification to the genus				000202
<i>Shigella flexneri</i> (group B)	66.20	0.53	INO 1		
<i>Shigella boydii</i> (group C)	33.64	0.43			
<i>Shigella dysenteriae</i> (group A)	0.16	-.02			
000203	Identification to the genus				000203
<i>Shigella boydii</i> (group C)	57.80	0.59	INO 1		
<i>Shigella flexneri</i> (group B)	40.76	0.59			
<i>Shigella dysenteriae</i> (group A)	0.44	0.18			
000213	Low discrimination				000213
<i>Klebsiella pneumoniae</i> subsp. ozaenae	50.59	0.39	ADO 97		
<i>Shigella boydii</i> (group C)	25.50	0.18			
<i>Shigella flexneri</i> (group B)	17.98	0.18			
000241	Identification to the genus				000241
<i>Shigella dysenteriae</i> (group A)	89.08	0.51	INO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella boydii</i> (group C)	6.41	0.25			
<i>Shigella flexneri</i> (group B)	4.16	0.25			
000242	Identification to the genus				000242
<i>Shigella flexneri</i> (group B)	51.25	0.45	INO 1		
<i>Shigella boydii</i> (group C)	48.10	0.41			
<i>Salmonella</i> serovar paratyphi	0.46	-0.9			
000243	Low discrimination				000243
<i>Shigella boydii</i> (group C)	62.70	0.56	INO 1		
<i>Shigella flexneri</i> (group B)	23.94	0.51			
<i>Salmonella</i> serovar paratyphi	10.53	0.33			
000253	Low discrimination				000253
<i>Yersinia kristensenii</i>	64.86	0.44	ORN 92		
<i>Klebsiella pneumoniae</i> subsp. ozaenae	13.35	0.44			
<i>Klebsiella pneumoniae</i> subsp. rhinoscleromatis	9.30	0.23			
000263	Good identification				000263
<i>Yersinia rohdei</i>	94.40	0.59	INO 1		
<i>Shigella boydii</i> (group C)	1.44	0.15			
<i>Citrobacter freundii</i>	1.04	0.26			
000273	Low discrimination				000273
<i>Yersinia rohdei</i>	59.75	0.49	INO 1		
<i>Klebsiella pneumoniae</i> subsp. rhinoscleromatis	27.88	0.33			
<i>Yersinia enterocolitica</i> ssp. enterocolitica	5.66	0.30			
000353	Good identification				000353
<i>Klebsiella pneumoniae</i> subsp. rhinoscleromatis	99.27	0.49	ADO 99		
<i>Yersinia kristensenii</i>	0.37	0.03			
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.23	0.13			
000373	Very good identification				000373
<i>Klebsiella pneumoniae</i> subsp. rhinoscleromatis	99.89	0.59	ADO 99		
<i>Yersinia rohdei</i>	0.11	0.08			
000400	Identification to the genus				000400
<i>Shigella dysenteriae</i> (group A)	77.26	0.39	ADO 1		
<i>Shigella flexneri</i> (group B)	16.79	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	5.01	0.12			
000401	Good identification				000401
<i>Shigella dysenteriae</i> (group A)	91.67	0.59	ADO 1		
<i>Shigella flexneri</i> (group B)	4.50	0.33			
<i>Shigella boydii</i> (group C)	3.75	0.28			
000402	Identification to the genus				000402
<i>Shigella flexneri</i> (group B)	66.08	0.53	ADO 1		
<i>Shigella boydii</i> (group C)	33.58	0.43			
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.18	0.11			
000403	Identification to the genus				000403

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella boydii</i> (group C)	56.33	0.59	ADO 1		
<i>Shigella flexneri</i> (group B)	39.72	0.59			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.60	0.46			
000413	Very good identification				000413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.52	0.68			
<i>Shigella boydii</i> (group C)	1.84	0.18			
<i>Shigella flexneri</i> (group B)	1.30	0.18			
000433	Very good identification				000433
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.82	0.56			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	2.96	0.06			
<i>Yersinia rohdei</i>	1.22	0.08			
000441	Identification to the genus				000441
<i>Shigella dysenteriae</i> (group A)	88.72	0.51	ADO 1		
<i>Shigella boydii</i> (group C)	6.38	0.25			
<i>Shigella flexneri</i> (group B)	4.15	0.25			
000442	Identification to the genus				000442
<i>Shigella flexneri</i> (group B)	50.82	0.45	ADO 1		
<i>Shigella boydii</i> (group C)	47.69	0.41			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.63	0.17			
000443	Low discrimination				000443
<i>Shigella boydii</i> (group C)	58.82	0.56	ADO 1		
<i>Shigella flexneri</i> (group B)	22.46	0.51			
<i>Salmonella</i> serovar <i>paratyphi</i>	9.88	0.33			
000452	Low discrimination				000452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	82.91	0.39	TRE 98		
<i>Shigella flexneri</i> (group B)	5.91	0.04			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	5.63	-.04			
000453	Identification to the genus				000453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	85.37	0.73			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	11.72	0.38			
<i>Yersinia kristensenii</i>	0.90	0.19			
000463	Good identification				000463
<i>Yersinia rohdei</i>	90.67	0.59	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.88	0.39			
<i>Escherichia coli</i>	1.44	0.25			
000473	Low discrimination				000473
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	49.25	0.47	MAL 95 INO 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	29.90	0.61			
<i>Yersinia rohdei</i>	20.25	0.49			
000553	Very good identification				000553
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	98.83	0.64	INO 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.17	0.42			
000573	Very good identification				000573
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.88	0.74	INO 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.10	0.30			
<i>Yersinia rohdei</i>	0.02	0.08			
000603	Low discrimination				000603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.59	0.48	CEL 92		
<i>Shigella boydii</i> (group C)	13.73	0.18			
<i>Shigella flexneri</i> (group B)	9.68	0.18			
000613	Very good identification				000613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.15	0.70			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.85	0.23			
000623	Acceptable identification				000623
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.72	0.36	CEL 92		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	5.29	-.09			
000633	Identification to the genus				000633
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	67.55	0.57			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	32.45	0.33			
000643	Low discrimination				000643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	73.49	0.53	CEL 92		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	18.22	0.23			
<i>Shigella boydii</i> (group C)	5.35	0.15			
000653	Identification to the genus				000653
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	68.04	0.64	MAL 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	31.89	0.75			
<i>Yersinia kristensenii</i>	0.05	0.03			
000673	Very good identification				000673
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	96.22	0.74	MAL 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.76	0.63			
<i>Yersinia rohdei</i>	0.02	0.08			
000713	Good identification				000713
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	96.09	0.49	SOR 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.91	0.39			
000733	Very good identification				000733
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.61	0.59	SOR 99	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.34	0.26		1	
<i>Serratia rubidaea</i>	0.05	-.06		99	
000743	Good identification				000743
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.35	0.49	CEL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.65	0.22			
000751	Good identification				000751

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.49	MAN 99		
000752	Good identification				000752
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.85	0.49	TRE 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.15	0.09			
000753	Very good identification				000753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.92	0.90			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.08	0.44			
000763	Very good identification				000763
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.95	0.59	CEL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.06	0.10			
000771	Very good identification				000771
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.59	MAN 99		
000772	Very good identification				000772
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.59	TRE 99		
000773	Excellent identification				000773
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.99	1.00			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.01	0.32			
001000	Low discrimination				001000
<i>Shigella dysenteriae</i> (group A)	54.67	0.39	PHE 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	14.02	0.19	TRE 90		
<i>Shigella flexneri</i> (group B)	11.88	0.26			
001001	Low discrimination				001001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	54.31	0.64	URE 97		
<i>Shigella dysenteriae</i> (group A)	40.98	0.59			
<i>Shigella flexneri</i> (group B)	2.01	0.33			
001002	Identification to the genus				001002
<i>Shigella flexneri</i> (group B)	66.20	0.53	PHE 1		
<i>Shigella boydii</i> (group C)	33.64	0.43			
<i>Shigella dysenteriae</i> (group A)	0.16	-.02			
001003	Identification to the genus				001003
<i>Shigella boydii</i> (group C)	57.53	0.59	PHE 1		
<i>Shigella flexneri</i> (group B)	40.57	0.59			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.58	0.23			
001020	Identification to the genus				001020
<i>Proteus penneri</i>	89.23	0.57	URE 99		
<i>Proteus vulgaris</i>	10.64	0.47			
<i>Shigella dysenteriae</i> (group A)	0.08	-.02			
001021	Good identification				001021
<i>Proteus penneri</i>	90.31	0.59	URE 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.91	0.39			
<i>Proteus vulgaris</i>	3.78	0.40			
001041	Identification to the genus				001041
<i>Shigella dysenteriae</i> (group A)	86.67	0.51	PHE 1		
<i>Shigella boydii</i> (group C)	6.23	0.25			
<i>Shigella flexneri</i> (group B)	4.05	0.25			
001042	Identification to the genus				001042
<i>Shigella flexneri</i> (group B)	51.25	0.45	PHE 1		
<i>Shigella boydii</i> (group C)	48.10	0.41			
<i>Salmonella</i> serovar <i>paratyphi</i>	0.46	-.09			
001043	Low discrimination				001043
<i>Shigella boydii</i> (group C)	63.61	0.56	PHE 1		
<i>Shigella flexneri</i> (group B)	24.29	0.51			
<i>Salmonella</i> serovar <i>paratyphi</i>	10.69	0.33			
001063	Very good identification				001063
<i>Yersinia rohdei</i>	96.23	0.59	PHE 1		
<i>Shigella boydii</i> (group C)	1.47	0.15			
<i>Citrobacter freundii</i>	1.06	0.26			
001073	Good identification				001073
<i>Yersinia rohdei</i>	97.12	0.49	PHE 1		
<i>Citrobacter freundii</i>	2.52	0.23			
<i>Citrobacter youngae</i>	0.37	0.04			
001201	Low discrimination				001201
<i>Providencia stuartii</i>	85.52	0.42	IND 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	8.25	0.23	SCI 93		
<i>Shigella dysenteriae</i> (group A)	6.23	0.18			
001221	Low discrimination				001221
<i>Providencia stuartii</i>	88.96	0.42	IND 98		
<i>Proteus penneri</i>	10.08	0.18	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.55	-.02			
001753	Good identification				001753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.49	PHE 1		
001773	Very good identification				001773
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.59	PHE 1		
002000	Identification to the genus				002000
<i>Shigella dysenteriae</i> (group A)	77.99	0.39	ESL 1		
<i>Shigella flexneri</i> (group B)	16.95	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	5.06	0.12			
002001	Low discrimination				002001
<i>Shigella dysenteriae</i> (group A)	87.03	0.59	ESL 1		
<i>Yersinia pseudotuberculosis</i>	5.06	0.25			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella flexneri</i> (group B)	4.27	0.33			
002002	Low discrimination				002002
<i>Shigella flexneri</i> (group B)	61.08	0.53	ESL 1		
<i>Shigella boydii</i> (group C)	31.03	0.43			
<i>Yersinia pseudotuberculosis</i>	7.74	0.25			
002003	Low discrimination				002003
<i>Yersinia pseudotuberculosis</i>	71.48	0.66	URE 95		
<i>Shigella boydii</i> (group C)	16.40	0.59			
<i>Shigella flexneri</i> (group B)	11.57	0.59			
002013	Low discrimination				002013
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	46.93	0.49	ADO 97		
<i>Yersinia pseudotuberculosis</i>	31.50	0.25			
<i>Escherichia vulneris</i>	9.24	0.16			
002033	Low discrimination				002033
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.55	0.37	ADO 97		
<i>Pantoea agglomerans</i>	11.51	0.03			
<i>Yersinia rohdei</i>	7.76	0.08			
002041	Identification to the genus				002041
<i>Shigella dysenteriae</i> (group A)	88.36	0.51	ESL 1		
<i>Shigella boydii</i> (group C)	6.36	0.25			
<i>Shigella flexneri</i> (group B)	4.13	0.25			
002042	Identification to the genus				002042
<i>Shigella flexneri</i> (group B)	50.71	0.45	ESL 1		
<i>Shigella boydii</i> (group C)	47.58	0.41			
<i>Escherichia coli</i>	1.06	0.17			
002043	Low discrimination				002043
<i>Shigella boydii</i> (group C)	57.72	0.56	ESL 1		
<i>Shigella flexneri</i> (group B)	22.04	0.51			
<i>Salmonella</i> serovar <i>paratyphi</i>	9.70	0.33			
002053	Low discrimination				002053
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	72.59	0.55	ADO 97		
<i>Citrobacter youngae</i>	7.37	0.30			
<i>Yersinia kristensenii</i>	6.17	0.19			
002063	Low discrimination				002063
<i>Yersinia rohdei</i>	88.39	0.59	ESL 1		
<i>Escherichia coli</i>	6.65	0.39			
<i>Shigella boydii</i> (group C)	1.35	0.15			
002073	Low discrimination				002073
<i>Yersinia rohdei</i>	71.45	0.49	ESL 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	13.05	0.42			
<i>Serratia ficaria</i>	5.90	0.16			
002123	Good identification				002123

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
<i>Pantoea agglomerans</i>		100.0	0.47	ONP 99		
002133	Good identification					002133
<i>Pantoea agglomerans</i>		97.04	0.44	ONP 99		
<i>Escherichia vulneris</i>		2.50	0.09			
<i>Leclercia adecarboxylata</i>		0.27	-0.05			
002213	Good identification					002213
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.51	ADO 97		
002233	Good identification					002233
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		96.23	0.39	ADO 97	1	
<i>Cronobacter sakazakii</i>		3.77	-0.03		99	
002253	Good identification					002253
<i>Klebsiella pneumoniae subsp. ozaenae</i>		91.35	0.57	ADO 97		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>		6.82	0.15			
<i>Yersinia kristensenii</i>		1.12	0.03			
002273	Low discrimination					002273
<i>Klebsiella pneumoniae subsp. ozaenae</i>		39.45	0.44	ADO 97		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>		35.35	0.25			
<i>Serratia ficaria</i>		17.83	0.18			
002353	Good identification					002353
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>		97.87	0.42	ADO 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>		2.13	0.26			
002373	Good identification					002373
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>		99.82	0.51	ADO 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>		0.18	0.13			
002403	Low discrimination					002403
<i>Klebsiella pneumoniae subsp. ozaenae</i>		75.07	0.58	CEL 92		
<i>Yersinia pseudotuberculosis</i>		17.92	0.25			
<i>Shigella boydii</i> (group C)		4.11	0.18			
002411	Good identification					002411
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.39	MAN 99		
002412	Good identification					002412
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.46	TRE 98		
002413	Very good identification					002413
<i>Klebsiella pneumoniae subsp. ozaenae</i>		99.97	0.80			
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>		0.03	-0.11			
002423	Good identification					002423
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.46	CEL 92		
002433	Very good identification					002433

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.98	0.68		1	
<i>Serratia rubidaea</i>	0.56	0.06		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.33	-.01		1	
002443	Very good identification				002443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.71	0.64	CEL 92		
<i>Shigella boydii</i> (group C)	2.13	0.15			
<i>Escherichia coli</i>	0.83	0.17			
002451	Good identification				002451
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.55	0.45	MAN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	1.45	-.11			
002452	Good identification				002452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.28	0.51	TRE 98		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.72	-.11			
002453	Very good identification				002453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.55	0.86			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	1.45	0.30			
002463	Acceptable identification				002463
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	90.69	0.52	CEL 92		
<i>Yersinia rohdei</i>	5.35	0.18			
<i>Escherichia coli</i>	2.10	0.13			
002472	Acceptable identification				002472
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.97	0.39	TRE 98		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	8.03	-.01			
002473	Identification to the genus				002473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	84.88	0.73			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	14.98	0.40			
<i>Yersinia rohdei</i>	0.15	0.08			
002513	Low discrimination				002513
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.91	0.49	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	13.55	0.15			
<i>Leclercia adecarboxylata</i>	5.65	0.12			
002553	Good identification				002553
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	90.04	0.56	INO 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	9.96	0.55			
002573	Very good identification				002573
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.09	0.66	INO 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.91	0.42			
002603	Very good identification				002603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.60	CEL 92		
002611	Good identification				002611

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	MAN 99		
002612	Good identification				002612
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.47	TRE 98		
002613	Very good identification				002613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.57	0.82			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.43	0.15			
002623	Good identification				002623
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.48	CEL 92		
002633	Good identification				002633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.00	0.70		1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	4.89	0.25		1	
<i>Serratia rubidaea</i>	0.11	-0.06		99	
002643	Very good identification				002643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.41	0.66	CEL 92		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	2.59	0.15			
002651	Identification to the genus				002651
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.39	0.47	MAN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	18.61	0.15			
002652	Identification to the genus				002652
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	89.83	0.53	TRE 98		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	10.17	0.15			
002653	Identification to the genus				002653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.38	0.88		1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	18.61	0.56		1	
<i>Serratia odorifera</i> biovar 2	0.01	0.00		99	
002663	Identification to the genus				002663
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.83	0.53	CEL 92		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	24.17	0.25			
002673	Identification to the genus				002673
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	73.29	0.66	MAL 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	26.71	0.75			
002713	Identification to the genus				002713
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	72.49	0.42	SOR 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	27.51	0.51			
002733	Good identification				002733
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	95.22	0.51	SOR 99	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.01	0.39		1	
<i>Serratia rubidaea</i>	1.77	0.18		99	
002743	Acceptable identification				002743

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	94.23	0.42	CEL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.78	0.35			
002751	Good identification				002751
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.29	0.42	MAN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.71	0.16			
002752	Good identification				002752
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	98.58	0.42	TRE 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.42	0.22			
002753	Very good identification				002753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.29	0.83			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.71	0.57			
002763	Good identification				002763
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.49	0.51	CEL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.51	0.22			
002771	Good identification				002771
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.51	MAN 99		
002772	Good identification				002772
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.88	0.51	TRE 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.12	0.09			
002773	Very good identification				002773
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.94	0.92			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.06	0.44			
003020	Acceptable identification				003020
<i>Proteus vulgaris</i>	92.19	0.47	H2S 95		
<i>Proteus penneri</i>	7.81	0.16	URE 95		
003021	Identification to the genus				003021
<i>Proteus vulgaris</i>	79.70	0.40	H2S 95		
<i>Proteus penneri</i>	19.26	0.18	URE 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.05	-.02			
003413	Good identification				003413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.39	PHE 1		
003453	Good identification				003453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.55	0.45	PHE 1		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	1.45	-.11			
003613	Good identification				003613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	PHE 1		
003653	Identification to the genus				003653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.39	0.47	PHE 1		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	18.61	0.15			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
003753	Good identification				003753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.29	0.42	PHE 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.71	0.16			
003773	Good identification				003773
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.51	PHE 1		
004000	Identification to the genus				004000
<i>Shigella dysenteriae</i> (group A)	77.26	0.39	SCI 1		
<i>Shigella flexneri</i> (group B)	16.79	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	5.01	0.12			
004001	Good identification				004001
<i>Shigella dysenteriae</i> (group A)	91.24	0.59	SCI 1		
<i>Shigella flexneri</i> (group B)	4.47	0.33			
<i>Shigella boydii</i> (group C)	3.73	0.28			
004002	Identification to the genus				004002
<i>Shigella flexneri</i> (group B)	65.96	0.53	SCI 1		
<i>Shigella boydii</i> (group C)	33.51	0.43			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.37	0.03			
004003	Identification to the genus				004003
<i>Shigella boydii</i> (group C)	57.32	0.59	SCI 1		
<i>Shigella flexneri</i> (group B)	40.42	0.59			
<i>Citrobacter youngae</i>	0.47	0.27			
004023	Low discrimination				004023
<i>Citrobacter freundii</i>	47.34	0.38	ONP 88		
<i>Shigella boydii</i> (group C)	21.74	0.18	SOR 99		
<i>Shigella flexneri</i> (group B)	15.33	0.18			
004033	Low discrimination				004033
<i>Citrobacter freundii</i>	76.75	0.36	ONP 88		
<i>Citrobacter youngae</i>	7.97	0.13	SOR 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	7.80	0.17			
004041	Identification to the genus				004041
<i>Shigella dysenteriae</i> (group A)	85.97	0.51	SCI 1		
<i>Shigella boydii</i> (group C)	6.18	0.25			
<i>Shigella flexneri</i> (group B)	4.02	0.25			
004042	Low discrimination				004042
<i>Shigella flexneri</i> (group B)	46.24	0.45	SCI 1		
<i>Shigella boydii</i> (group C)	43.39	0.41			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	5.66	0.23			
004043	Low discrimination				004043
<i>Citrobacter youngae</i>	32.81	0.68	ONP 90		
<i>Shigella boydii</i> (group C)	30.28	0.56			
<i>Shigella flexneri</i> (group B)	11.56	0.51			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
004053	Identification to the genus				004053
<i>Citrobacter youngae</i>	48.90	0.66	ONP 90		
<i>Citrobacter braakii</i>	32.05	0.63			
<i>Citrobacter freundii</i>	15.46	0.58			
004061	Low discrimination				004061
<i>Citrobacter freundii</i>	67.64	0.38	ONP 88		
<i>Yersinia rohdei</i>	15.54	0.18	MAN 99		
<i>Shigella dysenteriae</i> (group A)	10.08	0.10			
004062	Low discrimination				004062
<i>Citrobacter freundii</i>	68.69	0.38	ONP 88		
<i>Yersinia rohdei</i>	15.78	0.18	TRE 99		
<i>Citrobacter youngae</i>	6.85	0.15			
004063	Low discrimination				004063
<i>Citrobacter freundii</i>	74.46	0.79	ONP 88		
<i>Yersinia rohdei</i>	17.10	0.59			
<i>Citrobacter youngae</i>	7.43	0.56			
004071	Low discrimination				004071
<i>Citrobacter freundii</i>	83.24	0.36	ONP 88		
<i>Citrobacter youngae</i>	8.65	0.13	MAN 99		
<i>Yersinia rohdei</i>	8.11	0.08			
004072	Low discrimination				004072
<i>Citrobacter freundii</i>	83.24	0.36	ONP 88		
<i>Citrobacter youngae</i>	8.65	0.13	TRE 99		
<i>Yersinia rohdei</i>	8.11	0.08			
004073	Low discrimination				004073
<i>Citrobacter freundii</i>	81.08	0.77	ONP 88		
<i>Citrobacter youngae</i>	8.42	0.54			
<i>Yersinia rohdei</i>	7.90	0.49			
004143	Low discrimination				004143
<i>Citrobacter youngae</i>	44.92	0.41	ONP 90		
<i>Citrobacter freundii</i>	24.44	0.38	MAL 5		
<i>Citrobacter werkmanii</i>	16.04	0.15			
004153	Identification to the genus				004153
<i>Citrobacter youngae</i>	60.67	0.40	ONP 90		
<i>Citrobacter freundii</i>	31.70	0.36	MAL 5		
<i>Citrobacter braakii</i>	7.63	0.22			
004163	Good identification				004163
<i>Citrobacter freundii</i>	91.99	0.57	ONP 88		
<i>Citrobacter youngae</i>	5.56	0.30	MAL 8		
<i>Yersinia rohdei</i>	2.46	0.18			
004173	Low discrimination				004173

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	85.20	0.55	ONP 88	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	8.03	0.25	MAL 8	99	
<i>Citrobacter youngae</i>	5.36	0.28		1	
004201	Acceptable identification				004201
<i>Providencia stuartii</i>	90.57	0.39	IND 98		
<i>Shigella dysenteriae</i> (group A)	9.43	0.18	PHE 95		
004221	Good identification				004221
<i>Providencia stuartii</i>	100.0	0.39	IND 98		
004243	Low discrimination				004243
<i>Citrobacter youngae</i>	67.39	0.41	ONP 90		
<i>Shigella boydii</i> (group C)	11.94	0.15	INO 5		
<i>Shigella flexneri</i> (group B)	4.56	0.10			
004253	Low discrimination				004253
				VPT	
<i>Citrobacter youngae</i>	42.00	0.40	ONP 90	1	
<i>Serratia odorifera</i> biovar 2	28.96	0.33	INO 5	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	19.03	0.37		1	
004263	Low discrimination				004263
<i>Citrobacter freundii</i>	57.16	0.38	ONP 88		
<i>Citrobacter youngae</i>	29.71	0.30	INO 1		
<i>Yersinia rohdei</i>	13.13	0.18			
004273	Low discrimination				004273
<i>Citrobacter freundii</i>	34.06	0.36	ONP 88		
<i>Serratia ficaria</i>	33.15	0.18	INO 1		
<i>Citrobacter youngae</i>	18.44	0.28			
004403	Low discrimination				004403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	53.43	0.39	CEL 92		
<i>Shigella boydii</i> (group C)	27.31	0.18			
<i>Shigella flexneri</i> (group B)	19.26	0.18			
004413	Very good identification				004413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.60			
004433	Acceptable identification				004433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.97	0.48		1	
<i>Serratia rubidaea</i>	6.03	0.08		99	
004443	Low discrimination				004443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	59.51	0.44	CEL 92		
<i>Citrobacter youngae</i>	13.39	0.27			
<i>Shigella boydii</i> (group C)	12.36	0.15			
004453	Very good identification				004453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.64	0.66			
<i>Citrobacter youngae</i>	1.55	0.25			
<i>Citrobacter braakii</i>	1.01	0.22			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
004463	Low discrimination				004463
<i>Citrobacter freundii</i>	57.26	0.38	ONP 88		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	23.88	0.32	ADO 1		
<i>Yersinia rohdei</i>	13.15	0.18			
004473	Low discrimination				004473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.97	0.54			
<i>Citrobacter freundii</i>	13.10	0.36			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.11	0.06			
004603	Good identification				004603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.40	CEL 92		
004613	Very good identification				004613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.62			
004633	Good identification				004633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.61	0.50		1	
<i>Serratia rubidaea</i>	1.28	-.05		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	1.11	-.09		1	
004643	Good identification				004643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.46	CEL 92		
004653	Good identification				004653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	90.27	0.68		1	
<i>Serratia odorifera</i> biovar 2	5.19	0.34		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	4.54	0.23		1	
004673	Identification to the genus				004673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	62.36	0.55			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	37.64	0.33			
004753	Good identification				004753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	96.87	0.49	SCI 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.14	0.37			
004773	Very good identification				004773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.68	0.59	SCI 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.27	0.24		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.06	0.00		99	
005001	Low discrimination				005001
<i>Providencia stuartii</i>	79.05	0.39	IND 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	10.91	0.23	INO 95		
<i>Shigella dysenteriae</i> (group A)	8.23	0.18			
005021	Low discrimination				005021
<i>Providencia stuartii</i>	77.57	0.39	IND 98		
<i>Proteus penneri</i>	12.57	0.18	INO 95		
<i>Proteus vulgaris</i>	9.18	0.24			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
005063	Low discrimination				005063
<i>Citrobacter freundii</i>	75.22	0.38	ONP 88		
<i>Yersinia rohdei</i>	17.28	0.18	PHE 1		
<i>Citrobacter youngae</i>	7.51	0.15			
005073	Low discrimination				005073
<i>Citrobacter freundii</i>	83.24	0.36	ONP 88		
<i>Citrobacter youngae</i>	8.65	0.13	PHE 1		
<i>Yersinia rohdei</i>	8.11	0.08			
005201	Very good identification				005201
<i>Providencia stuartii</i>	100.0	0.65	IND 98		
005203	Good identification				005203
<i>Providencia stuartii</i>	100.0	0.46	IND 98		
005211	Good identification				005211
<i>Providencia stuartii</i>	100.0	0.39	IND 98		
005221	Very good identification				005221
<i>Providencia stuartii</i>	100.0	0.65	IND 98		
005223	Good identification				005223
<i>Providencia stuartii</i>	100.0	0.46	IND 98		
005231	Good identification				005231
<i>Providencia stuartii</i>	100.0	0.39	IND 98		
005400	Very good identification				005400
<i>Providencia alcalifaciens</i>	100.0	0.59	IND 99		
005420	Good identification				005420
<i>Providencia alcalifaciens</i>	100.0	0.43	IND 99		
005601	Good identification				005601
<i>Providencia stuartii</i>	99.32	0.39	IND 98		
<i>Providencia alcalifaciens</i>	0.68	-.17	ADO 5		
005621	Good identification				005621
<i>Providencia stuartii</i>	100.0	0.39	IND 98		
006013	Good identification				006013
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.42	ADO 97		
006043	Low discrimination				006043
<i>Citrobacter youngae</i>	66.35	0.41	ONP 90		
<i>Shigella boydii (group C)</i>	11.75	0.15	ESL 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	7.00	0.25			
006053	Low discrimination				006053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	48.16	0.47	ADO 97		
<i>Citrobacter youngae</i>	32.47	0.40			
<i>Serratia ficaria</i>	12.70	0.16			
006063	Low discrimination				006063
<i>Citrobacter freundii</i>	41.21	0.38	ONP 88		
<i>Serratia ficaria</i>	25.78	0.16	ESL 1		
<i>Citrobacter youngae</i>	21.42	0.30			
006073	Very good identification				006073
<i>Serratia ficaria</i>	96.92	0.57	ONP 99		
<i>Citrobacter freundii</i>	1.23	0.36			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.93	0.35			
006123	Very good identification				006123
<i>Pantoea agglomerans</i>	99.95	0.59	ONP 99		
<i>Serratia rubidaea</i>	0.05	-0.09			
006133	Very good identification				006133
<i>Pantoea agglomerans</i>	98.53	0.57	ONP 99		
<i>Serratia rubidaea</i>	0.90	0.16			
<i>Cronobacter sakazakii</i>	0.57	0.15			
006213	Good identification				006213
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.77	0.43	ADO 97	1	
<i>Cronobacter sakazakii</i>	2.23	-0.03		99	
006233	Low discrimination				006233
				VPT	
<i>Cronobacter sakazakii</i>	75.34	0.38	ONP 99	99	
<i>Serratia ficaria</i>	16.32	0.18	ORN 91	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	8.34	0.31		1	
006253	Low discrimination				006253
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	64.67	0.49	ADO 97	1	
<i>Serratia ficaria</i>	17.05	0.18		75	
<i>Serratia odorifera</i> biovar 2	16.40	0.29		99	
006273	Very good identification				006273
				VPT	
<i>Serratia ficaria</i>	98.98	0.59	ONP 99	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.95	0.37		1	
<i>Cronobacter sakazakii</i>	0.05	-0.03		99	
006403	Good identification				006403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.51	CEL 92		
006412	Good identification				006412
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.38	TRE 98		
006413	Very good identification				006413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.94	0.73		1	
<i>Serratia rubidaea</i>	0.06	-0.09		99	
006423	Low discrimination				006423

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	84.42	0.39	CEL 92	1	
<i>Serratia rubidaea</i>	15.59	0.08		99	
006433	Low discrimination				006433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.90	0.60		1	
<i>Serratia rubidaea</i>	20.10	0.33		99	
006443	Very good identification				006443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.56	CEL 92		
006451	Good identification				006451
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	MAN 99		
006452	Good identification				006452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	TRE 98		
006453	Very good identification				006453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.97	0.78			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.04	-.11			
006463	Good identification				006463
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.44	CEL 92		
006473	Very good identification				006473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.18	0.66			
<i>Serratia ficaria</i>	3.14	0.16			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.40	-.01			
006513	Low discrimination				006513
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.66	0.42	MAL 3	1	
<i>Serratia rubidaea</i>	24.34	0.16		99	
006533	Very good identification				006533
				VPT	
<i>Serratia rubidaea</i>	98.13	0.57	ONP 99	99	
<i>Pantoea agglomerans</i>	1.10	0.16		64	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.77	0.29		1	
006553	Identification to the genus				006553
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	82.44	0.47	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	17.56	0.15			
006603	Good identification				006603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.53	CEL 92		
006612	Good identification				006612
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.40	TRE 98		
006613	Very good identification				006613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.75			
006623	Good identification				006623

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.36	0.40	CEL 92	1	006633
<i>Serratia rubidaea</i>	3.64	-.05		99	
006633	Good identification				006633
				VPT	006643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.85	0.62		1	
<i>Serratia rubidaea</i>	4.88	0.20		99	
<i>Cronobacter sakazakii</i>	0.27	-.03		99	
006643	Very good identification				006643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.58	CEL 92		006651
006651	Good identification				006651
				VPT	006652
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.15	0.39	MAN 99	1	
<i>Serratia odorifera</i> biovar 2	2.85	0.00		99	
006652	Good identification				006652
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.45	TRE 98		006653
006653	Very good identification				006653
				VPT	006663
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.53	0.80		1	
<i>Serratia odorifera</i> biovar 2	0.94	0.31		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.53	0.15		1	
006663	Good identification				006663
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.46	CEL 92		006673
006673	Good identification				006673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.13	0.68			006713
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	5.89	0.25			
<i>Serratia ficaria</i>	2.97	0.18			
006713	Low discrimination				006713
				VPT	006733
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	88.66	0.43	MAL 3	1	
<i>Serratia rubidaea</i>	5.84	0.04		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	5.51	0.00		1	
006733	Acceptable identification				006733
				VPT	006753
<i>Serratia rubidaea</i>	93.72	0.45	ONP 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.60	0.31		1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	2.68	0.10		1	
006753	Identification to the genus				006753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	76.80	0.42	SCI 1		006773
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	23.20	0.49			
006773	Good identification				006773
				VPT	007123
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	96.69	0.51	SCI 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.43	0.37		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.38	-.02		98	
007123	Good identification				007123
<i>Pantoea agglomerans</i>	100.0	0.38	ONP 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
007133	Acceptable identification				007133
<i>Pantoea agglomerans</i>	94.51	0.36	ONP 99		
<i>Cronobacter sakazakii</i>	5.49	0.15	PHE 9		
007233	Good identification				007233
<i>Cronobacter sakazakii</i>	100.0	0.38	ONP 99		
007453	Good identification				007453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.37	PHE 1		
007653	Good identification				007653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.39	PHE 1		
010000	Identification to the genus				010000
<i>Shigella dysenteriae</i> (group A)	77.17	0.79	TRE 90		
<i>Shigella flexneri</i> (group B)	20.50	0.67			
<i>Shigella boydii</i> (group C)	2.04	0.44			
010001	Good identification				010001
<i>Shigella dysenteriae</i> (group A)	92.74	0.98			
<i>Shigella flexneri</i> (group B)	5.56	0.74			
<i>Shigella boydii</i> (group C)	1.54	0.59			
010002	Identification to the genus				010002
<i>Shigella flexneri</i> (group B)	85.33	0.94			
<i>Shigella boydii</i> (group C)	14.45	0.75			
<i>Shigella dysenteriae</i> (group A)	0.17	0.38			
010003	Identification to the genus				010003
<i>Shigella flexneri</i> (group B)	67.25	1.00			
<i>Shigella boydii</i> (group C)	31.79	0.90			
<i>Shigella dysenteriae</i> (group A)	0.60	0.57			
010010	Identification to the genus				010010
<i>Shigella dysenteriae</i> (group A)	77.39	0.38	CEL 1		
<i>Shigella flexneri</i> (group B)	20.56	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	2.05	0.03			
010011	Good identification				010011
<i>Shigella dysenteriae</i> (group A)	92.68	0.57	CEL 1		
<i>Shigella flexneri</i> (group B)	5.55	0.33			
<i>Shigella boydii</i> (group C)	1.54	0.18			
010012	Identification to the genus				010012
<i>Shigella flexneri</i> (group B)	85.37	0.53	CEL 1		
<i>Shigella boydii</i> (group C)	14.46	0.34			
<i>Shigella dysenteriae</i> (group A)	0.17	-0.04			
010013	Identification to the genus				010013
<i>Shigella flexneri</i> (group B)	65.47	0.59	CEL 1		
<i>Shigella boydii</i> (group C)	30.95	0.49			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	1.76	0.24			
010020	Identification to the genus				010020
<i>Shigella dysenteriae</i> (group A)	75.85	0.38	SUC 1		
<i>Shigella flexneri</i> (group B)	20.15	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	2.01	0.03			
010021	Low discrimination				010021
<i>Shigella dysenteriae</i> (group A)	88.63	0.57	SUC 1		
<i>Shigella flexneri</i> (group B)	5.31	0.33			
<i>Providencia stuartii</i>	2.04	0.24			
010022	Identification to the genus				010022
<i>Shigella flexneri</i> (group B)	82.84	0.53	SUC 1		
<i>Shigella boydii</i> (group C)	14.03	0.34			
<i>Escherichia coli</i>	2.96	0.29			
010023	Low discrimination				010023
<i>Shigella flexneri</i> (group B)	54.65	0.59	SUC 1		
<i>Shigella boydii</i> (group C)	25.84	0.49			
<i>Escherichia coli</i>	18.30	0.56			
010040	Identification to the genus				010040
<i>Shigella dysenteriae</i> (group A)	76.80	0.71	TRE 90		
<i>Shigella flexneri</i> (group B)	19.44	0.59			
<i>Shigella boydii</i> (group C)	3.57	0.41			
010041	Good identification				010041
<i>Shigella dysenteriae</i> (group A)	91.60	0.91			
<i>Shigella flexneri</i> (group B)	5.23	0.66			
<i>Shigella boydii</i> (group C)	2.68	0.57			
010042	Identification to the genus				010042
<i>Shigella flexneri</i> (group B)	75.48	0.86			
<i>Shigella boydii</i> (group C)	23.61	0.72			
<i>Escherichia coli</i>	0.74	0.51			
010043	Low discrimination				010043
<i>Shigella flexneri</i> (group B)	50.44	0.92			
<i>Shigella boydii</i> (group C)	44.04	0.88			
<i>Escherichia coli</i>	4.60	0.77			
010051	Identification to the genus				010051
<i>Shigella dysenteriae</i> (group A)	89.58	0.50	CEL 1		
<i>Shigella flexneri</i> (group B)	5.12	0.25			
<i>Shigella boydii</i> (group C)	2.63	0.16			
010052	Identification to the genus				010052
<i>Shigella flexneri</i> (group B)	73.05	0.45	CEL 1		
<i>Shigella boydii</i> (group C)	22.85	0.31			
<i>Yersinia kristensenii</i>	2.29	0.11			
010053	Low discrimination				010053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia kristensenii</i>	37.06	0.52	ORN 92		
<i>Shigella flexneri</i> (group B)	24.30	0.51			
<i>Shigella boydii</i> (group C)	21.22	0.47			
010061	Low discrimination				010061
<i>Shigella dysenteriae</i> (group A)	68.54	0.50	SUC 1		
<i>Escherichia coli</i>	23.54	0.47			
<i>Shigella flexneri</i> (group B)	3.91	0.25			
010062	Low discrimination				010062
<i>Shigella flexneri</i> (group B)	49.75	0.45	SUC 1		
<i>Escherichia coli</i>	31.96	0.47			
<i>Shigella boydii</i> (group C)	15.56	0.31			
010063	Low discrimination				010063
<i>Escherichia coli</i>	56.37	0.73			
<i>Yersinia rohdei</i>	16.29	0.59			
<i>Shigella flexneri</i> (group B)	9.38	0.51			
010073	Low discrimination				010073
<i>Citrobacter freundii</i>	42.84	0.58	ONP 88		
<i>Yersinia rohdei</i>	33.91	0.49			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	7.49	0.38			
010100	Identification to the genus				010100
<i>Shigella dysenteriae</i> (group A)	77.39	0.38	MAL 1		
<i>Shigella flexneri</i> (group B)	20.56	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	2.05	0.03			
010101	Good identification				010101
<i>Shigella dysenteriae</i> (group A)	92.78	0.57	MAL 1		
<i>Shigella flexneri</i> (group B)	5.56	0.33			
<i>Shigella boydii</i> (group C)	1.54	0.18			
010102	Identification to the genus				010102
<i>Shigella flexneri</i> (group B)	85.37	0.53	MAL 1		
<i>Shigella boydii</i> (group C)	14.46	0.34			
<i>Shigella dysenteriae</i> (group A)	0.17	-0.04			
010103	Identification to the genus				010103
<i>Shigella flexneri</i> (group B)	67.27	0.59	MAL 1		
<i>Shigella boydii</i> (group C)	31.80	0.49			
<i>Shigella dysenteriae</i> (group A)	0.60	0.16			
010141	Acceptable identification				010141
<i>Shigella dysenteriae</i> (group A)	91.61	0.50	MAL 1		
<i>Shigella flexneri</i> (group B)	5.23	0.25			
<i>Shigella boydii</i> (group C)	2.68	0.16			
010142	Identification to the genus				010142
<i>Shigella flexneri</i> (group B)	75.61	0.45	MAL 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella boydii</i> (group C)	23.65	0.31			
<i>Escherichia coli</i>	0.74	0.10			
010143	Low discrimination				010143
<i>Shigella flexneri</i> (group B)	50.07	0.51	MAL 1		
<i>Shigella boydii</i> (group C)	43.71	0.47			
<i>Escherichia coli</i>	4.56	0.36			
010163	Low discrimination				010163
<i>Citrobacter freundii</i>	44.83	0.38	ONP 88		
<i>Escherichia coli</i>	33.62	0.32	MAL 8		
<i>Yersinia rohdei</i>	9.71	0.18			
010173	Low discrimination				010173
<i>Citrobacter freundii</i>	85.73	0.36	ONP 88		
<i>Yersinia rohdei</i>	7.88	0.08	MAL 8		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.68	-.09			
010200	Low discrimination				010200
<i>Shigella dysenteriae</i> (group A)	72.87	0.38	INO 1		
<i>Shigella flexneri</i> (group B)	19.36	0.26	TRE 90		
<i>Providencia stuartii</i>	5.85	0.16			
010201	Low discrimination				010201
<i>Shigella dysenteriae</i> (group A)	66.00	0.57	INO 1		
<i>Providencia stuartii</i>	28.86	0.51			
<i>Shigella flexneri</i> (group B)	3.96	0.33			
010202	Identification to the genus				010202
<i>Shigella flexneri</i> (group B)	85.24	0.53	INO 1		
<i>Shigella boydii</i> (group C)	14.44	0.34			
<i>Shigella dysenteriae</i> (group A)	0.17	-.04			
010203	Identification to the genus				010203
<i>Shigella flexneri</i> (group B)	65.39	0.59	INO 1		
<i>Shigella boydii</i> (group C)	30.91	0.49			
<i>Providencia stuartii</i>	2.79	0.31			
010221	Good identification				010221
<i>Providencia stuartii</i>	97.74	0.51	PHE 95		
<i>Shigella dysenteriae</i> (group A)	2.26	0.16	SCI 93		
010241	Acceptable identification				010241
<i>Shigella dysenteriae</i> (group A)	90.75	0.50	INO 1		
<i>Shigella flexneri</i> (group B)	5.18	0.25			
<i>Shigella boydii</i> (group C)	2.66	0.16			
010242	Identification to the genus				010242
<i>Shigella flexneri</i> (group B)	75.61	0.45	INO 1		
<i>Shigella boydii</i> (group C)	23.65	0.31			
<i>Escherichia coli</i>	0.74	0.10			
010243	Low discrimination				010243

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella flexneri</i> (group B)	50.25	0.51	INO 1		
<i>Shigella boydii</i> (group C)	43.88	0.47			
<i>Escherichia coli</i>	4.58	0.36			
010253	Low discrimination				010253
<i>Yersinia kristensenii</i>	88.10	0.37	ORN 92		
<i>Shigella flexneri</i> (group B)	3.31	0.10			
<i>Shigella boydii</i> (group C)	2.89	0.06			
010401	Good identification				010401
<i>Shigella dysenteriae</i> (group A)	92.26	0.57	ADO 1		
<i>Shigella flexneri</i> (group B)	5.53	0.33			
<i>Shigella boydii</i> (group C)	1.54	0.18			
010402	Identification to the genus				010402
<i>Shigella flexneri</i> (group B)	84.74	0.53	ADO 1		
<i>Shigella boydii</i> (group C)	14.35	0.34			
<i>Providencia alcalifaciens</i>	0.50	-.04			
010403	Identification to the genus				010403
<i>Shigella flexneri</i> (group B)	66.31	0.59	ADO 1		
<i>Shigella boydii</i> (group C)	31.35	0.49			
<i>Escherichia coli</i>	1.75	0.33			
010441	Identification to the genus				010441
<i>Shigella dysenteriae</i> (group A)	89.81	0.50	ADO 1		
<i>Shigella flexneri</i> (group B)	5.13	0.25			
<i>Shigella boydii</i> (group C)	2.63	0.16			
010442	Identification to the genus				010442
<i>Shigella flexneri</i> (group B)	73.34	0.45	ADO 1		
<i>Shigella boydii</i> (group C)	22.94	0.31			
<i>Escherichia coli</i>	3.72	0.24			
010443	Low discrimination				010443
<i>Shigella flexneri</i> (group B)	42.26	0.51	ADO 1		
<i>Shigella boydii</i> (group C)	36.90	0.47			
<i>Escherichia coli</i>	20.06	0.51			
010463	Low discrimination				010463
<i>Escherichia coli</i>	87.34	0.47	ADO 5		
<i>Yersinia rohdei</i>	4.84	0.18			
<i>Shigella flexneri</i> (group B)	2.79	0.10			
010753	Good identification				010753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.49	IND 1		
010773	Very good identification				010773
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	100.0	0.59	IND 1		
011000	Low discrimination				011000

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	66.22	0.45	ORN 95		
<i>Providencia alcalifaciens</i>	16.31	0.30	URE 96		
<i>Shigella dysenteriae</i> (group A)	11.12	0.38			
011001	Low discrimination				011001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	51.49	0.64	URE 97		
<i>Shigella dysenteriae</i> (group A)	31.79	0.57			
<i>Providencia stuartii</i>	13.90	0.51			
011002	Identification to the genus				011002
<i>Shigella flexneri</i> (group B)	83.97	0.53	PHE 1		
<i>Shigella boydii</i> (group C)	14.22	0.34			
<i>Morganella morganii</i> subsp. <i>morganii</i>	1.00	0.04			
011003	Identification to the genus				011003
<i>Shigella flexneri</i> (group B)	64.78	0.59	PHE 1		
<i>Shigella boydii</i> (group C)	30.62	0.49			
<i>Providencia stuartii</i>	2.76	0.31			
011020	Low discrimination				011020
<i>Proteus vulgaris</i>	74.88	0.47	H2S 95		
<i>Providencia alcalifaciens</i>	11.61	0.15	URE 95		
<i>Proteus penneri</i>	6.34	0.16			
011021	Low discrimination				011021
<i>Providencia stuartii</i>	67.33	0.51	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	15.92	0.39	INO 95		
<i>Proteus vulgaris</i>	12.24	0.40			
011041	Low discrimination				011041
<i>Shigella dysenteriae</i> (group A)	87.71	0.50	PHE 1		
<i>Shigella flexneri</i> (group B)	5.01	0.25			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	3.35	0.23			
011042	Identification to the genus				011042
<i>Shigella flexneri</i> (group B)	75.61	0.45	PHE 1		
<i>Shigella boydii</i> (group C)	23.65	0.31			
<i>Escherichia coli</i>	0.74	0.10			
011043	Low discrimination				011043
<i>Shigella flexneri</i> (group B)	50.51	0.51	PHE 1		
<i>Shigella boydii</i> (group C)	44.10	0.47			
<i>Escherichia coli</i>	4.60	0.36			
011200	Acceptable identification				011200
<i>Providencia stuartii</i>	94.72	0.42	SCI 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.73	0.04	TRE 98		
<i>Providencia alcalifaciens</i>	0.92	-.11			
011201	Very good identification				011201
<i>Providencia stuartii</i>	99.68	0.77	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.20	0.23			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella dysenteriae</i> (group A)	0.12	0.16			
011203	Very good identification				011203
<i>Providencia stuartii</i>	98.20	0.57	SCI 93		
<i>Shigella flexneri</i> (group B)	1.22	0.18	MAN 10		
<i>Shigella boydii</i> (group C)	0.58	0.08			
011211	Good identification				011211
<i>Providencia stuartii</i>	100.0	0.51	SCI 93		
011220	Good identification				011220
<i>Providencia stuartii</i>	98.91	0.42	SCI 93		
<i>Proteus vulgaris</i>	1.09	0.06	TRE 98		
011221	Very good identification				011221
<i>Providencia stuartii</i>	99.98	0.77	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.01	-.02			
<i>Proteus vulgaris</i>	0.01	-.01			
011223	Very good identification				011223
<i>Providencia stuartii</i>	100.0	0.57	SCI 93		
011231	Good identification				011231
<i>Providencia stuartii</i>	100.0	0.51	SCI 93		
011241	Good identification				011241
<i>Providencia stuartii</i>	95.10	0.36	SCI 93		
<i>Shigella dysenteriae</i> (group A)	4.91	0.09	SOR 1		
011261	Good identification				011261
<i>Providencia stuartii</i>	100.0	0.36	SCI 93		
011301	Good identification				011301
<i>Providencia stuartii</i>	100.0	0.36	SCI 93		
011321	Good identification				011321
<i>Providencia stuartii</i>	100.0	0.36	SCI 93		
011400	Very good identification				011400
<i>Providencia alcalifaciens</i>	99.90	0.65	SCI 98		
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.08	0.04			
<i>Shigella dysenteriae</i> (group A)	0.01	-.04			
011420	Good identification				011420
<i>Providencia alcalifaciens</i>	99.87	0.50	SCI 98		
<i>Proteus vulgaris</i>	0.13	0.06			
011601	Good identification				011601
<i>Providencia stuartii</i>	99.63	0.51	SCI 93		
<i>Providencia alcalifaciens</i>	0.38	-.11	ADO 5		
011602	Good identification				011602

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Providencia rettgeri</i>	98.88	0.39	URE 98		
<i>Providencia alcalifaciens</i>	0.70	-.11	SCI 95		
<i>Providencia stuartii</i>	0.42	-.04			
011621	Good identification				011621
<i>Providencia stuartii</i>	100.0	0.51	SCI 93		
012000	Identification to the genus				012000
<i>Shigella dysenteriae</i> (group A)	77.39	0.38	ESL 1		
<i>Shigella flexneri</i> (group B)	20.56	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	2.05	0.03			
012001	Good identification				012001
<i>Shigella dysenteriae</i> (group A)	92.14	0.57	ESL 1		
<i>Shigella flexneri</i> (group B)	5.52	0.33			
<i>Shigella boydii</i> (group C)	1.53	0.18			
012002	Identification to the genus				012002
<i>Shigella flexneri</i> (group B)	84.40	0.53	ESL 1		
<i>Shigella boydii</i> (group C)	14.30	0.34			
<i>Escherichia coli</i>	1.13	0.21			
012003	Low discrimination				012003
<i>Shigella flexneri</i> (group B)	59.90	0.59	ESL 1		
<i>Shigella boydii</i> (group C)	28.31	0.49			
<i>Escherichia coli</i>	7.52	0.47			
012023	Low discrimination				012023
<i>Escherichia coli</i>	84.91	0.43	SOR 88		
<i>Shigella flexneri</i> (group B)	10.25	0.18			
<i>Shigella boydii</i> (group C)	4.84	0.08			
012041	Low discrimination				012041
<i>Shigella dysenteriae</i> (group A)	82.29	0.50	ESL 1		
<i>Escherichia coli</i>	10.60	0.38			
<i>Shigella flexneri</i> (group B)	4.70	0.25			
012042	Low discrimination				012042
<i>Shigella flexneri</i> (group B)	64.36	0.45	ESL 1		
<i>Shigella boydii</i> (group C)	20.13	0.31			
<i>Escherichia coli</i>	15.51	0.38			
012043	Low discrimination				012043
<i>Escherichia coli</i>	54.32	0.65			
<i>Shigella flexneri</i> (group B)	24.09	0.51			
<i>Shigella boydii</i> (group C)	21.03	0.47			
012063	Very good identification				012063
<i>Escherichia coli</i>	96.01	0.61			
<i>Yersinia rohdei</i>	1.12	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.91	0.18			
012133	Good identification				012133

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	96.41	0.36	ONP 99		
<i>Pantoea agglomerans</i>	3.59	0.03	ADO 93		
012433	Acceptable identification				012433
<i>Leclercia adecarboxylata</i>	92.60	0.36	ONP 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	7.40	0.27	MAL 93		
012443	Low discrimination				012443
<i>Escherichia coli</i>	79.32	0.38	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	8.03	0.23			
<i>Shigella flexneri (group B)</i>	6.75	0.10			
012453	Good identification				012453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.88	0.45	IND 1		
<i>Escherichia coli</i>	1.70	0.04			
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	1.43	-.11			
012513	Very good identification				012513
<i>Leclercia adecarboxylata</i>	99.17	0.53	ONP 99		
<i>Escherichia fergusonii</i>	0.68	0.12			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.14	0.08			
012533	Very good identification				012533
<i>Leclercia adecarboxylata</i>	100.0	0.59	ONP 99		
012613	Good identification				012613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	IND 1		
012653	Identification to the genus				012653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	80.57	0.47	IND 1	1	
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	18.42	0.15		1	
<i>Serratia odorifera biovar 2</i>	1.01	0.00		99	
012753	Good identification				012753
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	99.29	0.42	IND 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.71	0.16			
012773	Good identification				012773
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	100.0	0.51	IND 1		
013020	Good identification				013020
<i>Proteus vulgaris</i>	100.0	0.47	H2S 95		
013021	Acceptable identification				013021
<i>Proteus vulgaris</i>	93.57	0.40	H2S 95		
<i>Providencia stuartii</i>	5.20	0.10	URE 95		
<i>Morganella morganii subsp. sibonii</i>	1.23	-.02			
013201	Good identification				013201
<i>Providencia stuartii</i>	100.0	0.36	ESL 1		
013221	Good identification				013221

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	99.05	0.36	ESL 1		
<i>Proteus vulgaris</i>	0.95	-.01	SCI 93		
014001	Low discrimination				014001
<i>Shigella dysenteriae</i> (group A)	72.10	0.57	SCI 1		
<i>Providencia stuartii</i>	22.05	0.47			
<i>Shigella flexneri</i> (group B)	4.32	0.33			
014002	Identification to the genus				014002
<i>Shigella flexneri</i> (group B)	84.94	0.53	SCI 1		
<i>Shigella boydii</i> (group C)	14.39	0.34			
<i>Providencia alcalifaciens</i>	0.50	-.04			
014003	Identification to the genus				014003
<i>Shigella flexneri</i> (group B)	65.70	0.59	SCI 1		
<i>Shigella boydii</i> (group C)	31.06	0.49			
<i>Providencia stuartii</i>	1.96	0.28			
014021	Good identification				014021
<i>Providencia stuartii</i>	96.80	0.47	PHE 95		
<i>Shigella dysenteriae</i> (group A)	3.20	0.16	INO 95		
014041	Identification to the genus				014041
<i>Shigella dysenteriae</i> (group A)	89.81	0.50	SCI 1		
<i>Shigella flexneri</i> (group B)	5.13	0.25			
<i>Shigella boydii</i> (group C)	2.63	0.16			
014042	Identification to the genus				014042
<i>Shigella flexneri</i> (group B)	74.08	0.45	SCI 1		
<i>Shigella boydii</i> (group C)	23.17	0.31			
<i>Citrobacter youngae</i>	0.76	0.11			
014043	Low discrimination				014043
<i>Shigella flexneri</i> (group B)	30.19	0.51	SCI 1		
<i>Shigella boydii</i> (group C)	26.36	0.47			
<i>Citrobacter youngae</i>	15.12	0.52			
014053	Low discrimination				014053
<i>Citrobacter braakii</i>	39.00	0.56	ORN 93		
<i>Citrobacter youngae</i>	21.32	0.50			
<i>Citrobacter amalonaticus</i>	18.98	0.33			
014063	Good identification				014063
<i>Citrobacter freundii</i>	93.52	0.73	ONP 88		
<i>Citrobacter youngae</i>	3.34	0.40			
<i>Escherichia coli</i>	1.53	0.32			
014073	Good identification				014073
<i>Citrobacter freundii</i>	93.59	0.70	ONP 88		
<i>Citrobacter youngae</i>	3.48	0.39			
<i>Citrobacter braakii</i>	1.80	0.33			

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
014163	Good identification					014163
<i>Citrobacter freundii</i>		97.88	0.51	ONP 88		
<i>Citrobacter youngae</i>		2.12	0.14	MAL 8		
014173	Good identification					014173
<i>Citrobacter freundii</i>		97.80	0.49	ONP 88		
<i>Citrobacter youngae</i>		2.20	0.12	MAL 8		
014200	Good identification					014200
<i>Providencia stuartii</i>		97.72	0.39	PHE 95		
<i>Providencia alcalifaciens</i>		1.36	-.11	TRE 98		
<i>Shigella dysenteriae</i> (group A)		0.93	-.04			
014201	Very good identification					014201
<i>Providencia stuartii</i>		99.83	0.74	PHE 95		
<i>Shigella dysenteriae</i> (group A)		0.17	0.16			
014203	Very good identification					014203
<i>Providencia stuartii</i>		97.44	0.54	PHE 95		
<i>Shigella flexneri</i> (group B)		1.74	0.18	MAN 10		
<i>Shigella boydii</i> (group C)		0.82	0.08			
014211	Good identification					014211
<i>Providencia stuartii</i>		100.0	0.47	PHE 95		
014220	Good identification					014220
<i>Providencia stuartii</i>		100.0	0.39	PHE 95		
014221	Very good identification					014221
<i>Providencia stuartii</i>		100.0	0.74	PHE 95		
014223	Very good identification					014223
<i>Providencia stuartii</i>		100.0	0.54	PHE 95		
014231	Good identification					014231
<i>Providencia stuartii</i>		100.0	0.47	PHE 95		
014400	Very good identification					014400
<i>Providencia alcalifaciens</i>		99.99	0.65	PHE 98		
<i>Shigella dysenteriae</i> (group A)		0.01	-.04			
014420	Good identification					014420
<i>Providencia alcalifaciens</i>		100.0	0.50	PHE 98		
014601	Good identification					014601
<i>Providencia stuartii</i>		99.47	0.47	PHE 95		
<i>Providencia alcalifaciens</i>		0.54	-.11	ADO 5		
014621	Good identification					014621
<i>Providencia stuartii</i>		100.0	0.47	PHE 95		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
015000	Very good identification					015000
<i>Providencia alcalifaciens</i>		98.43	0.65	ADO 98		
<i>Providencia stuartii</i>		1.46	0.39			
<i>Morganella morganii</i> subsp. <i>morganii</i>		0.08	0.04			
015001	Very good identification					015001
<i>Providencia stuartii</i>		96.84	0.74	INO 95		
<i>Providencia alcalifaciens</i>		2.72	0.30			
<i>Morganella morganii</i> subsp. <i>sibonii</i>		0.27	0.23			
015003	Very good identification					015003
<i>Providencia stuartii</i>		96.96	0.54	INO 95		
<i>Shigella flexneri</i> (group B)		1.73	0.18	MAN 10		
<i>Shigella boydii</i> (group C)		0.82	0.08			
015011	Good identification					015011
<i>Providencia stuartii</i>		99.47	0.47	INO 95		
<i>Providencia alcalifaciens</i>		0.54	-.11	CEL 5		
015020	Acceptable identification					015020
<i>Providencia alcalifaciens</i>		90.30	0.50	ADO 98		
<i>Providencia stuartii</i>		7.60	0.39			
<i>Proteus vulgaris</i>		2.10	0.32			
015021	Very good identification					015021
<i>Providencia stuartii</i>		99.25	0.74	INO 95		
<i>Providencia alcalifaciens</i>		0.49	0.15			
<i>Proteus vulgaris</i>		0.24	0.24			
015023	Very good identification					015023
<i>Providencia stuartii</i>		100.0	0.54	INO 95		
015031	Good identification					015031
<i>Providencia stuartii</i>		100.0	0.47	INO 95		
015200	Very good identification					015200
<i>Providencia stuartii</i>		96.55	0.65	TRE 98		
<i>Providencia alcalifaciens</i>		3.46	0.24			
015201	Excellent identification					015201
<i>Providencia stuartii</i>		100.0	1.00			
<i>Providencia alcalifaciens</i>		0.00	-.11			
015202	Identification to the genus					015202
<i>Providencia stuartii</i>		84.36	0.46	TRE 98		
<i>Providencia rettgeri</i>		15.08	0.24	MAN 10		
<i>Providencia alcalifaciens</i>		0.55	-.11			
015203	Very good identification					015203
<i>Providencia stuartii</i>		100.0	0.80	MAN 10		
015210	Good identification					015210

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	99.32	0.39	CEL 5		
<i>Providencia alcalifaciens</i>	0.68	-1.17	TRE 98		
015211	Very good identification				015211
<i>Providencia stuartii</i>	100.0	0.74	CEL 5		
015213	Very good identification				015213
<i>Providencia stuartii</i>	100.0	0.54	CEL 5		
015220	Very good identification				015220
<i>Providencia stuartii</i>	99.37	0.65	TRE 98		
<i>Providencia alcalifaciens</i>	0.63	0.09			
015221	Excellent identification				015221
<i>Providencia stuartii</i>	100.0	1.00			
015222	Good identification				015222
<i>Providencia stuartii</i>	96.94	0.46	TRE 98		
<i>Providencia rettgeri</i>	3.06	0.09	MAN 10		
015223	Very good identification				015223
<i>Providencia stuartii</i>	100.0	0.80	MAN 10		
015230	Good identification				015230
<i>Providencia stuartii</i>	100.0	0.39	CEL 5		
015231	Very good identification				015231
<i>Providencia stuartii</i>	100.0	0.74	CEL 5		
015233	Very good identification				015233
<i>Providencia stuartii</i>	100.0	0.54	CEL 5		
015241	Very good identification				015241
<i>Providencia stuartii</i>	100.0	0.59	SOR 1		
015243	Good identification				015243
<i>Providencia stuartii</i>	100.0	0.39	SOR 1		
015261	Very good identification				015261
<i>Providencia stuartii</i>	100.0	0.59	SOR 1		
015263	Good identification				015263
<i>Providencia stuartii</i>	100.0	0.39	SOR 1		
015301	Very good identification				015301
<i>Providencia stuartii</i>	100.0	0.59	MAL 1		
015303	Good identification				015303
<i>Providencia stuartii</i>	100.0	0.39	MAL 1		
015321	Very good identification				015321

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>		100.0	0.59	MAL 1		
015323	Good identification					015323
<i>Providencia stuartii</i>		100.0	0.39	MAL 1		
015400	Excellent identification					015400
<i>Providencia alcalifaciens</i>		100.0	1.00			
<i>Providencia stuartii</i>		0.00	0.13			
<i>Providencia rettgeri</i>		0.00	0.05			
015401	Very good identification					015401
<i>Providencia alcalifaciens</i>		96.31	0.65	TRE 2		
<i>Providencia stuartii</i>		3.69	0.47			
015402	Good identification					015402
<i>Providencia alcalifaciens</i>		94.19	0.65	MAN 2		
<i>Providencia rettgeri</i>		5.81	0.46			
015410	Very good identification					015410
<i>Providencia alcalifaciens</i>		100.0	0.59	CEL 1		
015420	Very good identification					015420
<i>Providencia alcalifaciens</i>		99.99	0.85			
<i>Providencia stuartii</i>		0.01	0.13			
<i>Providencia rettgeri</i>		0.00	-.11			
015421	Identification to the genus					015421
<i>Providencia alcalifaciens</i>		82.16	0.50	TRE 2		
<i>Providencia stuartii</i>		17.84	0.47			
015422	Acceptable identification					015422
<i>Providencia alcalifaciens</i>		94.19	0.50	MAN 2		
<i>Providencia rettgeri</i>		5.81	0.30			
015430	Good identification					015430
<i>Providencia alcalifaciens</i>		100.0	0.43	CEL 1		
015440	Very good identification					015440
<i>Providencia alcalifaciens</i>		100.0	0.59	SOR 1		
015460	Good identification					015460
<i>Providencia alcalifaciens</i>		100.0	0.43	SOR 1		
015500	Very good identification					015500
<i>Providencia alcalifaciens</i>		100.0	0.59	MAL 1		
015520	Good identification					015520
<i>Providencia alcalifaciens</i>		100.0	0.43	MAL 1		
015600	Very good identification					015600
<i>Providencia alcalifaciens</i>		96.03	0.59	INO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	2.88	0.39			
<i>Providencia rettgeri</i>	1.09	0.24			
015601	Very good identification				015601
<i>Providencia stuartii</i>	98.63	0.74	ADO 5		
<i>Providencia alcalifaciens</i>	1.37	0.24			
015602	Very good identification				015602
<i>Providencia rettgeri</i>	97.93	0.65	URE 98		
<i>Providencia alcalifaciens</i>	1.78	0.24			
<i>Providencia stuartii</i>	0.29	0.19			
015603	Good identification				015603
<i>Providencia stuartii</i>	93.29	0.54	ADO 5		
<i>Providencia rettgeri</i>	6.47	0.24	MAN 10		
<i>Providencia alcalifaciens</i>	0.24	-.11			
015611	Good identification				015611
<i>Providencia stuartii</i>	99.73	0.47	ADO 5		
<i>Providencia alcalifaciens</i>	0.27	-.17	CEL 5		
015620	Identification to the genus				015620
<i>Providencia alcalifaciens</i>	84.64	0.43	INO 1		
<i>Providencia stuartii</i>	14.40	0.39			
<i>Providencia rettgeri</i>	0.96	0.09			
015621	Very good identification				015621
<i>Providencia stuartii</i>	99.76	0.74	ADO 5		
<i>Providencia alcalifaciens</i>	0.24	0.09			
015622	Good identification				015622
<i>Providencia rettgeri</i>	96.61	0.50	URE 98		
<i>Providencia alcalifaciens</i>	1.76	0.09			
<i>Providencia stuartii</i>	1.63	0.19			
015623	Very good identification				015623
<i>Providencia stuartii</i>	98.79	0.54	ADO 5		
<i>Providencia rettgeri</i>	1.21	0.09	MAN 10		
015631	Good identification				015631
<i>Providencia stuartii</i>	100.0	0.47	ADO 5		
016453	Good identification				016453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.37	IND 1		
016653	Low discrimination				016653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	51.31	0.39	IND 1	1	
<i>Serratia odorifera biovar 2</i>	48.69	0.31		99	
017201	Very good identification				017201
<i>Providencia stuartii</i>	100.0	0.59	ESL 1		
017203	Good identification				017203

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	100.0	0.39	ESL 1		
017221	Very good identification				017221
<i>Providencia stuartii</i>	100.0	0.59	ESL 1		
017223	Good identification				017223
<i>Providencia stuartii</i>	100.0	0.39	ESL 1		
017400	Very good identification				017400
<i>Providencia alcalifaciens</i>	99.93	0.59	ESL 1		
<i>Providencia rettgeri</i>	0.07	-.01			
017402	Identification to the genus				017402
<i>Providencia rettgeri</i>	76.68	0.40	URE 98		
<i>Providencia alcalifaciens</i>	23.32	0.24	INO 90		
017420	Good identification				017420
<i>Providencia alcalifaciens</i>	100.0	0.43	ESL 1		
017602	Very good identification				017602
<i>Providencia rettgeri</i>	99.97	0.60	URE 98		
<i>Providencia alcalifaciens</i>	0.03	-.17			
017622	Good identification				017622
<i>Providencia rettgeri</i>	100.0	0.44	URE 98		
020000	Low discrimination				020000
<i>Shigella dysenteriae</i> (group A)	57.36	0.39	ORN 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	14.71	0.19	TRE 90		
<i>Shigella flexneri</i> (group B)	12.47	0.26			
020001	Low discrimination				020001
<i>Shigella dysenteriae</i> (group A)	55.06	0.59	ORN 1		
<i>Shigella sonnei</i>	20.71	0.39			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	9.77	0.46			
020002	Low discrimination				020002
<i>Salmonella enterica</i> subsp. <i>enterica</i>	37.91	0.54	LYS 95		
<i>Shigella flexneri</i> (group B)	22.96	0.53	SOR 90		
<i>Shigella sonnei</i>	18.82	0.39			
020003	Low discrimination				020003
<i>Shigella sonnei</i>	66.08	0.80	ONP 90		
<i>Salmonella</i> serovar <i>paratyphi</i>	29.42	0.74			
<i>Shigella boydii</i> (group C)	2.34	0.59			
020013	Low discrimination				020013
<i>Shigella sonnei</i>	63.14	0.54	ONP 90		
<i>Salmonella</i> serovar <i>paratyphi</i>	28.11	0.47	CEL 5		
<i>Yersinia kristensenii</i>	5.07	0.41			
020023	Low discrimination				020023

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella sonnei</i>	44.66	0.39	ONP 90		
<i>Yersinia rohdei</i>	26.16	0.49	SUC 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	19.88	0.33			
020033	Low discrimination				020033
<i>Yersinia rohdei</i>	52.71	0.39	SOR 99		
<i>Escherichia hermannii</i>	14.72	0.22			
<i>Shigella sonnei</i>	14.21	0.13			
020040	Low discrimination				020040
<i>Salmonella enterica</i> subsp. <i>enterica</i>	59.19	0.39	LYS 95		
<i>Shigella dysenteriae</i> (group A)	20.26	0.32	MAN 98		
<i>Salmonella</i> serovar <i>paratyphi</i>	13.67	0.18			
020041	Low discrimination				020041
<i>Salmonella</i> serovar <i>paratyphi</i>	85.86	0.59	MAN 99		
<i>Shigella dysenteriae</i> (group A)	11.57	0.51			
<i>Shigella boydii</i> (group C)	0.83	0.25			
020042	Identification to the genus				020042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	65.53	0.74	LYS 95		
<i>Salmonella</i> serovar <i>paratyphi</i>	30.58	0.59			
<i>Shigella flexneri</i> (group B)	1.80	0.45			
020043	Very good identification				020043
<i>Salmonella</i> serovar <i>paratyphi</i>	98.68	1.00			
<i>Citrobacter braakii</i>	0.40	0.70			
<i>Shigella boydii</i> (group C)	0.31	0.56			
020053	Low discrimination				020053
<i>Salmonella</i> serovar <i>paratyphi</i>	47.48	0.74	CEL 5		
<i>Yersinia kristensenii</i>	44.61	0.82			
<i>Citrobacter braakii</i>	7.35	0.76			
020061	Low discrimination				020061
<i>Yersinia rohdei</i>	80.01	0.49	MAN 99		
<i>Salmonella</i> serovar <i>paratyphi</i>	11.67	0.18			
<i>Escherichia coli</i>	4.12	0.26			
020062	Low discrimination				020062
<i>Yersinia rohdei</i>	64.12	0.49	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	20.05	0.33			
<i>Salmonella</i> serovar <i>paratyphi</i>	9.35	0.18			
020063	Low discrimination				020063
<i>Yersinia rohdei</i>	85.05	0.90			
<i>Salmonella</i> serovar <i>paratyphi</i>	12.41	0.59			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.20	0.54			
020071	Low discrimination				020071
<i>Yersinia rohdei</i>	75.29	0.39	MAN 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	19.35	0.29			
<i>Citrobacter braakii</i>	2.00	0.12			
020072	Low discrimination				020072
<i>Yersinia rohdei</i>	74.76	0.39	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	19.21	0.29			
<i>Citrobacter braakii</i>	1.99	0.12			
020073	Low discrimination				020073
<i>Yersinia rohdei</i>	83.11	0.80			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.57	0.64			
<i>Citrobacter braakii</i>	2.21	0.53			
020103	Low discrimination				020103
<i>Shigella sonnei</i>	49.14	0.39	ONP 90		
<i>Hafnia alvei</i>	26.01	0.59	MAL 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	21.88	0.33			
020113	Low discrimination				020113
<i>Hafnia alvei</i>	50.20	0.43	LYS 99		
<i>Shigella sonnei</i>	28.29	0.13			
<i>Salmonella</i> serovar <i>paratyphi</i>	12.59	0.06			
020123	Low discrimination				020123
<i>Hafnia alvei</i>	74.14	0.39	LYS 99		
<i>Shigella sonnei</i>	12.73	-.02	SUC 10		
<i>Yersinia rohdei</i>	7.46	0.08			
020143	Very good identification				020143
<i>Salmonella</i> serovar <i>paratyphi</i>	98.63	0.59	MAL 1		
<i>Citrobacter braakii</i>	0.40	0.29			
<i>Shigella boydii</i> (group C)	0.31	0.15			
020163	Low discrimination				020163
<i>Yersinia rohdei</i>	85.16	0.49	MAL 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	12.42	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.20	0.13			
020173	Low discrimination				020173
				VPT	
<i>Yersinia rohdei</i>	78.51	0.39	MAL 1	1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.99	0.23		2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	4.80	0.12		99	
020203	Low discrimination				020203
<i>Shigella sonnei</i>	66.18	0.39	ONP 90		
<i>Salmonella</i> serovar <i>paratyphi</i>	29.46	0.33	INO 1		
<i>Shigella boydii</i> (group C)	2.35	0.18			
020243	Very good identification				020243
<i>Salmonella</i> serovar <i>paratyphi</i>	97.51	0.59	INO 1		
<i>Yersinia kristensenii</i>	0.85	0.25			
<i>Citrobacter braakii</i>	0.39	0.29			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
020253	Good identification				020253
<i>Yersinia kristensenii</i>	92.70	0.66			
<i>Salmonella</i> serovar <i>paratyphi</i>	5.65	0.33			
<i>Citrobacter braakii</i>	0.87	0.35			
020263	Low discrimination				020263
<i>Yersinia rohdei</i>	56.83	0.49	INO 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	34.08	0.47			
<i>Salmonella</i> serovar <i>paratyphi</i>	8.29	0.18			
020273	Identification to the genus				020273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	78.92	0.56	ONP 95		
<i>Yersinia rohdei</i>	14.62	0.39			
<i>Yersinia kristensenii</i>	5.53	0.25			
020403	Low discrimination				020403
<i>Shigella sonnei</i>	65.59	0.39	ONP 90		
<i>Salmonella</i> serovar <i>paratyphi</i>	29.19	0.33	ADO 1		
<i>Shigella boydii</i> (group C)	2.33	0.18			
020413	Low discrimination				020413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	30.83	0.37	ORN 3		
<i>Shigella sonnei</i>	28.18	0.13			
<i>Escherichia fergusonii</i>	26.19	0.25			
020443	Very good identification				020443
<i>Salmonella</i> serovar <i>paratyphi</i>	98.17	0.59	ADO 1		
<i>Escherichia coli</i>	0.53	0.30			
<i>Citrobacter braakii</i>	0.39	0.29			
020463	Low discrimination				020463
<i>Yersinia rohdei</i>	81.98	0.49	ADO 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	11.96	0.18			
<i>Escherichia coli</i>	4.22	0.26			
020473	Low discrimination				020473
<i>Yersinia rohdei</i>	70.97	0.39	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	9.72	0.30			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.03	0.23			
020613	Good identification				020613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.39	ORN 3		
020653	Low discrimination				020653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	43.56	0.44	ORN 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	30.36	0.23			
<i>Yersinia kristensenii</i>	24.59	0.25			
020753	Good identification				020753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.77	0.49	ORN 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.23	0.13			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
020773	Very good identification				020773
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	100.0	0.59	ORN 1		
021000	Good identification				021000
<i>Morganella morganii subsp. morganii</i>	95.44	0.45	IND 95		
<i>Morganella morganii subsp. sibonii</i>	4.20	0.28	URE 96		
<i>Shigella dysenteriae (group A)</i>	0.20	-.02			
021001	Very good identification				021001
<i>Morganella morganii subsp. sibonii</i>	97.21	0.69	URE 97		
<i>Proteus mirabilis</i>	1.92	0.25			
<i>Shigella dysenteriae (group A)</i>	0.42	0.18			
021003	Low discrimination				021003
<i>Shigella sonnei</i>	63.52	0.39	ONP 90		
<i>Salmonella serovar paratyphi</i>	28.28	0.33	PHE 1		
<i>Morganella morganii subsp. sibonii</i>	4.02	0.28			
021021	Low discrimination				021021
<i>Morganella morganii subsp. sibonii</i>	85.94	0.44	URE 97		
<i>Proteus penneri</i>	8.98	0.18	SUC 6		
<i>Proteus mirabilis</i>	4.70	0.09			
021043	Very good identification				021043
<i>Salmonella serovar paratyphi</i>	98.69	0.59	PHE 1		
<i>Citrobacter braakii</i>	0.40	0.29			
<i>Shigella boydii (group C)</i>	0.31	0.15			
021063	Low discrimination				021063
<i>Yersinia rohdei</i>	85.16	0.49	PHE 1		
<i>Salmonella serovar paratyphi</i>	12.42	0.18			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.20	0.13			
021073	Low discrimination				021073
<i>Yersinia rohdei</i>	83.44	0.39	PHE 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	10.61	0.23			
<i>Citrobacter braakii</i>	2.22	0.12			
022003	Low discrimination				022003
<i>Shigella sonnei</i>	57.20	0.39	ONP 90		
<i>Salmonella serovar paratyphi</i>	25.46	0.33	ESL 1		
<i>Yersinia pseudotuberculosis</i>	8.84	0.25			
022043	Very good identification				022043
<i>Salmonella serovar paratyphi</i>	96.22	0.59	ESL 1		
<i>Escherichia coli</i>	2.44	0.44			
<i>Citrobacter braakii</i>	0.39	0.29			
022063	Low discrimination				022063
<i>Yersinia rohdei</i>	53.73	0.49	ESL 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	25.06	0.44			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	13.14	0.40			
022073	Identification to the genus				022073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	79.19	0.54	ONP 95		
<i>Yersinia rohdei</i>	18.87	0.39			
<i>Citrobacter braakii</i>	0.50	0.12			
022103	Low discrimination				022103
<i>Hafnia alvei</i>	80.11	0.39	LYS 99		
<i>Shigella sonnei</i>	13.76	-.02	ESL 10		
<i>Salmonella</i> serovar <i>paratyphi</i>	6.13	-.09			
022263	Acceptable identification				022263
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	92.32	0.37	ONP 95	2	
<i>Yersinia rohdei</i>	4.67	0.08		1	
<i>Serratia marcescens</i>	3.01	-.02		98	
022273	Good identification				022273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.32	0.47	ONP 95		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.13	0.13			
<i>Yersinia rohdei</i>	0.55	-.02			
022413	Low discrimination				022413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	84.68	0.49	ORN 3		
<i>Escherichia fergusonii</i>	15.32	0.23			
022433	Good identification				022433
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	ORN 3		
022453	Very good identification				022453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.54	0.55	ORN 3		
<i>Salmonella</i> serovar <i>paratyphi</i>	1.03	-.09			
<i>Yersinia kristensenii</i>	0.96	-.01			
022473	Low discrimination				022473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	86.69	0.42	ORN 3		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.71	0.13			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	5.00	-.01			
022613	Good identification				022613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.51	ORN 3		
022633	Good identification				022633
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.39	ORN 3		
022653	Good identification				022653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.05	0.57	ORN 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	6.95	0.15			
022673	Identification to the genus				022673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	52.00	0.44	ORN 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	46.59	0.25			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.41	0.05			
022753	Good identification				022753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	97.87	0.42	ORN 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.13	0.26			
022773	Good identification				022773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.40	0.51	ORN 1	1	
<i>Enterobacter aerogenes</i>	0.42	-.02		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.18	0.13		1	
024002	Acceptable identification				024002
<i>Salmonella enterica</i> subsp. <i>enterica</i>	94.57	0.44	LYS 95		
<i>Shigella flexneri</i> (group B)	1.74	0.12	SOR 90		
<i>Shigella sonnei</i>	1.42	-.02			
024003	Low discrimination				024003
<i>Shigella sonnei</i>	46.01	0.39	ONP 90		
<i>Hafnia alvei</i>	24.35	0.59	SCI 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	20.48	0.33			
024013	Low discrimination				024013
<i>Citrobacter braakii</i>	49.55	0.45	SOR 99		
<i>Hafnia alvei</i>	22.40	0.43			
<i>Shigella sonnei</i>	12.62	0.13			
024023	Low discrimination				024023
<i>Hafnia alvei</i>	67.61	0.39	LYS 99		
<i>Shigella sonnei</i>	11.61	-.02	SUC 10		
<i>Citrobacter braakii</i>	8.81	0.15			
024041	Low discrimination				024041
<i>Citrobacter braakii</i>	49.76	0.38	MAN 99		
<i>Salmonella</i> serovar <i>paratyphi</i>	41.77	0.18			
<i>Shigella dysenteriae</i> (group A)	5.63	0.10			
024042	Very good identification				024042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	96.75	0.64	LYS 95		
<i>Citrobacter braakii</i>	1.63	0.38			
<i>Salmonella</i> serovar <i>paratyphi</i>	1.37	0.18			
024043	Low discrimination				024043
<i>Citrobacter braakii</i>	51.90	0.80			
<i>Salmonella</i> serovar <i>paratyphi</i>	43.57	0.59			
<i>Salmonella</i> serovar <i>enteritidis</i>	2.96	0.39			
024051	Acceptable identification				024051
<i>Citrobacter braakii</i>	94.32	0.45	MAN 99		
<i>Salmonella</i> serovar <i>paratyphi</i>	2.05	-.09			
<i>Yersinia kristensenii</i>	1.93	-.01			
024052	Low discrimination				024052

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	73.77	0.45	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	21.79	0.23			
<i>Salmonella serovar paratyphi</i>	1.61	-0.09			
024053	Good identification				024053
<i>Citrobacter braakii</i>	93.57	0.86			
<i>Salmonella serovar paratyphi</i>	2.04	0.33			
<i>Yersinia kristensenii</i>	1.91	0.41			
024063	Low discrimination				024063
<i>Citrobacter braakii</i>	48.69	0.56	SUC 7		
<i>Yersinia rohdei</i>	37.61	0.49			
<i>Salmonella serovar paratyphi</i>	5.49	0.18			
024073	Low discrimination				024073
				VPT	
<i>Citrobacter braakii</i>	67.76	0.63	SUC 7	1	
<i>Enterobacter cloacae subsp. cloacae</i>	17.35	0.44		99	
<i>Yersinia rohdei</i>	8.59	0.39		1	
024103	Very good identification				024103
<i>Hafnia alvei</i>	97.32	0.59	LYS 99		
<i>Shigella sonnei</i>	1.86	-0.02			
<i>Salmonella serovar paratyphi</i>	0.83	-0.09			
024113	Good identification				024113
				VPT	
<i>Hafnia alvei</i>	95.88	0.43	LYS 99	85	
<i>Citrobacter braakii</i>	2.14	0.04		1	
<i>Enterobacter cloacae subsp. cloacae</i>	1.98	-0.04		99	
024123	Good identification				024123
<i>Hafnia alvei</i>	100.0	0.39	LYS 99		
024143	Low discrimination				024143
<i>Citrobacter braakii</i>	36.06	0.38	MAL 1		
<i>Salmonella serovar paratyphi</i>	30.27	0.18			
<i>Salmonella enterica subsp. salamae</i>	25.32	0.18			
024153	Low discrimination				024153
				VPT	
<i>Citrobacter braakii</i>	75.88	0.45	MAL 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	13.43	0.22		99	
<i>Citrobacter sedlakii</i>	4.71	0.04		1	
024173	Very good identification				024173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	98.11	0.53	ONP 99	99	
<i>Citrobacter braakii</i>	1.29	0.22		1	
<i>Citrobacter freundii</i>	0.44	0.14		1	
024253	Low discrimination				024253
<i>Citrobacter braakii</i>	66.09	0.45	INO 1		
<i>Yersinia kristensenii</i>	23.61	0.25			
<i>Salmonella serovar enteritidis</i>	5.21	0.07			
024373	Good identification				024373

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.38	ONP 99		
024443	Low discrimination				024443
<i>Citrobacter braakii</i>	50.98	0.38	ADO 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	42.80	0.18			
<i>Salmonella</i> serovar <i>enteritidis</i>	2.91	-.02			
024453	Low discrimination				024453
<i>Citrobacter braakii</i>	76.08	0.45	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	16.88	0.35			
<i>Salmonella</i> serovar <i>paratyphi</i>	1.66	-.09			
024573	Good identification				024573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.23	0.44	ONP 99	99	
<i>Citrobacter koseri</i>	4.11	0.14		1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.67	-.09		1	
024653	Good identification				024653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.41	0.37	ORN 3		
<i>Citrobacter braakii</i>	3.59	0.04			
025043	Low discrimination				025043
<i>Citrobacter braakii</i>	52.73	0.38	PHE 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	44.27	0.18			
<i>Salmonella</i> serovar <i>enteritidis</i>	3.01	-.02			
025053	Acceptable identification				025053
<i>Citrobacter braakii</i>	94.32	0.45	PHE 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	2.05	-.09			
<i>Yersinia kristensenii</i>	1.93	-.01			
026003	Low discrimination				026003
<i>Hafnia alvei</i>	80.11	0.39	LYS 99		
<i>Shigella sonnei</i>	13.76	-.02	ESL 10		
<i>Salmonella</i> serovar <i>paratyphi</i>	6.13	-.09			
026033	Good identification				026033
<i>Cronobacter sakazakii</i>	99.04	0.49	ONP 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.96	0.10			
026043	Low discrimination				026043
<i>Citrobacter braakii</i>	45.38	0.38	ESL 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	38.09	0.18			
<i>Salmonella</i> serovar <i>enteritidis</i>	13.48	0.13			
026053	Low discrimination				026053
<i>Citrobacter braakii</i>	77.51	0.45	ESL 1		
<i>Citrobacter amalonaticus</i>	13.69	0.12			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.13	0.16			
026073	Low discrimination				026073

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	65.48	0.36	ONP 99	99	
<i>Serratia ficaria</i>	18.74	0.16		75	
<i>Citrobacter braakii</i>	6.03	0.22		1	
026103	Good identification				026103
<i>Hafnia alvei</i>	100.0	0.39	LYS 99		
026133	Low discrimination				026133
<i>Cronobacter sakazakii</i>	72.55	0.36	ONP 99		
<i>Pantoea agglomerans</i>	12.63	0.16			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	9.59	0.20			
026173	Good identification				026173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.74	0.46	ONP 99	99	
<i>Kluyvera ascorbata</i>	1.87	0.02		1	
<i>Cronobacter sakazakii</i>	0.39	-.06		99	
026233	Very good identification				026233
<i>Cronobacter sakazakii</i>	100.0	0.59	ONP 99		
026333	Good identification				026333
<i>Cronobacter sakazakii</i>	99.23	0.45	ONP 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.77	0.04			
026413	Acceptable identification				026413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.04	0.42	ORN 3		
<i>Escherichia fergusonii</i>	7.96	0.09			
026453	Good identification				026453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.96	0.47	ORN 3	1	
<i>Citrobacter braakii</i>	1.12	0.04		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.93	-.05		99	
026573	Acceptable identification				026573
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.68	0.36	ONP 99		
<i>Enterobacter aerogenes</i>	5.32	-.02			
026613	Good identification				026613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	ORN 3		
026653	Good identification				026653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.49	ORN 3		
026673	Low discrimination				026673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.92	0.37	ORN 3	1	
<i>Serratia odorifera</i> biovar 1	19.59	0.14		50	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	9.74	0.11		99	
027033	Good identification				027033
<i>Cronobacter sakazakii</i>	100.0	0.49	ONP 99		
027133	Good identification				027133

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Cronobacter sakazakii</i>	98.31	0.36	ONP 99		
<i>Pantoea agglomerans</i>	1.69	-.05			
027233	Very good identification				027233
<i>Cronobacter sakazakii</i>	100.0	0.59	ONP 99		
027333	Good identification				027333
<i>Cronobacter sakazakii</i>	100.0	0.45	ONP 99		
030000	Low discrimination				030000
<i>Morganella morganii</i> subsp. <i>morganii</i>	77.11	0.45	URE 96		
<i>Shigella dysenteriae</i> (group A)	12.95	0.38	PHE 95		
<i>Edwardsiella tarda</i>	5.70	0.18			
030001	Low discrimination				030001
<i>Shigella dysenteriae</i> (group A)	74.61	0.57	ORN 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	16.17	0.46			
<i>Shigella flexneri</i> (group B)	4.47	0.33			
030002	Low discrimination				030002
<i>Shigella flexneri</i> (group B)	78.63	0.53	ORN 1		
<i>Shigella boydii</i> (group C)	13.32	0.34			
<i>Escherichia coli</i>	4.57	0.34			
030003	Low discrimination				030003
<i>Shigella flexneri</i> (group B)	36.94	0.59	ORN 1		
<i>Escherichia coli</i>	20.10	0.60			
<i>Shigella boydii</i> (group C)	17.46	0.49			
030013	Good identification				030013
<i>Escherichia hermannii</i>	92.51	0.65	ONP 98		
<i>Escherichia fergusonii</i>	2.53	0.36			
<i>Yersinia kristensenii</i>	2.51	0.33			
030023	Low discrimination				030023
<i>Escherichia coli</i>	79.44	0.56	SOR 88		
<i>Escherichia hermannii</i>	14.76	0.32			
<i>Shigella flexneri</i> (group B)	2.21	0.18			
030033	Very good identification				030033
<i>Escherichia hermannii</i>	98.06	0.63	ONP 98		
<i>Citrobacter farmeri</i>	1.01	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.45	0.23			
030041	Low discrimination				030041
<i>Shigella dysenteriae</i> (group A)	56.79	0.50	ORN 1		
<i>Escherichia coli</i>	31.69	0.52			
<i>Salmonella</i> serovar <i>paratyphi</i>	5.20	0.18			
030042	Low discrimination				030042
<i>Escherichia coli</i>	35.60	0.52	TRE 95		
<i>Shigella flexneri</i> (group B)	34.10	0.45			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>enterica</i>	12.53	0.33			
030043	Low discrimination				030043
<i>Escherichia coli</i>	44.61	0.78			
<i>Salmonella</i> serovar <i>paratyphi</i>	38.17	0.59			
<i>Citrobacter braakii</i>	7.47	0.63			
030053	Low discrimination				030053
<i>Yersinia kristensenii</i>	80.34	0.74			
<i>Citrobacter braakii</i>	15.21	0.70			
<i>Salmonella</i> serovar <i>paratyphi</i>	2.02	0.33			
030061	Acceptable identification				030061
<i>Escherichia coli</i>	91.54	0.48	MAN 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.42	0.19			
<i>Shigella dysenteriae</i> (group A)	2.49	0.09			
030062	Acceptable identification				030062
<i>Escherichia coli</i>	92.16	0.48	TRE 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.44	0.19			
<i>Yersinia rohdei</i>	1.57	0.08			
030063	Low discrimination				030063
<i>Escherichia coli</i>	79.48	0.74			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.89	0.54			
<i>Yersinia rohdei</i>	7.07	0.49			
030073	Low discrimination				030073
<i>Citrobacter farmeri</i>	62.62	0.59	ONP 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	27.93	0.64			
<i>Citrobacter braakii</i>	2.87	0.47			
030143	Low discrimination				030143
<i>Escherichia coli</i>	44.78	0.37	MAL 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	38.32	0.18			
<i>Citrobacter braakii</i>	7.50	0.22			
030243	Low discrimination				030243
<i>Escherichia coli</i>	36.81	0.37	INO 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	31.50	0.18			
<i>Yersinia kristensenii</i>	11.66	0.18			
030253	Very good identification				030253
<i>Yersinia kristensenii</i>	97.03	0.59			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.72	0.30			
<i>Citrobacter braakii</i>	1.05	0.29			
030263	Low discrimination				030263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	82.90	0.47	ONP 95		
<i>Escherichia coli</i>	15.71	0.33			
<i>Yersinia rohdei</i>	1.40	0.08			
030273	Good identification				030273

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	91.98	0.56	ONP 95		
<i>Citrobacter farmeri</i>	4.86	0.18			
<i>Yersinia kristensenii</i>	2.76	0.18			
030413	Very good identification				030413
<i>Escherichia fergusonii</i>	97.23	0.60	LYS 95		
<i>Escherichia hermannii</i>	2.70	0.24			
<i>Yersinia kristensenii</i>	0.07	-.08			
030443	Low discrimination				030443
<i>Escherichia coli</i>	80.87	0.52	ADO 5		
<i>Salmonella</i> serovar <i>paratyphi</i>	13.28	0.18			
<i>Citrobacter braakii</i>	2.60	0.22			
030463	Good identification				030463
<i>Escherichia coli</i>	96.07	0.48	ADO 5		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.29	0.13			
<i>Yersinia rohdei</i>	1.64	0.08			
030513	Very good identification				030513
<i>Escherichia fergusonii</i>	100.0	0.54	LYS 95		
031000	Very good identification				031000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.75	0.72	URE 96		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.23	0.28			
<i>Shigella dysenteriae</i> (group A)	0.01	-.04			
031001	Very good identification				031001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	95.28	0.69	URE 97		
<i>Morganella morganii</i> subsp. <i>morganii</i>	4.20	0.31			
<i>Shigella dysenteriae</i> (group A)	0.33	0.16			
031021	Good identification				031021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.58	0.44	URE 97		
<i>Providencia stuartii</i>	2.32	0.10	SUC 6		
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.67	-.11			
031043	Low discrimination				031043
<i>Escherichia coli</i>	44.78	0.37	PHE 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	38.32	0.18			
<i>Citrobacter braakii</i>	7.50	0.22			
031201	Low discrimination				031201
<i>Providencia stuartii</i>	73.43	0.36	ORN 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	25.45	0.28	SCI 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	1.12	-.11			
031221	Good identification				031221
<i>Providencia stuartii</i>	97.84	0.36	ORN 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2.16	0.03	SCI 93		
032003	Low discrimination				032003

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	63.28	0.48	SOR 88		
<i>Escherichia hermannii</i>	25.54	0.31			
<i>Shigella flexneri</i> (group B)	4.70	0.18			
032013	Very good identification				032013
<i>Escherichia hermannii</i>	96.44	0.62	ONP 98		
<i>Escherichia fergusonii</i>	3.37	0.35			
<i>Escherichia coli</i>	0.15	0.13			
032023	Identification to the genus				032023
<i>Escherichia coli</i>	66.33	0.44	SOR 88		
<i>Escherichia hermannii</i>	32.86	0.29			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.82	0.03			
032033	Very good identification				032033
<i>Escherichia hermannii</i>	99.64	0.60	ONP 98		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.23	0.13			
<i>Escherichia coli</i>	0.13	0.09			
032041	Acceptable identification				032041
<i>Escherichia coli</i>	93.25	0.39	MAN 95		
<i>Shigella dysenteriae</i> (group A)	6.75	0.09			
032042	Acceptable identification				032042
<i>Escherichia coli</i>	94.97	0.39	TRE 95		
<i>Shigella flexneri</i> (group B)	3.68	0.04			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	1.35	-.09			
032043	Good identification				032043
<i>Escherichia coli</i>	94.73	0.65			
<i>Salmonella</i> serovar <i>paratyphi</i>	3.28	0.18			
<i>Citrobacter braakii</i>	0.64	0.22			
032061	Acceptable identification				032061
<i>Escherichia coli</i>	93.96	0.35	MAN 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.04	0.09			
032062	Acceptable identification				032062
<i>Escherichia coli</i>	93.96	0.35	TRE 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.04	0.09			
032063	Low discrimination				032063
<i>Escherichia coli</i>	85.51	0.62			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.18	0.44			
<i>Yersinia rohdei</i>	0.31	0.08			
032073	Low discrimination				032073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	86.13	0.54	ONP 95		
<i>Citrobacter farmeri</i>	5.85	0.18			
<i>Escherichia hermannii</i>	3.82	0.19			
032263	Low discrimination				032263

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	87.56	0.37	ONP 95		
<i>Escherichia coli</i>	12.44	0.21			
032273	Good identification				032273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.47	ONP 95		
032413	Very good identification				032413
<i>Escherichia fergusonii</i>	97.76	0.58	LYS 95		
<i>Escherichia hermannii</i>	2.13	0.21			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.11	0.08			
032443	Good identification				032443
<i>Escherichia coli</i>	100.0	0.39	ADO 5		
032463	Good identification				032463
<i>Escherichia coli</i>	96.92	0.35	ADO 5		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.08	0.03			
032513	Good identification				032513
<i>Escherichia fergusonii</i>	98.54	0.53	LYS 95		
<i>Leclercia adecarboxylata</i>	1.46	0.12			
034013	Low discrimination				034013
<i>Citrobacter braakii</i>	38.32	0.38	SOR 99		
<i>Escherichia hermannii</i>	25.09	0.24			
<i>Citrobacter amalonaticus</i>	21.99	0.17			
034043	Good identification				034043
<i>Citrobacter braakii</i>	94.46	0.73			
<i>Escherichia coli</i>	1.90	0.37			
<i>Salmonella</i> serovar <i>paratyphi</i>	1.63	0.18			
034051	Identification to the genus				034051
<i>Citrobacter braakii</i>	62.83	0.38	MAN 99		
<i>Citrobacter amalonaticus</i>	36.06	0.17			
<i>Yersinia kristensenii</i>	1.12	-0.08			
034052	Identification to the genus				034052
<i>Citrobacter braakii</i>	62.83	0.38	TRE 99		
<i>Citrobacter amalonaticus</i>	36.06	0.17			
<i>Yersinia kristensenii</i>	1.12	-0.08			
034053	Identification to the genus				034053
<i>Citrobacter braakii</i>	62.68	0.80			
<i>Citrobacter amalonaticus</i>	35.97	0.58			
<i>Yersinia kristensenii</i>	1.12	0.33			
034063	Low discrimination				034063
<i>Citrobacter braakii</i>	73.76	0.50	SUC 7		
<i>Escherichia coli</i>	13.14	0.33			
<i>Citrobacter freundii</i>	7.52	0.32			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
034073	Identification to the genus				034073
<i>Citrobacter braakii</i>	41.84	0.56	SUC 7		
<i>Citrobacter farmeri</i>	33.78	0.39			
<i>Citrobacter amalonaticus</i>	20.36	0.33			
034253	Low discrimination				034253
<i>Citrobacter braakii</i>	53.06	0.38	INO 1		
<i>Citrobacter amalonaticus</i>	30.45	0.17			
<i>Yersinia kristensenii</i>	16.49	0.18			
034413	Good identification				034413
<i>Escherichia fergusonii</i>	98.45	0.45	LYS 95		
<i>Citrobacter koseri</i>	1.55	0.07			
034513	Low discrimination				034513
<i>Escherichia fergusonii</i>	68.59	0.40	LYS 95		
<i>Citrobacter koseri</i>	31.41	0.31			
034553	Very good identification				034553
<i>Citrobacter koseri</i>	99.86	0.56	ONP 99		
<i>Escherichia fergusonii</i>	0.14	-.01			
034573	Very good identification				034573
				VPT	
<i>Citrobacter koseri</i>	99.76	0.55	ONP 99	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.24	0.03		99	
035053	Identification to the genus				035053
<i>Citrobacter braakii</i>	62.83	0.38	PHE 1		
<i>Citrobacter amalonaticus</i>	36.06	0.17			
<i>Yersinia kristensenii</i>	1.12	-.08			
035201	Very good identification				035201
<i>Providencia stuartii</i>	100.0	0.59	ORN 1		
035203	Good identification				035203
<i>Providencia stuartii</i>	100.0	0.39	ORN 1		
035221	Very good identification				035221
<i>Providencia stuartii</i>	100.0	0.59	ORN 1		
035223	Good identification				035223
<i>Providencia stuartii</i>	100.0	0.39	ORN 1		
035400	Very good identification				035400
<i>Providencia alcalifaciens</i>	99.97	0.59	ORN 1		
<i>Morganella morganii subsp. morganii</i>	0.03	-.11			
035420	Good identification				035420
<i>Providencia alcalifaciens</i>	100.0	0.43	ORN 1		
036053	Identification to the genus				036053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter amalonaticus</i>	84.66	0.37	ONP 94		
<i>Citrobacter braakii</i>	15.07	0.38	URE 88		
<i>Yersinia kristensenii</i>	0.27	-.08	ESL 9		
036233	Good identification				036233
<i>Cronobacter sakazakii</i>	100.0	0.40	ONP 99		
036413	Good identification				036413
<i>Escherichia fergusonii</i>	100.0	0.44	LYS 95		
036513	Good identification				036513
<i>Escherichia fergusonii</i>	100.0	0.38	LYS 95		
037233	Good identification				037233
<i>Cronobacter sakazakii</i>	100.0	0.40	ONP 99		
040000	Low discrimination				040000
<i>Shigella dysenteriae</i> (group A)	49.43	0.39	URE 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	16.01	0.21	TRE 90		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	14.49	0.31			
040001	Low discrimination				040001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	73.49	0.72	PHE 93		
<i>Shigella dysenteriae</i> (group A)	22.78	0.59			
<i>Yersinia pseudotuberculosis</i>	1.33	0.25			
040002	Low discrimination				040002
<i>Shigella flexneri</i> (group B)	61.08	0.53	URE 1		
<i>Shigella boydii</i> (group C)	31.03	0.43			
<i>Yersinia pseudotuberculosis</i>	7.74	0.25			
040003	Low discrimination				040003
<i>Yersinia pseudotuberculosis</i>	71.19	0.66	ESL 95		
<i>Shigella boydii</i> (group C)	16.33	0.59			
<i>Shigella flexneri</i> (group B)	11.52	0.59			
040020	Very good identification				040020
<i>Proteus penneri</i>	97.52	0.57	PHE 99		
<i>Proteus vulgaris</i>	2.23	0.33			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.16	0.06			
040021	Low discrimination				040021
<i>Proteus penneri</i>	86.95	0.59	PHE 99		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	11.51	0.47			
<i>Proteus vulgaris</i>	0.70	0.25			
040023	Low discrimination				040023
<i>Yersinia rohdei</i>	82.37	0.56	SOR 99		
<i>Yersinia pseudotuberculosis</i>	9.61	0.25			
<i>Proteus penneri</i>	2.60	0.18			
040033	Good identification				040033

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Yersinia rohdei</i>	95.51	0.47	SOR 99		
<i>Citrobacter freundii</i>	2.58	0.21			
<i>Citrobacter youngae</i>	1.07	0.11			
040041	Low discrimination				040041
<i>Shigella dysenteriae</i> (group A)	81.17	0.51	URE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	6.17	0.31			
<i>Shigella boydii</i> (group C)	5.84	0.25			
040042	Identification to the genus				040042
<i>Shigella flexneri</i> (group B)	49.33	0.45	URE 1		
<i>Shigella boydii</i> (group C)	46.29	0.41			
<i>Citrobacter youngae</i>	2.25	0.24			
040043	Low discrimination				040043
<i>Shigella boydii</i> (group C)	31.80	0.56	URE 1		
<i>Citrobacter youngae</i>	26.95	0.66			
<i>Yersinia rohdei</i>	15.91	0.56			
040053	Low discrimination				040053
<i>Yersinia kristensenii</i>	80.96	0.71	ORN 92		
<i>Citrobacter youngae</i>	12.34	0.64			
<i>Yersinia rohdei</i>	2.97	0.47			
040061	Good identification				040061
<i>Yersinia rohdei</i>	94.13	0.56	MAN 99		
<i>Proteus penneri</i>	2.97	0.18			
<i>Citrobacter freundii</i>	1.08	0.23			
040062	Very good identification				040062
<i>Yersinia rohdei</i>	97.53	0.56	TRE 99		
<i>Citrobacter freundii</i>	1.12	0.23			
<i>Citrobacter youngae</i>	0.44	0.13			
040063	Very good identification				040063
<i>Yersinia rohdei</i>	98.29	0.98			
<i>Citrobacter freundii</i>	1.13	0.64			
<i>Citrobacter youngae</i>	0.45	0.54			
040071	Acceptable identification				040071
<i>Yersinia rohdei</i>	94.69	0.47	MAN 99		
<i>Citrobacter freundii</i>	2.56	0.21			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.70	0.13			
040072	Acceptable identification				040072
<i>Yersinia rohdei</i>	94.69	0.47	TRE 99		
<i>Citrobacter freundii</i>	2.56	0.21			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.70	0.13			
040073	Very good identification				040073
<i>Yersinia rohdei</i>	95.20	0.88			
<i>Citrobacter freundii</i>	2.57	0.62			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	1.06	0.52			
040143	Low discrimination				040143
<i>Citrobacter youngae</i>	48.60	0.39	ONP 90		
<i>Citrobacter werkmanii</i>	22.20	0.15	MAL 5		
<i>Shigella boydii</i> (group C)	11.01	0.15			
040163	Low discrimination				040163
<i>Yersinia rohdei</i>	89.11	0.56	MAL 1		
<i>Citrobacter freundii</i>	8.78	0.43			
<i>Citrobacter youngae</i>	2.11	0.27			
040173	Low discrimination				040173
<i>Yersinia rohdei</i>	76.59	0.47	MAL 1		
<i>Citrobacter freundii</i>	17.80	0.40			
<i>Citrobacter youngae</i>	4.46	0.26			
040243	Low discrimination				040243
<i>Citrobacter youngae</i>	59.29	0.39	ONP 90		
<i>Shigella boydii</i> (group C)	13.43	0.15	INO 5		
<i>Yersinia kristensenii</i>	10.78	0.14			
040253	Good identification				040253
<i>Yersinia kristensenii</i>	94.34	0.55	ORN 92		
<i>Citrobacter youngae</i>	4.29	0.37			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.64	0.25			
040263	Good identification				040263
<i>Yersinia rohdei</i>	92.85	0.56	INO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	3.88	0.30			
<i>Citrobacter youngae</i>	2.20	0.27			
040273	Low discrimination				040273
<i>Yersinia rohdei</i>	65.58	0.47	INO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	24.69	0.40			
<i>Citrobacter youngae</i>	3.82	0.26			
040413	Good identification				040413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.48	URE 10		
040433	Acceptable identification				040433
<i>Klebsiella pneumoniae subsp. ozaenae</i>	92.06	0.36	URE 10		
<i>Yersinia rohdei</i>	7.94	0.06			
040453	Low discrimination				040453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	71.56	0.54	URE 10		
<i>Yersinia kristensenii</i>	22.67	0.30			
<i>Citrobacter youngae</i>	3.46	0.23			
040463	Very good identification				040463
<i>Yersinia rohdei</i>	97.82	0.56	ADO 1		
<i>Citrobacter freundii</i>	1.12	0.23			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.62	0.20			
040473	Low discrimination				040473
<i>Yersinia rohdei</i>	77.10	0.47	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	16.76	0.41			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	2.51	0.06			
040613	Good identification				040613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.50	URE 10		
040633	Good identification				040633
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.82	0.38	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	4.18	-0.09			
040653	Identification to the genus				040653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	80.66	0.56	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	15.65	0.23			
<i>Yersinia kristensenii</i>	3.69	0.14			
040753	Good identification				040753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.17	0.49	URE 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.83	0.25			
040773	Very good identification				040773
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.93	0.59	URE 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.07	0.12			
041000	Low discrimination				041000
<i>Proteus penneri</i>	51.33	0.57	SUC 99		
<i>Morganella morganii</i> subsp. <i>morganii</i>	27.57	0.47			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	17.46	0.54			
041001	Very good identification				041001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.32	0.95			
<i>Proteus penneri</i>	3.50	0.59			
<i>Proteus vulgaris</i>	0.09	0.35			
041003	Low discrimination				041003
<i>Morganella morganii</i> subsp. <i>sibonii</i>	81.75	0.54	MAN 1		
<i>Yersinia pseudotuberculosis</i>	10.99	0.25			
<i>Proteus penneri</i>	2.97	0.18			
041011	Very good identification				041011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.50	0.54	CEL 1		
<i>Proteus penneri</i>	3.50	0.18			
041020	Very good identification				041020
<i>Proteus penneri</i>	97.74	0.98			
<i>Proteus vulgaris</i>	2.24	0.74			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.02	0.29			
041021	Very good identification				041021

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus penneri</i>	97.48	1.00			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.73	0.70			
<i>Proteus vulgaris</i>	0.78	0.66			
041022	Very good identification				041022
<i>Proteus penneri</i>	97.76	0.57	MAN 1		
<i>Proteus vulgaris</i>	2.24	0.33			
041023	Very good identification				041023
<i>Proteus penneri</i>	97.18	0.59	MAN 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.73	0.29			
<i>Proteus vulgaris</i>	0.78	0.25			
041030	Very good identification				041030
<i>Proteus penneri</i>	97.76	0.57	CEL 1		
<i>Proteus vulgaris</i>	2.24	0.33			
041031	Very good identification				041031
<i>Proteus penneri</i>	97.49	0.59	CEL 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.73	0.29			
<i>Proteus vulgaris</i>	0.78	0.25			
041041	Very good identification				041041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	95.57	0.54	SOR 1		
<i>Proteus penneri</i>	3.47	0.18			
<i>Shigella dysenteriae</i> (group A)	0.96	0.10			
041060	Very good identification				041060
<i>Proteus penneri</i>	97.76	0.57	SOR 1		
<i>Proteus vulgaris</i>	2.24	0.33			
041061	Very good identification				041061
<i>Proteus penneri</i>	97.18	0.59	SOR 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.73	0.29			
<i>Proteus vulgaris</i>	0.78	0.25			
041063	Very good identification				041063
<i>Yersinia rohdei</i>	95.46	0.56	PHE 1		
<i>Proteus penneri</i>	3.01	0.18			
<i>Citrobacter freundii</i>	1.09	0.23			
041073	Good identification				041073
<i>Yersinia rohdei</i>	95.51	0.47	PHE 1		
<i>Citrobacter freundii</i>	2.58	0.21			
<i>Citrobacter youngae</i>	1.07	0.11			
041101	Very good identification				041101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.50	0.54	MAL 1		
<i>Proteus penneri</i>	3.50	0.18			
041120	Very good identification				041120
<i>Proteus penneri</i>	97.76	0.57	MAL 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus vulgaris</i>	2.24	0.33			
041121	Very good identification				041121
<i>Proteus penneri</i>	97.49	0.59	MAL 1		
<i>Morganella morganii subsp. sibonii</i>	1.73	0.29			
<i>Proteus vulgaris</i>	0.78	0.25			
041201	Low discrimination				041201
<i>Morganella morganii subsp. sibonii</i>	85.20	0.54	INO 1		
<i>Providencia stuartii</i>	11.70	0.35			
<i>Proteus penneri</i>	3.09	0.18			
041220	Very good identification				041220
<i>Proteus penneri</i>	97.67	0.57	INO 1		
<i>Proteus vulgaris</i>	2.24	0.33			
<i>Providencia stuartii</i>	0.09	0.00			
041221	Good identification				041221
<i>Proteus penneri</i>	93.99	0.59	INO 1		
<i>Providencia stuartii</i>	3.59	0.35			
<i>Morganella morganii subsp. sibonii</i>	1.67	0.29			
041401	Very good identification				041401
<i>Morganella morganii subsp. sibonii</i>	96.50	0.54	ADO 1		
<i>Proteus penneri</i>	3.50	0.18			
041420	Very good identification				041420
<i>Proteus penneri</i>	97.76	0.57	ADO 1		
<i>Proteus vulgaris</i>	2.24	0.33			
041421	Very good identification				041421
<i>Proteus penneri</i>	97.49	0.59	ADO 1		
<i>Morganella morganii subsp. sibonii</i>	1.73	0.29			
<i>Proteus vulgaris</i>	0.78	0.25			
042001	Good identification				042001
<i>Yersinia pseudotuberculosis</i>	96.28	0.51	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	2.84	0.31			
<i>Shigella dysenteriae (group A)</i>	0.88	0.18			
042002	Good identification				042002
<i>Yersinia pseudotuberculosis</i>	99.37	0.51	TRE 99		
<i>Shigella flexneri (group B)</i>	0.42	0.12			
<i>Shigella boydii (group C)</i>	0.21	0.02			
042003	Very good identification				042003
<i>Yersinia pseudotuberculosis</i>	99.98	0.92			
<i>Shigella boydii (group C)</i>	0.01	0.18			
<i>Shigella flexneri (group B)</i>	0.01	0.18			
042013	Good identification				042013
<i>Yersinia pseudotuberculosis</i>	99.14	0.51	CEL 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.86	0.30			
042023	Good identification				042023
<i>Yersinia pseudotuberculosis</i>	99.55	0.51	SUC 1		
<i>Yersinia rohdei</i>	0.45	0.15			
042043	Acceptable identification				042043
<i>Yersinia pseudotuberculosis</i>	94.13	0.51	SOR 1		
<i>Citrobacter youngae</i>	3.79	0.39			
<i>Shigella boydii</i> (group C)	0.86	0.15			
042063	Good identification				042063
<i>Yersinia rohdei</i>	91.74	0.56	ESL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.99	0.28			
<i>Citrobacter youngae</i>	2.17	0.27			
042073	Low discrimination				042073
<i>Yersinia rohdei</i>	71.18	0.47	ESL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.84	0.38			
<i>Citrobacter youngae</i>	4.14	0.26			
042103	Good identification				042103
<i>Yersinia pseudotuberculosis</i>	100.0	0.51	MAL 1		
042203	Good identification				042203
<i>Yersinia pseudotuberculosis</i>	99.91	0.51	INO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.09	0.10			
042253	Low discrimination				042253
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	66.33	0.37	URE 10		
<i>Yersinia kristensenii</i>	24.53	0.14	ADO 97		
<i>Citrobacter youngae</i>	5.81	0.11			
042403	Good identification				042403
<i>Yersinia pseudotuberculosis</i>	97.61	0.51	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.39	0.39			
042413	Very good identification				042413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.54	0.61	URE 10		
<i>Yersinia pseudotuberculosis</i>	3.46	0.10			
042433	Good identification				042433
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.86	0.48	URE 10		
<i>Leclercia adecarboxylata</i>	1.14	-.05			
042443	Low discrimination				042443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.83	0.44	URE 10		
<i>Yersinia pseudotuberculosis</i>	18.17	0.10	CEL 92		
042453	Very good identification				042453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.87	0.66	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.13	-.11			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
042473	Very good identification				042473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.31	0.54	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	1.56	-.01			
<i>Yersinia rohdei</i>	1.13	0.06			
042553	Identification to the genus				042553
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.90	0.35	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	45.10	0.15	MAL 3		
042603	Low discrimination				042603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	74.77	0.41	URE 10		
<i>Yersinia pseudotuberculosis</i>	25.23	0.10	CEL 92		
042613	Very good identification				042613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.62	URE 10		
042633	Good identification				042633
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.50	URE 10		
042643	Good identification				042643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.46	URE 10		
042653	Very good identification				042653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.96	0.68	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	2.04	0.15			
042673	Identification to the genus				042673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	80.04	0.56	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	19.96	0.25			
042753	Acceptable identification				042753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	92.74	0.42	URE 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	7.26	0.37			
042773	Good identification				042773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.20	0.51	URE 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.65	0.25		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.15	-.11		98	
043000	Low discrimination				043000
<i>Proteus vulgaris</i>	78.70	0.43	H2S 95		
<i>Proteus penneri</i>	11.35	0.16	SUC 97		
<i>Morganella morganii</i> subsp. <i>morganii</i>	6.10	0.06			
043001	Low discrimination				043001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	86.93	0.54	ESL 1		
<i>Proteus vulgaris</i>	7.67	0.35			
<i>Proteus penneri</i>	3.16	0.18			
043003	Good identification				043003
<i>Yersinia pseudotuberculosis</i>	99.61	0.51	PHE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.39	0.13			
043020	Identification to the genus				043020
<i>Proteus vulgaris</i>	69.37	0.74	H2S 95		
<i>Proteus penneri</i>	30.63	0.57			
043021	Identification to the genus				043021
<i>Proteus penneri</i>	55.19	0.59	ESL 1		
<i>Proteus vulgaris</i>	43.83	0.66			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.98	0.29			
044023	Low discrimination				044023
<i>Citrobacter freundii</i>	66.53	0.36	ONP 88		
<i>Citrobacter youngae</i>	18.80	0.22	SOR 99		
<i>Yersinia rohdei</i>	14.67	0.15			
044043	Identification to the genus				044043
<i>Citrobacter youngae</i>	82.90	0.75	ONP 90		
<i>Citrobacter freundii</i>	9.64	0.58			
<i>Citrobacter braakii</i>	6.03	0.52			
044053	Identification to the genus				044053
<i>Citrobacter youngae</i>	74.06	0.73	ONP 90		
<i>Citrobacter braakii</i>	13.37	0.58			
<i>Citrobacter freundii</i>	8.27	0.56			
044061	Low discrimination				044061
<i>Citrobacter freundii</i>	66.53	0.36	ONP 88		
<i>Citrobacter youngae</i>	18.80	0.22	MAN 99		
<i>Yersinia rohdei</i>	14.67	0.15			
044062	Low discrimination				044062
<i>Citrobacter freundii</i>	66.53	0.36	ONP 88		
<i>Citrobacter youngae</i>	18.80	0.22	TRE 99		
<i>Yersinia rohdei</i>	14.67	0.15			
044063	Low discrimination				044063
<i>Citrobacter freundii</i>	66.27	0.77	ONP 88		
<i>Citrobacter youngae</i>	18.73	0.63			
<i>Yersinia rohdei</i>	14.62	0.56			
044073	Low discrimination				044073
<i>Citrobacter freundii</i>	70.79	0.75	ONP 88		
<i>Citrobacter youngae</i>	20.84	0.61			
<i>Yersinia rohdei</i>	6.62	0.47			
044143	Identification to the genus				044143
<i>Citrobacter werkmanii</i>	60.48	0.37	ONP 99		
<i>Citrobacter youngae</i>	32.77	0.49	H2S 92		
<i>Citrobacter freundii</i>	6.29	0.36			
044153	Low discrimination				044153

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	76.62	0.47	ONP 90		
<i>Citrobacter freundii</i>	14.13	0.34	MAL 5		
<i>Citrobacter sedlakii</i>	3.57	0.04			
044163	Identification to the genus				044163
<i>Citrobacter freundii</i>	82.73	0.55	ONP 88		
<i>Citrobacter youngae</i>	14.15	0.37	MAL 8		
<i>Yersinia rohdei</i>	2.12	0.15			
044173	Low discrimination				044173
				VPT	
<i>Citrobacter freundii</i>	70.83	0.53	ONP 88	1	
<i>Enterobacter cloacae subsp. cloacae</i>	15.78	0.31	MAL 8	99	
<i>Citrobacter youngae</i>	12.62	0.35		1	
044243	Good identification				044243
<i>Citrobacter youngae</i>	96.50	0.49	ONP 90		
<i>Citrobacter freundii</i>	2.15	0.17	INO 5		
<i>Citrobacter braakii</i>	1.35	0.11			
044253	Low discrimination				044253
<i>Citrobacter youngae</i>	85.98	0.47	ONP 90		
<i>Yersinia kristensenii</i>	6.71	0.14	INO 5		
<i>Citrobacter braakii</i>	2.98	0.17			
044263	Low discrimination				044263
<i>Citrobacter youngae</i>	54.68	0.37	ONP 90		
<i>Citrobacter freundii</i>	37.13	0.36	INO 5		
<i>Yersinia rohdei</i>	8.19	0.15			
044413	Good identification				044413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	URE 10		
044453	Low discrimination				044453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	70.18	0.46	URE 10		
<i>Citrobacter youngae</i>	22.51	0.32			
<i>Citrobacter braakii</i>	4.06	0.17			
044463	Low discrimination				044463
<i>Citrobacter freundii</i>	64.01	0.36	ONP 88		
<i>Citrobacter youngae</i>	18.09	0.22	ADO 1		
<i>Yersinia rohdei</i>	14.12	0.15			
044613	Good identification				044613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.43	URE 10		
044653	Good identification				044653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.64	0.48	URE 10		
<i>Citrobacter youngae</i>	1.36	0.06			
044673	Acceptable identification				044673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	91.70	0.36	URE 10	1	
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	5.03	-.09		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	3.27	-.05		99	
045001	Low discrimination				045001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	80.19	0.54	SCI 1		
<i>Proteus mirabilis</i>	7.94	0.24			
<i>Providencia stuartii</i>	7.70	0.31			
045020	Identification to the genus				045020
<i>Proteus penneri</i>	71.41	0.57	SCI 1		
<i>Proteus vulgaris</i>	28.54	0.58			
<i>Providencia stuartii</i>	0.05	-.04			
045021	Identification to the genus				045021
<i>Proteus penneri</i>	84.07	0.59	SCI 1		
<i>Proteus vulgaris</i>	11.78	0.51			
<i>Providencia stuartii</i>	2.25	0.31			
045063	Low discrimination				045063
<i>Citrobacter freundii</i>	66.53	0.36	ONP 88		
<i>Citrobacter youngae</i>	18.80	0.22	PHE 1		
<i>Yersinia rohdei</i>	14.67	0.15			
045201	Very good identification				045201
<i>Providencia stuartii</i>	99.45	0.58	IND 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.55	0.13			
045203	Good identification				045203
<i>Providencia stuartii</i>	100.0	0.38	IND 98		
045221	Very good identification				045221
<i>Providencia stuartii</i>	97.78	0.58	IND 98		
<i>Proteus penneri</i>	1.95	0.18			
<i>Proteus vulgaris</i>	0.27	0.10			
045223	Good identification				045223
<i>Providencia stuartii</i>	100.0	0.38	IND 98		
045402	Good identification				045402
<i>Providencia rettgeri</i>	99.67	0.39	IND 99		
<i>Providencia alcalifaciens</i>	0.33	-.17	INO 90		
045602	Very good identification				045602
<i>Providencia rettgeri</i>	100.0	0.59	IND 99		
045622	Good identification				045622
<i>Providencia rettgeri</i>	100.0	0.43	IND 99		
046003	Good identification				046003
<i>Yersinia pseudotuberculosis</i>	99.88	0.51	SCI 1		
<i>Citrobacter youngae</i>	0.12	0.07			
046043	Low discrimination				046043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	88.51	0.49	ONP 90		
<i>Yersinia pseudotuberculosis</i>	7.81	0.10	ESL 5		
<i>Citrobacter freundii</i>	1.98	0.17			
046053	Low discrimination				046053
<i>Citrobacter youngae</i>	83.88	0.47	ONP 90		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	6.21	0.28	ESL 5		
<i>Citrobacter amalonaticus</i>	5.21	0.06			
046063	Low discrimination				046063
<i>Citrobacter youngae</i>	54.68	0.37	ONP 90		
<i>Citrobacter freundii</i>	37.13	0.36	ESL 5		
<i>Yersinia rohdei</i>	8.19	0.15			
046413	Very good identification				046413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.53	URE 10		
046433	Good identification				046433
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.58	0.41	URE 10	1	
<i>Serratia rubidaea</i>	4.42	-0.02		99	
046443	Acceptable identification				046443
<i>Klebsiella pneumoniae subsp. ozaenae</i>	94.40	0.37	URE 10		
<i>Citrobacter youngae</i>	5.60	0.07	CEL 92		
046453	Very good identification				046453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.58	0.59	URE 10		
<i>Citrobacter youngae</i>	0.42	0.06			
046473	Good identification				046473
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.42	0.46	URE 10	1	
<i>Enterobacter cloacae subsp. cloacae</i>	2.58	0.03		99	
046613	Very good identification				046613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.55	URE 10		
046633	Good identification				046633
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.43	URE 10		
046643	Good identification				046643
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.39	URE 10		
046653	Very good identification				046653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.60	URE 10		
046673	Acceptable identification				046673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	94.23	0.48	URE 10	1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	5.78	0.01		98	
047020	Very good identification				047020
<i>Proteus vulgaris</i>	97.54	0.58	H2S 95		
<i>Proteus penneri</i>	2.47	0.16			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
047021	Acceptable identification				047021
<i>Proteus vulgaris</i>	93.28	0.51	H2S 95		
<i>Proteus penneri</i>	6.72	0.18			
047602	Very good identification				047602
<i>Providencia rettgeri</i>	100.0	0.53	IND 99		
047622	Good identification				047622
<i>Providencia rettgeri</i>	100.0	0.38	IND 99		
050000	Low discrimination				050000
<i>Morganella morganii subsp. morganii</i>	81.91	0.47	ORN 95		
<i>Shigella dysenteriae (group A)</i>	10.89	0.38	PHE 95		
<i>Morganella morganii subsp. sibonii</i>	3.90	0.31			
050001	Low discrimination				050001
<i>Morganella morganii subsp. sibonii</i>	78.26	0.72	PHE 93		
<i>Shigella dysenteriae (group A)</i>	19.85	0.57			
<i>Shigella flexneri (group B)</i>	1.19	0.33			
050002	Identification to the genus				050002
<i>Shigella flexneri (group B)</i>	84.29	0.53	URE 1		
<i>Shigella boydii (group C)</i>	14.28	0.34			
<i>Morganella morganii subsp. morganii</i>	1.27	0.06			
050003	Low discrimination				050003
<i>Shigella flexneri (group B)</i>	63.03	0.59	URE 1		
<i>Shigella boydii (group C)</i>	29.79	0.49			
<i>Yersinia pseudotuberculosis</i>	3.94	0.25			
050021	Low discrimination				050021
<i>Morganella morganii subsp. sibonii</i>	82.22	0.47	PHE 93		
<i>Proteus penneri</i>	6.28	0.18	SUC 6		
<i>Proteus vulgaris</i>	4.98	0.25			
050041	Low discrimination				050041
<i>Shigella dysenteriae (group A)</i>	84.12	0.50	URE 1		
<i>Morganella morganii subsp. sibonii</i>	7.82	0.31			
<i>Shigella flexneri (group B)</i>	4.80	0.25			
050042	Identification to the genus				050042
<i>Shigella flexneri (group B)</i>	75.16	0.45	URE 1		
<i>Shigella boydii (group C)</i>	23.51	0.31			
<i>Escherichia coli</i>	0.73	0.10			
050043	Low discrimination				050043
<i>Shigella flexneri (group B)</i>	38.36	0.51	URE 1		
<i>Shigella boydii (group C)</i>	33.49	0.47			
<i>Citrobacter youngae</i>	15.02	0.50			
050053	Low discrimination				050053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia kristensenii</i>	89.22	0.63	ORN 92		
<i>Citrobacter youngae</i>	5.60	0.48			
<i>Citrobacter braakii</i>	2.68	0.42			
050063	Low discrimination				050063
<i>Yersinia rohdei</i>	55.54	0.56	IND 1		
<i>Citrobacter freundii</i>	31.01	0.58			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.42	0.38			
050073	Low discrimination				050073
<i>Citrobacter freundii</i>	36.22	0.56	ONP 88		
<i>Yersinia rohdei</i>	27.53	0.47			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	24.18	0.47			
050163	Low discrimination				050163
<i>Citrobacter freundii</i>	77.27	0.36	ONP 88		
<i>Yersinia rohdei</i>	16.08	0.15	MAL 8		
<i>Citrobacter youngae</i>	6.66	0.12			
050201	Low discrimination				050201
<i>Providencia stuartii</i>	78.97	0.43	PHE 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	16.78	0.31	SCI 93		
<i>Shigella dysenteriae</i> (group A)	4.26	0.16			
050221	Good identification				050221
<i>Providencia stuartii</i>	98.66	0.43	PHE 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.34	0.06	SCI 93		
050253	Good identification				050253
<i>Yersinia kristensenii</i>	97.25	0.48	ORN 92		
<i>Citrobacter youngae</i>	1.82	0.22			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.93	0.14			
050273	Low discrimination				050273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	87.36	0.40	ONP 95		
<i>Yersinia kristensenii</i>	4.84	0.06	ORN 95		
<i>Citrobacter freundii</i>	3.08	0.15			
050602	Good identification				050602
<i>Providencia rettgeri</i>	100.0	0.39	PHE 98		
051000	Very good identification				051000
<i>Morganella morganii</i> subsp. <i>morganii</i>	96.01	0.74	ORN 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	3.20	0.54			
<i>Proteus vulgaris</i>	0.66	0.43			
051001	Excellent identification				051001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.20	0.95			
<i>Providencia stuartii</i>	0.36	0.43			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.30	0.33			
051003	Good identification				051003

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	93.07	0.54	MAN 1		
<i>Providencia stuartii</i>	3.66	0.23			
<i>Shigella flexneri</i> (group B)	2.02	0.18			
051011	Very good identification				051011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.88	0.54	CEL 1		
<i>Providencia stuartii</i>	1.83	0.17			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.30	-.09			
051020	Identification to the genus				051020
<i>Proteus vulgaris</i>	66.77	0.74	H2S 95		
<i>Proteus penneri</i>	29.48	0.57			
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.04	0.33			
051021	Low discrimination				051021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	48.15	0.70	SUC 6		
<i>Proteus penneri</i>	27.38	0.59			
<i>Proteus vulgaris</i>	21.75	0.66			
051041	Very good identification				051041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	98.54	0.54	SOR 1		
<i>Shigella dysenteriae</i> (group A)	0.81	0.09			
<i>Providencia stuartii</i>	0.35	0.02			
051101	Very good identification				051101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.34	0.54	MAL 1		
<i>Providencia stuartii</i>	0.36	0.02			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.30	-.09			
051201	Low discrimination				051201
<i>Providencia stuartii</i>	87.03	0.69	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	12.93	0.54			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.04	-.09			
051203	Good identification				051203
<i>Providencia stuartii</i>	98.38	0.50	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.33	0.13	MAN 10		
<i>Providencia rettgeri</i>	0.29	-.09			
051211	Good identification				051211
<i>Providencia stuartii</i>	97.23	0.43	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2.77	0.13	CEL 5		
051221	Very good identification				051221
<i>Providencia stuartii</i>	98.12	0.69	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.93	0.29			
<i>Proteus penneri</i>	0.53	0.18			
051223	Good identification				051223
<i>Providencia stuartii</i>	100.0	0.50	SCI 93		
051231	Good identification				051231

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	100.0	0.43	SCI 93		
051401	Very good identification				051401
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.58	0.54	ADO 1		
<i>Providencia stuartii</i>	1.82	0.17			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.30	-.09			
051402	Very good identification				051402
<i>Providencia rettgeri</i>	99.74	0.54	SCI 95		
<i>Providencia alcalifaciens</i>	0.13	-.11	INO 90		
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.13	-.09			
051422	Good identification				051422
<i>Providencia rettgeri</i>	100.0	0.39	SCI 95		
051601	Good identification				051601
<i>Providencia stuartii</i>	96.64	0.43	SCI 93		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2.76	0.13	ADO 5		
<i>Providencia rettgeri</i>	0.60	-.09			
051602	Very good identification				051602
<i>Providencia rettgeri</i>	100.0	0.74	SCI 95		
051612	Good identification				051612
<i>Providencia rettgeri</i>	100.0	0.43	SCI 95		
051621	Good identification				051621
<i>Providencia stuartii</i>	100.0	0.43	SCI 93		
051622	Very good identification				051622
<i>Providencia rettgeri</i>	100.0	0.58	SCI 95		
052003	Good identification				052003
<i>Yersinia pseudotuberculosis</i>	98.66	0.51	IND 1		
<i>Shigella flexneri</i> (group B)	0.84	0.18			
<i>Shigella boydii</i> (group C)	0.40	0.08			
052073	Low discrimination				052073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	89.69	0.38	ONP 95		
<i>Citrobacter freundii</i>	4.07	0.15	ORN 95		
<i>Citrobacter youngae</i>	3.14	0.10			
052133	Good identification				052133
<i>Leclercia adecarboxylata</i>	100.0	0.36	ONP 99		
052433	Good identification				052433
<i>Leclercia adecarboxylata</i>	99.12	0.36	ONP 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.88	0.07	MAL 93		
052513	Very good identification				052513
<i>Leclercia adecarboxylata</i>	100.0	0.53	ONP 99		
052533	Very good identification				052533

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	100.0	0.59	ONP 99		
053001	Good identification				053001
<i>Morganella morganii subsp. sibonii</i>	91.33	0.54	ESL 1		
<i>Proteus vulgaris</i>	8.06	0.35			
<i>Providencia stuartii</i>	0.33	0.02			
053020	Very good identification				053020
<i>Proteus vulgaris</i>	99.51	0.74	H2S 95		
<i>Proteus penneri</i>	0.44	0.16			
<i>Morganella morganii subsp. morganii</i>	0.05	-.09			
053021	Very good identification				053021
<i>Proteus vulgaris</i>	96.49	0.66	H2S 95		
<i>Morganella morganii subsp. sibonii</i>	2.16	0.29			
<i>Proteus penneri</i>	1.23	0.18			
053402	Good identification				053402
<i>Providencia rettgeri</i>	100.0	0.49	SCI 95		
053602	Very good identification				053602
<i>Providencia rettgeri</i>	100.0	0.68	SCI 95		
053612	Good identification				053612
<i>Providencia rettgeri</i>	100.0	0.37	SCI 95		
053622	Good identification				053622
<i>Providencia rettgeri</i>	100.0	0.53	SCI 95		
054001	Low discrimination				054001
<i>Providencia stuartii</i>	72.42	0.40	PHE 95		
<i>Morganella morganii subsp. sibonii</i>	22.00	0.31	INO 95		
<i>Shigella dysenteriae (group A)</i>	5.58	0.16			
054021	Good identification				054021
<i>Providencia stuartii</i>	96.16	0.40	PHE 95		
<i>Proteus vulgaris</i>	1.98	0.10	INO 95		
<i>Morganella morganii subsp. sibonii</i>	1.87	0.06			
054043	Identification to the genus				054043
<i>Citrobacter youngae</i>	63.75	0.59	ONP 90		
<i>Citrobacter freundii</i>	20.68	0.52			
<i>Citrobacter braakii</i>	12.94	0.46			
054053	Low discrimination				054053
<i>Citrobacter amalonaticus</i>	61.04	0.51	ONP 94		
<i>Citrobacter youngae</i>	20.81	0.58	ORN 94		
<i>Citrobacter braakii</i>	10.48	0.52			
054063	Identification to the genus				054063
<i>Citrobacter freundii</i>	89.91	0.70	ONP 88		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	9.11	0.48			
<i>Citrobacter braakii</i>	0.52	0.23			
054073	Identification to the genus				054073
<i>Citrobacter freundii</i>	83.31	0.68	ONP 88		
<i>Citrobacter youngae</i>	8.79	0.46			
<i>Citrobacter amalonaticus</i>	6.19	0.26			
054163	Acceptable identification				054163
<i>Citrobacter freundii</i>	94.23	0.49	ONP 88		
<i>Citrobacter youngae</i>	5.78	0.21	MAL 8		
054173	Acceptable identification				054173
<i>Citrobacter freundii</i>	93.24	0.47	ONP 88		
<i>Citrobacter youngae</i>	5.95	0.19	MAL 8		
<i>Citrobacter amalonaticus</i>	0.80	-.15			
054201	Very good identification				054201
<i>Providencia stuartii</i>	100.0	0.66	PHE 95		
054203	Good identification				054203
<i>Providencia stuartii</i>	100.0	0.47	PHE 95		
054211	Good identification				054211
<i>Providencia stuartii</i>	100.0	0.40	PHE 95		
054221	Very good identification				054221
<i>Providencia stuartii</i>	100.0	0.66	PHE 95		
054223	Good identification				054223
<i>Providencia stuartii</i>	100.0	0.47	PHE 95		
054231	Good identification				054231
<i>Providencia stuartii</i>	100.0	0.40	PHE 95		
054402	Good identification				054402
<i>Providencia rettgeri</i>	99.67	0.46	PHE 98		
<i>Providencia alcalifaciens</i>	0.33	-.11	INO 90		
054601	Good identification				054601
<i>Providencia stuartii</i>	100.0	0.40	PHE 95		
054602	Very good identification				054602
<i>Providencia rettgeri</i>	100.0	0.65	PHE 98		
054621	Good identification				054621
<i>Providencia stuartii</i>	100.0	0.40	PHE 95		
054622	Good identification				054622
<i>Providencia rettgeri</i>	100.0	0.50	PHE 98		
055001	Low discrimination				055001

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	82.13	0.66	INO 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	17.45	0.54			
<i>Proteus vulgaris</i>	0.27	0.20			
055002	Good identification				055002
<i>Providencia rettgeri</i>	96.47	0.39	INO 90		
<i>Providencia stuartii</i>	2.24	0.12	ADO 99		
<i>Providencia alcalifaciens</i>	0.65	-.11			
055003	Good identification				055003
<i>Providencia stuartii</i>	97.26	0.47	INO 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.88	0.13	MAN 10		
<i>Providencia rettgeri</i>	0.87	-.02			
055011	Good identification				055011
<i>Providencia stuartii</i>	96.08	0.40	INO 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	3.92	0.13	CEL 5		
055020	Low discrimination				055020
<i>Proteus vulgaris</i>	88.30	0.58	H2S 95		
<i>Providencia stuartii</i>	7.22	0.31			
<i>Proteus penneri</i>	2.23	0.16			
055021	Low discrimination				055021
<i>Providencia stuartii</i>	88.63	0.66	INO 95		
<i>Proteus vulgaris</i>	9.49	0.51			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.20	0.29			
055023	Good identification				055023
<i>Providencia stuartii</i>	99.04	0.47	INO 95		
<i>Proteus vulgaris</i>	0.96	0.10	MAN 10		
055031	Good identification				055031
<i>Providencia stuartii</i>	97.99	0.40	INO 95		
<i>Proteus vulgaris</i>	2.01	0.10	CEL 5		
055200	Very good identification				055200
<i>Providencia stuartii</i>	97.52	0.58	TRE 98		
<i>Providencia rettgeri</i>	2.24	0.18			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.16	-.09			
055201	Very good identification				055201
<i>Providencia stuartii</i>	99.99	0.92			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.01	0.13			
055202	Very good identification				055202
<i>Providencia rettgeri</i>	95.34	0.59	ADO 99		
<i>Providencia stuartii</i>	4.66	0.38			
055203	Very good identification				055203
<i>Providencia stuartii</i>	99.58	0.73	MAN 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia rettgeri</i>	0.42	0.18			
055211	Very good identification				055211
<i>Providencia stuartii</i>	100.0	0.66	CEL 5		
055213	Good identification				055213
<i>Providencia stuartii</i>	100.0	0.47	CEL 5		
055220	Very good identification				055220
<i>Providencia stuartii</i>	98.96	0.58	TRE 98		
<i>Proteus vulgaris</i>	0.64	0.17			
<i>Providencia rettgeri</i>	0.40	0.02			
055221	Very good identification				055221
<i>Providencia stuartii</i>	99.99	0.92			
<i>Proteus vulgaris</i>	0.01	0.10			
055222	Identification to the genus				055222
<i>Providencia rettgeri</i>	78.30	0.43	ADO 99		
<i>Providencia stuartii</i>	21.70	0.38			
055223	Very good identification				055223
<i>Providencia stuartii</i>	99.93	0.73	MAN 10		
<i>Providencia rettgeri</i>	0.07	0.02			
055231	Very good identification				055231
<i>Providencia stuartii</i>	100.0	0.66	CEL 5		
055233	Good identification				055233
<i>Providencia stuartii</i>	100.0	0.47	CEL 5		
055241	Good identification				055241
<i>Providencia stuartii</i>	100.0	0.51	SOR 1		
055261	Good identification				055261
<i>Providencia stuartii</i>	100.0	0.51	SOR 1		
055301	Good identification				055301
<i>Providencia stuartii</i>	100.0	0.51	MAL 1		
055321	Good identification				055321
<i>Providencia stuartii</i>	100.0	0.51	MAL 1		
055400	Good identification				055400
<i>Providencia alcalifaciens</i>	94.09	0.59	URE 1		
<i>Providencia rettgeri</i>	5.80	0.39			
<i>Providencia stuartii</i>	0.06	0.05			
055401	Identification to the genus				055401
<i>Providencia stuartii</i>	59.71	0.40	INO 95		
<i>Providencia alcalifaciens</i>	36.73	0.24	ADO 5		
<i>Morganella morganii subsp. sibonii</i>	2.44	0.13			

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
055402	Very good identification					055402
<i>Providencia rettgeri</i>		99.67	0.80	INO 90		
<i>Providencia alcalifaciens</i>		0.33	0.24			
055403	Acceptable identification					055403
<i>Providencia rettgeri</i>		93.76	0.39	INO 90		
<i>Providencia stuartii</i>		5.60	0.20	TRE 1		
<i>Providencia alcalifaciens</i>		0.63	-.11			
055412	Good identification					055412
<i>Providencia rettgeri</i>		99.89	0.49	INO 90		
<i>Providencia alcalifaciens</i>		0.11	-.17	CEL 3		
055420	Acceptable identification					055420
<i>Providencia alcalifaciens</i>		93.06	0.43	URE 1		
<i>Providencia rettgeri</i>		5.74	0.24			
<i>Proteus vulgaris</i>		0.84	0.17			
055421	Identification to the genus					055421
<i>Providencia stuartii</i>		88.57	0.40	INO 95		
<i>Providencia alcalifaciens</i>		9.62	0.09	ADO 5		
<i>Proteus vulgaris</i>		1.82	0.10			
055422	Very good identification					055422
<i>Providencia rettgeri</i>		99.67	0.65	INO 90		
<i>Providencia alcalifaciens</i>		0.33	0.09			
055442	Good identification					055442
<i>Providencia rettgeri</i>		99.67	0.39	INO 90		
<i>Providencia alcalifaciens</i>		0.33	-.17	SOR 1		
055502	Good identification					055502
<i>Providencia rettgeri</i>		99.67	0.39	MAL 1		
<i>Providencia alcalifaciens</i>		0.33	-.17	INO 90		
055600	Very good identification					055600
<i>Providencia rettgeri</i>		96.03	0.59	MAN 99		
<i>Providencia stuartii</i>		2.23	0.31			
<i>Providencia alcalifaciens</i>		1.75	0.18			
055601	Very good identification					055601
<i>Providencia stuartii</i>		99.09	0.66	ADO 5		
<i>Providencia rettgeri</i>		0.88	0.18			
<i>Providencia alcalifaciens</i>		0.03	-.17			
055602	Excellent identification					055602
<i>Providencia rettgeri</i>		100.0	1.00			
<i>Providencia stuartii</i>		0.00	0.12			
<i>Providencia alcalifaciens</i>		0.00	-.17			
055603	Identification to the genus					055603

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia rettgeri</i>	88.80	0.59	TRE 1		
<i>Providencia stuartii</i>	11.20	0.47			
055611	Good identification				055611
<i>Providencia stuartii</i>	100.0	0.40	ADO 5		
055612	Very good identification				055612
<i>Providencia rettgeri</i>	100.0	0.69	CEL 3		
055620	Identification to the genus				055620
<i>Providencia rettgeri</i>	87.00	0.43	MAN 99		
<i>Providencia stuartii</i>	11.42	0.31			
<i>Providencia alcalifaciens</i>	1.58	0.02			
055621	Very good identification				055621
<i>Providencia stuartii</i>	99.84	0.66	ADO 5		
<i>Providencia rettgeri</i>	0.16	0.02			
055622	Very good identification				055622
<i>Providencia rettgeri</i>	99.99	0.85			
<i>Providencia stuartii</i>	0.02	0.12			
055623	Identification to the genus				055623
<i>Providencia rettgeri</i>	58.31	0.43	TRE 1		
<i>Providencia stuartii</i>	41.69	0.47			
055631	Good identification				055631
<i>Providencia stuartii</i>	100.0	0.40	ADO 5		
055632	Very good identification				055632
<i>Providencia rettgeri</i>	100.0	0.53	CEL 3		
055642	Very good identification				055642
<i>Providencia rettgeri</i>	100.0	0.59	SOR 1		
055662	Good identification				055662
<i>Providencia rettgeri</i>	100.0	0.43	SOR 1		
055702	Very good identification				055702
<i>Providencia rettgeri</i>	100.0	0.59	MAL 1		
055722	Good identification				055722
<i>Providencia rettgeri</i>	100.0	0.43	MAL 1		
056402	Good identification				056402
<i>Providencia rettgeri</i>	100.0	0.40	PHE 98		
056602	Very good identification				056602
<i>Providencia rettgeri</i>	100.0	0.60	PHE 98		
056622	Good identification				056622

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia rettgeri</i>	100.0	0.44	PHE 98		
057020	Very good identification				057020
<i>Proteus vulgaris</i>	100.0	0.58	H2S 95		
057021	Acceptable identification				057021
<i>Proteus vulgaris</i>	91.38	0.51	H2S 95		
<i>Providencia stuartii</i>	8.62	0.25			
057201	Good identification				057201
<i>Providencia stuartii</i>	100.0	0.51	ESL 1		
057202	Very good identification				057202
<i>Providencia rettgeri</i>	99.91	0.53	ADO 99		
<i>Providencia stuartii</i>	0.09	-.03			
057221	Good identification				057221
<i>Providencia stuartii</i>	99.44	0.51	ESL 1		
<i>Proteus vulgaris</i>	0.56	0.10			
057222	Good identification				057222
<i>Providencia rettgeri</i>	99.48	0.38	ADO 99		
<i>Providencia stuartii</i>	0.52	-.03			
057402	Very good identification				057402
<i>Providencia rettgeri</i>	99.99	0.75	INO 90		
<i>Providencia alcalifaciens</i>	0.01	-.17			
057412	Good identification				057412
<i>Providencia rettgeri</i>	100.0	0.44	INO 90		
057422	Very good identification				057422
<i>Providencia rettgeri</i>	100.0	0.59	INO 90		
057600	Very good identification				057600
<i>Providencia rettgeri</i>	100.0	0.53	MAN 99		
057602	Excellent identification				057602
<i>Providencia rettgeri</i>	100.0	0.95			
057603	Very good identification				057603
<i>Providencia rettgeri</i>	99.76	0.53	TRE 1		
<i>Providencia stuartii</i>	0.24	0.05			
057612	Very good identification				057612
<i>Providencia rettgeri</i>	100.0	0.63	CEL 3		
057620	Good identification				057620
<i>Providencia rettgeri</i>	100.0	0.38	MAN 99		
057622	Very good identification				057622

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia rettgeri</i>	100.0	0.79			
057623	Good identification				057623
<i>Providencia rettgeri</i>	98.68	0.38	TRE 1		
<i>Providencia stuartii</i>	1.32	0.05			
057632	Good identification				057632
<i>Providencia rettgeri</i>	100.0	0.48	CEL 3		
057642	Very good identification				057642
<i>Providencia rettgeri</i>	100.0	0.53	SOR 1		
057662	Good identification				057662
<i>Providencia rettgeri</i>	100.0	0.38	SOR 1		
057702	Very good identification				057702
<i>Providencia rettgeri</i>	100.0	0.53	MAL 1		
057722	Good identification				057722
<i>Providencia rettgeri</i>	100.0	0.38	MAL 1		
060000	Acceptable identification				060000
<i>Morganella morganii</i> subsp. <i>morganii</i>	91.93	0.47	IND 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	7.79	0.36	PHE 95		
<i>Shigella dysenteriae</i> (group A)	0.15	-.02			
060001	Very good identification				060001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	98.77	0.77	PHE 93		
<i>Proteus mirabilis</i>	0.80	0.25			
<i>Shigella dysenteriae</i> (group A)	0.17	0.18			
060003	Low discrimination				060003
<i>Shigella sonnei</i>	41.97	0.39	ONP 90		
<i>Hafnia alvei</i>	22.21	0.59	URE 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	18.68	0.33			
060011	Acceptable identification				060011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	91.59	0.36	PHE 93		
<i>Yersinia kristensenii</i>	8.41	0.10	CEL 1		
060013	Low discrimination				060013
<i>Yersinia kristensenii</i>	86.66	0.51	SOR 99		
<i>Hafnia alvei</i>	5.78	0.43			
<i>Shigella sonnei</i>	3.26	0.13			
060021	Acceptable identification				060021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	93.46	0.52	PHE 93		
<i>Proteus penneri</i>	4.01	0.18	SUC 6		
<i>Proteus mirabilis</i>	2.10	0.09			
060023	Low discrimination				060023
<i>Yersinia rohdei</i>	80.35	0.47	SOR 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	10.69	0.39			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.52	0.23			
060033	Low discrimination				060033
<i>Yersinia rohdei</i>	59.04	0.37	SOR 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	29.86	0.33			
<i>Yersinia kristensenii</i>	5.67	0.10			
060041	Low discrimination				060041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	52.56	0.36	PHE 93		
<i>Salmonella</i> serovar <i>paratyphi</i>	29.16	0.18	SOR 1		
<i>Citrobacter braakii</i>	7.10	0.24			
060043	Low discrimination				060043
<i>Salmonella</i> serovar <i>paratyphi</i>	66.96	0.59	URE 1		
<i>Citrobacter braakii</i>	16.30	0.65			
<i>Yersinia kristensenii</i>	11.08	0.51			
060051	Good identification				060051
<i>Yersinia kristensenii</i>	96.24	0.51	MAN 99		
<i>Citrobacter braakii</i>	2.90	0.31			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.55	0.13			
060052	Good identification				060052
<i>Yersinia kristensenii</i>	96.12	0.51	TRE 99		
<i>Citrobacter braakii</i>	2.90	0.31			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.54	0.13			
060053	Very good identification				060053
<i>Yersinia kristensenii</i>	96.35	0.92			
<i>Citrobacter braakii</i>	2.91	0.72			
<i>Salmonella</i> serovar <i>paratyphi</i>	0.31	0.33			
060061	Identification to the genus				060061
<i>Yersinia rohdei</i>	88.04	0.47	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.00	0.29			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.96	0.11			
060062	Identification to the genus				060062
<i>Yersinia rohdei</i>	89.47	0.47	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.16	0.29			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.37	-0.09			
060063	Good identification				060063
<i>Yersinia rohdei</i>	94.08	0.88			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.29	0.64			
<i>Citrobacter braakii</i>	0.33	0.42			
060071	Identification to the genus				060071
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	47.77	0.39	ONP 95		
<i>Yersinia rohdei</i>	46.74	0.37	MAN 98		
<i>Yersinia kristensenii</i>	4.49	0.10			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
060072	Identification to the genus				060072
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	47.77	0.39	ONP 95		
<i>Yersinia rohdei</i>	46.74	0.37	TRE 98		
<i>Yersinia kristensenii</i>	4.49	0.10			
060073	Identification to the genus				060073
<i>Yersinia rohdei</i>	61.39	0.78			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	31.05	0.74			
<i>Yersinia kristensenii</i>	5.89	0.51			
060101	Good identification				060101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	95.13	0.36	PHE 93		
<i>Hafnia alvei</i>	3.30	0.18	MAL 1		
<i>Proteus mirabilis</i>	1.56	-.10			
060103	Very good identification				060103
<i>Hafnia alvei</i>	97.32	0.59	LYS 99		
<i>Shigella sonnei</i>	1.86	-.02			
<i>Salmonella</i> serovar <i>paratyphi</i>	0.83	-.09			
060113	Low discrimination				060113
<i>Hafnia alvei</i>	84.78	0.43	LYS 99		
<i>Yersinia kristensenii</i>	12.84	0.10			
<i>Citrobacter sedlakii</i>	2.39	-.11			
060123	Acceptable identification				060123
<i>Hafnia alvei</i>	92.95	0.39	LYS 99		
<i>Yersinia rohdei</i>	7.05	0.06	SUC 10		
060153	Low discrimination				060153
<i>Yersinia kristensenii</i>	81.69	0.51	MAL 1		
<i>Citrobacter sedlakii</i>	15.19	0.31			
<i>Citrobacter braakii</i>	2.46	0.31			
060163	Acceptable identification				060163
<i>Yersinia rohdei</i>	94.68	0.47	MAL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.32	0.23			
060173	Low discrimination				060173
				VPT	
<i>Yersinia rohdei</i>	55.81	0.37	MAL 1	1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	28.23	0.33		2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	8.41	0.18		99	
060201	Good identification				060201
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.36	PHE 93		
060213	Good identification				060213
<i>Yersinia kristensenii</i>	100.0	0.36	SOR 99		
060243	Low discrimination				060243
<i>Yersinia kristensenii</i>	59.27	0.36	CEL 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar paratyphi</i>	20.50	0.18			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	13.30	0.30			
060251	Good identification				060251
<i>Yersinia kristensenii</i>	98.64	0.36	MAN 99		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.36	0.05			
060252	Good identification				060252
<i>Yersinia kristensenii</i>	98.64	0.36	TRE 99		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.36	0.05			
060253	Very good identification				060253
<i>Yersinia kristensenii</i>	99.12	0.77			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.67	0.40			
<i>Citrobacter braakii</i>	0.17	0.31			
060263	Identification to the genus				060263
<i>Yersinia enterocolitica ssp. enterocolitica</i>	70.34	0.56	ONP 95		
<i>Yersinia rohdei</i>	29.50	0.47			
<i>Yersinia kristensenii</i>	0.17	-.05			
060273	Identification to the genus				060273
<i>Yersinia enterocolitica ssp. enterocolitica</i>	88.83	0.66	ONP 95		
<i>Yersinia kristensenii</i>	6.94	0.36			
<i>Yersinia rohdei</i>	4.14	0.37			
060353	Good identification				060353
<i>Yersinia kristensenii</i>	98.95	0.36	MAL 1		
<i>Citrobacter sedlakii</i>	1.05	-.11			
060401	Good identification				060401
<i>Morganella morganii subsp. sibonii</i>	100.0	0.36	PHE 93		
060453	Good identification				060453
<i>Yersinia kristensenii</i>	95.73	0.51	ADO 1		
<i>Citrobacter braakii</i>	2.89	0.31			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.81	0.23			
060463	Acceptable identification				060463
<i>Yersinia rohdei</i>	94.68	0.47	ADO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	5.32	0.23			
060473	Identification to the genus				060473
<i>Yersinia rohdei</i>	60.23	0.37	ADO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	30.47	0.33			
<i>Yersinia kristensenii</i>	5.78	0.10			
060653	Acceptable identification				060653
<i>Yersinia kristensenii</i>	94.45	0.36	ADO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	5.55	0.25			
061000	Good identification				061000

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	94.00	0.74	IND 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	5.57	0.59			
<i>Proteus mirabilis</i>	0.34	0.25			
061001	Very good identification				061001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.91	1.00			
<i>Proteus mirabilis</i>	2.91	0.60			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.17	0.33			
061003	Very good identification				061003
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.02	0.59	MAN 1		
<i>Proteus mirabilis</i>	2.88	0.19			
<i>Shigella sonnei</i>	0.47	-.02			
061011	Very good identification				061011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.93	0.59	CEL 1		
<i>Proteus mirabilis</i>	2.91	0.19			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.17	-.09			
061020	Low discrimination				061020
<i>Proteus penneri</i>	85.40	0.57	ORN 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	8.80	0.33			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	3.30	0.34			
061021	Low discrimination				061021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	71.14	0.75	SUC 6		
<i>Proteus penneri</i>	22.76	0.59			
<i>Proteus mirabilis</i>	5.90	0.44			
061041	Very good identification				061041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.93	0.59	SOR 1		
<i>Proteus mirabilis</i>	2.91	0.19			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.17	-.09			
061053	Good identification				061053
<i>Yersinia kristensenii</i>	96.51	0.51	PHE 1		
<i>Citrobacter braakii</i>	2.91	0.31			
<i>Salmonella</i> serovar <i>paratyphi</i>	0.31	-.09			
061063	Acceptable identification				061063
<i>Yersinia rohdei</i>	94.68	0.47	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.32	0.23			
061073	Identification to the genus				061073
<i>Yersinia rohdei</i>	61.60	0.37	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	31.16	0.33			
<i>Yersinia kristensenii</i>	5.91	0.10			
061101	Good identification				061101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	94.13	0.59	MAL 1		
<i>Proteus mirabilis</i>	5.71	0.25			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.16	-.09			

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
061201	Very good identification					061201
<i>Morganella morganii</i> subsp. <i>sibonii</i>		96.93	0.59	INO 1		
<i>Proteus mirabilis</i>		2.91	0.19			
<i>Morganella morganii</i> subsp. <i>morganii</i>		0.17	-.09			
061253	Good identification					061253
<i>Yersinia kristensenii</i>		100.0	0.36	PHE 1		
061401	Very good identification					061401
<i>Morganella morganii</i> subsp. <i>sibonii</i>		96.93	0.59	ADO 1		
<i>Proteus mirabilis</i>		2.91	0.19			
<i>Morganella morganii</i> subsp. <i>morganii</i>		0.17	-.09			
062001	Low discrimination					062001
<i>Morganella morganii</i> subsp. <i>sibonii</i>		83.84	0.36	PHE 93		
<i>Yersinia pseudotuberculosis</i>		16.16	0.10	ESL 1		
062003	Good identification					062003
<i>Yersinia pseudotuberculosis</i>		97.56	0.51	ORN 1		
<i>Hafnia alvei</i>		1.95	0.39			
<i>Shigella sonnei</i>		0.34	-.02			
062053	Identification to the genus					062053
<i>Yersinia kristensenii</i>		88.51	0.51	ESL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		8.18	0.38			
<i>Citrobacter braakii</i>		2.67	0.31			
062063	Identification to the genus					062063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		64.97	0.54	ONP 95		
<i>Yersinia rohdei</i>		35.03	0.47			
062073	Good identification					062073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		93.61	0.64	ONP 95		
<i>Yersinia rohdei</i>		5.61	0.37			
<i>Yersinia kristensenii</i>		0.54	0.10			
062103	Low discrimination					062103
<i>Hafnia alvei</i>		66.46	0.39	LYS 99		
<i>Yersinia pseudotuberculosis</i>		33.54	0.10	ESL 10		
062253	Identification to the genus					062253
<i>Yersinia kristensenii</i>		81.19	0.36	ESL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		18.22	0.30			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		0.59	0.06			
062263	Good identification					062263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		98.75	0.47	ONP 95		
<i>Yersinia rohdei</i>		1.26	0.06			
062273	Very good identification					062273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		99.76	0.56	ONP 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia kristensenii</i>	0.24	-.05			
062453	Low discrimination				062453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	77.07	0.35	ORN 3		
<i>Yersinia kristensenii</i>	22.93	0.10	URE 10		
062653	Good identification				062653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.88	0.37	ORN 3		
<i>Yersinia kristensenii</i>	4.12	-.05	URE 10		
063001	Very good identification				063001
<i>Morganella morganii subsp. sibonii</i>	96.93	0.59	ESL 1		
<i>Proteus mirabilis</i>	2.91	0.19			
<i>Morganella morganii subsp. morganii</i>	0.17	-.09			
064003	Low discrimination				064003
<i>Hafnia alvei</i>	86.69	0.59	LYS 99		
<i>Citrobacter braakii</i>	10.22	0.34			
<i>Shigella sonnei</i>	1.65	-.02			
064013	Low discrimination				064013
<i>Citrobacter braakii</i>	48.42	0.40	SOR 99		
<i>Hafnia alvei</i>	35.72	0.43			
<i>Citrobacter amalonaticus</i>	10.45	0.10			
064023	Low discrimination				064023
<i>Hafnia alvei</i>	86.53	0.39	LYS 99		
<i>Citrobacter braakii</i>	6.91	0.11	SUC 10		
<i>Yersinia rohdei</i>	6.57	0.06			
064043	Good identification				064043
<i>Citrobacter braakii</i>	94.67	0.75			
<i>Citrobacter youngae</i>	3.03	0.44			
<i>Salmonella serovar paratyphi</i>	1.31	0.18			
064051	Low discrimination				064051
<i>Citrobacter braakii</i>	75.33	0.40	MAN 99		
<i>Citrobacter amalonaticus</i>	16.26	0.10			
<i>Yersinia kristensenii</i>	8.41	0.10			
064052	Low discrimination				064052
<i>Citrobacter braakii</i>	75.33	0.40	TRE 99		
<i>Citrobacter amalonaticus</i>	16.26	0.10			
<i>Yersinia kristensenii</i>	8.41	0.10			
064053	Low discrimination				064053
<i>Citrobacter braakii</i>	74.38	0.81			
<i>Citrobacter amalonaticus</i>	16.06	0.51			
<i>Yersinia kristensenii</i>	8.31	0.51			
064063	Low discrimination				064063
<i>Citrobacter braakii</i>	44.10	0.52	SUC 7		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia rohdei</i>	41.93	0.47			
<i>Citrobacter freundii</i>	5.76	0.36			
064073	Low discrimination				064073
				VPT	
<i>Citrobacter braakii</i>	43.29	0.58	SUC 7	1	
<i>Enterobacter cloacae subsp. cloacae</i>	33.58	0.49		99	
<i>Citrobacter amalonaticus</i>	7.93	0.26		1	
064103	Very good identification				064103
<i>Hafnia alvei</i>	100.0	0.59	LYS 99		
064113	Low discrimination				064113
				VPT	
<i>Hafnia alvei</i>	85.06	0.43	LYS 99	85	
<i>Citrobacter sedlakii</i>	11.69	0.04		1	
<i>Enterobacter cloacae subsp. cloacae</i>	3.26	0.02		99	
064123	Good identification				064123
<i>Hafnia alvei</i>	100.0	0.39	LYS 99		
064153	Low discrimination				064153
				VPT	
<i>Citrobacter sedlakii</i>	83.77	0.45	ONP 99	1	
<i>Citrobacter braakii</i>	8.35	0.40		1	
<i>Enterobacter cloacae subsp. cloacae</i>	4.48	0.28		99	
064173	Very good identification				064173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	98.63	0.59	ONP 99	99	
<i>Citrobacter sedlakii</i>	0.58	0.04		1	
<i>Citrobacter braakii</i>	0.43	0.17		1	
064253	Low discrimination				064253
<i>Yersinia kristensenii</i>	59.74	0.36	SCI 1		
<i>Citrobacter braakii</i>	30.62	0.40			
<i>Citrobacter amalonaticus</i>	6.61	0.10			
064373	Good identification				064373
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.43	ONP 99		
064453	Low discrimination				064453
<i>Citrobacter braakii</i>	69.39	0.40	ADO 1		
<i>Citrobacter amalonaticus</i>	14.98	0.10			
<i>Yersinia kristensenii</i>	7.75	0.10			
064473	Good identification				064473
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	95.58	0.39	ONP 99	99	
<i>Citrobacter braakii</i>	3.73	0.17		1	
<i>Citrobacter amalonaticus</i>	0.68	-0.15		1	
064573	Good identification				064573
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.77	0.49	ONP 99	99	
<i>Citrobacter koseri</i>	3.23	0.17		1	
065001	Low discrimination				065001

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus mirabilis</i>	84.63	0.65	H2S 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	15.34	0.59			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.03	-.09			
065021	Acceptable identification				065021
<i>Proteus mirabilis</i>	91.79	0.50	H2S 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	6.02	0.34			
<i>Proteus penneri</i>	1.93	0.18			
065053	Low discrimination				065053
<i>Citrobacter braakii</i>	75.33	0.40	PHE 1		
<i>Citrobacter amalonaticus</i>	16.26	0.10			
<i>Yersinia kristensenii</i>	8.41	0.10			
066003	Low discrimination				066003
<i>Hafnia alvei</i>	66.46	0.39	LYS 99		
<i>Yersinia pseudotuberculosis</i>	33.54	0.10	ESL 10		
066073	Low discrimination				066073
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	85.38	0.42	ONP 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.76	0.23		2	
<i>Citrobacter amalonaticus</i>	4.65	0.06		1	
066103	Good identification				066103
<i>Hafnia alvei</i>	100.0	0.39	LYS 99		
066173	Good identification				066173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.72	0.51	ONP 99	99	
<i>Citrobacter sedlakii</i>	0.28	-.11		1	
066373	Good identification				066373
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.36	ONP 99		
066573	Good identification				066573
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.42	ONP 99		
070000	Very good identification				070000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.55	0.74	PHE 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.44	0.36			
<i>Shigella dysenteriae</i> (group A)	0.01	-.04			
070001	Very good identification				070001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.61	0.77	PHE 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.23	0.33			
<i>Shigella dysenteriae</i> (group A)	0.14	0.16			
070003	Low discrimination				070003
<i>Morganella morganii</i> subsp. <i>sibonii</i>	62.53	0.36	PHE 93		
<i>Shigella flexneri</i> (group B)	10.16	0.18	MAN 1		
<i>Escherichia coli</i>	5.53	0.19			
070011	Acceptable identification				070011

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	94.14	0.36	PHE 93		
<i>Yersinia kristensenii</i>	3.71	0.03	CEL 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.15	-.09			
070013	Low discrimination				070013
<i>Yersinia kristensenii</i>	86.02	0.44	SOR 99		
<i>Escherichia hermannii</i>	9.55	0.24			
<i>Citrobacter braakii</i>	2.98	0.24			
070021	Good identification				070021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.64	0.52	PHE 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.36	-.09	SUC 6		
070041	Low discrimination				070041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	80.57	0.36	PHE 93		
<i>Citrobacter braakii</i>	5.36	0.18	SOR 1		
<i>Shigella dysenteriae</i> (group A)	4.93	0.09			
070043	Low discrimination				070043
<i>Citrobacter braakii</i>	51.50	0.59			
<i>Yersinia kristensenii</i>	30.48	0.44			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.57	0.38			
070051	Acceptable identification				070051
<i>Yersinia kristensenii</i>	94.78	0.44	MAN 99		
<i>Citrobacter braakii</i>	3.28	0.24			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.25	0.13			
070052	Acceptable identification				070052
<i>Yersinia kristensenii</i>	94.78	0.44	TRE 99		
<i>Citrobacter braakii</i>	3.28	0.24			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.25	0.13			
070053	Very good identification				070053
<i>Yersinia kristensenii</i>	95.27	0.85			
<i>Citrobacter braakii</i>	3.30	0.65			
<i>Citrobacter amalonaticus</i>	0.69	0.34			
070063	Low discrimination				070063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	79.26	0.64	ONP 95		
<i>Yersinia rohdei</i>	14.24	0.47			
<i>Citrobacter braakii</i>	2.46	0.36			
070071	Low discrimination				070071
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	75.80	0.39	ONP 95		
<i>Citrobacter farmeri</i>	21.15	0.15	MAN 98		
<i>Yersinia kristensenii</i>	3.05	0.03			
070072	Low discrimination				070072
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	75.80	0.39	ONP 95		
<i>Citrobacter farmeri</i>	21.15	0.15	TRE 98		
<i>Yersinia kristensenii</i>	3.05	0.03			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
070073	Low discrimination				070073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	59.14	0.74	ONP 95		
<i>Citrobacter farmeri</i>	33.34	0.56			
<i>Yersinia kristensenii</i>	4.81	0.44			
070101	Good identification				070101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.76	0.36	PHE 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.24	-.09	MAL 1		
070153	Low discrimination				070153
<i>Citrobacter sedlakii</i>	66.83	0.45	ONP 99		
<i>Yersinia kristensenii</i>	31.55	0.44			
<i>Citrobacter braakii</i>	1.09	0.24			
070201	Good identification				070201
<i>Morganella morganii</i> subsp. <i>sibonii</i>	95.27	0.36	PHE 93		
<i>Providencia stuartii</i>	2.55	0.02	INO 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.18	-.09			
070253	Very good identification				070253
<i>Yersinia kristensenii</i>	98.21	0.69			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.56	0.40			
<i>Citrobacter braakii</i>	0.20	0.24			
070263	Very good identification				070263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.58	0.56	ONP 95		
<i>Yersinia rohdei</i>	0.42	0.06			
070273	Very good identification				070273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	95.53	0.66	ONP 95		
<i>Yersinia kristensenii</i>	3.20	0.28			
<i>Citrobacter farmeri</i>	1.27	0.15			
070401	Good identification				070401
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.76	0.36	PHE 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.24	-.09	ADO 1		
070453	Good identification				070453
<i>Yersinia kristensenii</i>	95.12	0.44	ADO 1		
<i>Citrobacter braakii</i>	3.30	0.24			
<i>Citrobacter amalonaticus</i>	0.69	-.07			
071000	Excellent identification				071000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.69	1.00			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.59			
<i>Proteus vulgaris</i>	0.00	0.02			
071001	Very good identification				071001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.77	1.00			
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.17	0.59			
<i>Proteus mirabilis</i>	0.06	0.25			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
071002	Very good identification				071002
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.69	0.59	MAN 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			
071003	Very good identification				071003
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.83	0.59	MAN 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.17	0.18			
071010	Very good identification				071010
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.69	0.59	CEL 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			
071011	Very good identification				071011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.83	0.59	CEL 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.17	0.18			
071020	Very good identification				071020
<i>Morganella morganii</i> subsp. <i>morganii</i>	96.48	0.59	SUC 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.90	0.34			
<i>Proteus vulgaris</i>	1.13	0.33			
071021	Very good identification				071021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	98.72	0.75	SUC 6		
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.51	0.18			
<i>Proteus penneri</i>	0.32	0.18			
071040	Very good identification				071040
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.69	0.59	SOR 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			
071041	Very good identification				071041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.83	0.59	SOR 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.17	0.18			
071053	Good identification				071053
<i>Yersinia kristensenii</i>	95.38	0.44	PHE 1		
<i>Citrobacter braakii</i>	3.31	0.24			
<i>Citrobacter amalonaticus</i>	0.69	-.07			
071100	Very good identification				071100
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.69	0.59	MAL 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			
071101	Very good identification				071101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.72	0.59	MAL 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.17	0.18			
<i>Proteus mirabilis</i>	0.12	-.10			
071200	Very good identification				071200
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.69	0.59	INO 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
071201	Good identification				071201
<i>Morganella morganii</i> subsp. <i>sibonii</i>	93.37	0.59	INO 1		
<i>Providencia stuartii</i>	3.57	0.28			
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.06	0.18			
071400	Very good identification				071400
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.66	0.59	ADO 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			
<i>Providencia alcalifaciens</i>	0.03	-.17			
071401	Very good identification				071401
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.83	0.59	ADO 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.17	0.18			
072001	Good identification				072001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.76	0.36	PHE 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.24	-.09	ESL 1		
072053	Low discrimination				072053
<i>Yersinia kristensenii</i>	75.46	0.44	ESL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	16.27	0.38			
<i>Citrobacter amalonaticus</i>	5.33	0.14			
072063	Very good identification				072063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.49	0.54	ONP 95		
<i>Escherichia coli</i>	1.98	0.21			
<i>Yersinia rohdei</i>	0.53	0.06			
072073	Very good identification				072073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.98	0.64	ONP 95		
<i>Citrobacter farmeri</i>	1.67	0.15			
<i>Yersinia kristensenii</i>	0.24	0.03			
072263	Good identification				072263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.47	ONP 95		
072273	Very good identification				072273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.56	ONP 95		
073000	Very good identification				073000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.65	0.59	ESL 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			
<i>Proteus vulgaris</i>	0.04	0.02			
073001	Very good identification				073001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	96.83	0.59	ESL 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.17	0.18			
074001	Acceptable identification				074001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	93.28	0.36	PHE 93		
<i>Proteus mirabilis</i>	2.85	-.04	SCI 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.13	-.09			
074043	Identification to the genus				074043
<i>Citrobacter braakii</i>	86.54	0.69			
<i>Citrobacter amalonaticus</i>	12.19	0.34			
<i>Citrobacter youngae</i>	0.99	0.28			
074053	Identification to the genus				074053
<i>Citrobacter amalonaticus</i>	86.02	0.75	ONP 94		
<i>Citrobacter braakii</i>	12.53	0.75			
<i>Yersinia kristensenii</i>	1.22	0.44			
074063	Low discrimination				074063
<i>Citrobacter braakii</i>	69.50	0.46	SUC 7		
<i>Citrobacter freundii</i>	9.08	0.29			
<i>Citrobacter amalonaticus</i>	8.30	0.10			
074073	Identification to the genus				074073
<i>Citrobacter amalonaticus</i>	71.94	0.51	ONP 94		
<i>Citrobacter braakii</i>	12.36	0.52	SUC 6		
<i>Citrobacter farmeri</i>	12.28	0.37			
074153	Good identification				074153
<i>Citrobacter sedlakii</i>	90.24	0.59	ONP 99		
<i>Citrobacter amalonaticus</i>	6.23	0.34			
<i>Citrobacter koseri</i>	2.54	0.34			
074553	Very good identification				074553
<i>Citrobacter koseri</i>	97.61	0.59	ONP 99		
<i>Citrobacter sedlakii</i>	2.24	0.18			
<i>Citrobacter amalonaticus</i>	0.16	-.07			
074573	Very good identification				074573
				VPT	
<i>Citrobacter koseri</i>	99.70	0.58	ONP 99	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.30	0.08		99	
075000	Very good identification				075000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.59	0.59	SCI 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.31	0.18			
<i>Proteus mirabilis</i>	0.07	-.04			
075001	Low discrimination				075001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	85.32	0.59	SCI 1		
<i>Proteus mirabilis</i>	9.60	0.30			
<i>Morganella morganii</i> subsp. <i>morganii</i>	2.79	0.18			
075201	Good identification				075201
<i>Providencia stuartii</i>	97.84	0.51	ORN 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.95	0.18			
<i>Proteus mirabilis</i>	0.22	-.11			
075221	Good identification				075221

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	100.0	0.51	ORN 1		
075402	Good identification				075402
<i>Providencia rettgeri</i>	99.67	0.39	ORN 1		
<i>Providencia alcalifaciens</i>	0.33	-0.17	INO 90		
075602	Very good identification				075602
<i>Providencia rettgeri</i>	100.0	0.59	ORN 1		
075622	Good identification				075622
<i>Providencia rettgeri</i>	100.0	0.43	ORN 1		
076053	Very good identification				076053
<i>Citrobacter amalonaticus</i>	98.10	0.55	ONP 94		
<i>Citrobacter braakii</i>	1.46	0.34	ESL 9		
<i>Citrobacter sedlakii</i>	0.30	0.04			
076153	Good identification				076153
<i>Citrobacter sedlakii</i>	96.65	0.45	ONP 99		
<i>Citrobacter amalonaticus</i>	3.22	0.14			
<i>Citrobacter koseri</i>	0.13	-0.07			
077602	Very good identification				077602
<i>Providencia rettgeri</i>	100.0	0.53	ORN 1		
077622	Good identification				077622
<i>Providencia rettgeri</i>	100.0	0.38	ORN 1		
100000	Very good identification				100000
<i>Shigella dysenteriae</i> (group A)	97.84	0.73	TRE 90		
<i>Shigella boydii</i> (group C)	1.65	0.34			
<i>Shigella flexneri</i> (group B)	0.50	0.26			
100001	Very good identification				100001
<i>Shigella dysenteriae</i> (group A)	98.65	0.92			
<i>Shigella boydii</i> (group C)	1.05	0.49			
<i>Shigella sonnei</i>	0.16	0.24			
100002	Identification to the genus				100002
<i>Shigella boydii</i> (group C)	81.30	0.65	ONP 10		
<i>Shigella flexneri</i> (group B)	14.55	0.53			
<i>Shigella sonnei</i>	2.19	0.24			
100003	Low discrimination				100003
<i>Shigella boydii</i> (group C)	61.31	0.80	ONP 10		
<i>Shigella sonnei</i>	28.86	0.65			
<i>Shigella flexneri</i> (group B)	3.93	0.59			
100011	Low discrimination				100011
<i>Shigella dysenteriae</i> (group A)	84.72	0.51	CEL 1		
<i>Escherichia vulneris</i>	13.50	0.28			
<i>Shigella boydii</i> (group C)	0.90	0.08			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
100013	Good identification				100013
<i>Escherichia vulneris</i>	90.53	0.69			
<i>Shigella sonnei</i>	4.82	0.39			
<i>Shigella boydii</i> (group C)	1.97	0.39			
100021	Good identification				100021
<i>Shigella dysenteriae</i> (group A)	96.36	0.51	SUC 1		
<i>Yersinia rohdei</i>	1.50	0.18			
<i>Shigella boydii</i> (group C)	1.02	0.08			
100023	Low discrimination				100023
<i>Yersinia rohdei</i>	62.55	0.59	SOR 99		
<i>Shigella boydii</i> (group C)	13.89	0.39			
<i>Escherichia coli</i>	7.70	0.44			
100033	Low discrimination				100033
<i>Escherichia vulneris</i>	64.63	0.47	SUC 8		
<i>Yersinia rohdei</i>	24.23	0.49			
<i>Citrobacter freundii</i>	4.60	0.41			
100040	Very good identification				100040
<i>Shigella dysenteriae</i> (group A)	96.55	0.65	TRE 90		
<i>Shigella boydii</i> (group C)	2.86	0.31			
<i>Shigella flexneri</i> (group B)	0.47	0.18			
100041	Very good identification				100041
<i>Shigella dysenteriae</i> (group A)	97.52	0.85			
<i>Shigella boydii</i> (group C)	1.82	0.47			
<i>Escherichia coli</i>	0.25	0.39			
100042	Low discrimination				100042
<i>Shigella boydii</i> (group C)	86.14	0.62	ONP 10		
<i>Shigella flexneri</i> (group B)	8.35	0.45			
<i>Escherichia coli</i>	2.10	0.39			
100043	Low discrimination				100043
<i>Shigella boydii</i> (group C)	60.87	0.78	ONP 10		
<i>Citrobacter youngae</i>	18.96	0.78			
<i>Escherichia coli</i>	4.97	0.65			
100051	Low discrimination				100051
<i>Shigella dysenteriae</i> (group A)	68.43	0.44	CEL 1		
<i>Yersinia kristensenii</i>	11.89	0.26			
<i>Citrobacter youngae</i>	10.51	0.35			
100053	Low discrimination				100053
<i>Yersinia kristensenii</i>	39.20	0.67	ORN 92		
<i>Citrobacter youngae</i>	34.67	0.76			
<i>Citrobacter braakii</i>	11.69	0.67			
100061	Low discrimination				100061

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia rohdei</i>	69.71	0.59	MAN 99		
<i>Shigella dysenteriae</i> (group A)	19.37	0.44			
<i>Citrobacter freundii</i>	5.62	0.43			
100062	Low discrimination				100062
<i>Yersinia rohdei</i>	84.46	0.59	TRE 99		
<i>Citrobacter freundii</i>	6.81	0.43			
<i>Escherichia coli</i>	4.01	0.35			
100063	Good identification				100063
<i>Yersinia rohdei</i>	90.03	1.00			
<i>Citrobacter freundii</i>	7.26	0.84			
<i>Citrobacter youngae</i>	1.25	0.66			
100071	Low discrimination				100071
<i>Yersinia rohdei</i>	75.68	0.49	MAN 99		
<i>Citrobacter freundii</i>	14.38	0.41			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.48	0.29			
100072	Low discrimination				100072
<i>Yersinia rohdei</i>	75.95	0.49	TRE 99		
<i>Citrobacter freundii</i>	14.43	0.41			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.51	0.29			
100073	Low discrimination				100073
<i>Yersinia rohdei</i>	78.37	0.90			
<i>Citrobacter freundii</i>	14.89	0.82			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.32	0.64			
100101	Good identification				100101
<i>Shigella dysenteriae</i> (group A)	97.91	0.51	MAL 1		
<i>Shigella boydii</i> (group C)	1.04	0.08			
<i>Escherichia vulneris</i>	0.89	0.02			
100103	Low discrimination				100103
<i>Escherichia vulneris</i>	59.19	0.43	CEL 99		
<i>Shigella boydii</i> (group C)	22.46	0.39			
<i>Shigella sonnei</i>	10.57	0.24			
100111	Good identification				100111
<i>Escherichia vulneris</i>	98.89	0.43	MAN 99		
<i>Shigella dysenteriae</i> (group A)	1.11	0.10			
100112	Good identification				100112
<i>Escherichia vulneris</i>	100.0	0.43	TRE 99		
100113	Very good identification				100113
<i>Escherichia vulneris</i>	99.97	0.85			
<i>Pantoea agglomerans</i>	0.01	0.03			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.01	0.18			
100123	Low discrimination				100123

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Pantoea agglomerans</i>	89.66	0.47	ESL 99		
<i>Escherichia vulneris</i>	7.25	0.22			
<i>Yersinia rohdei</i>	1.44	0.18			
100133	Good identification				100133
				VPT	
<i>Escherichia vulneris</i>	90.76	0.63	SUC 8	1	
<i>Pantoea agglomerans</i>	8.91	0.44		64	
<i>Serratia rubidaea</i>	0.11	0.06		99	
100141	Good identification				100141
<i>Shigella dysenteriae</i> (group A)	96.33	0.44	MAL 1		
<i>Shigella boydii</i> (group C)	1.80	0.06			
<i>Citrobacter youngae</i>	0.95	0.11			
100143	Low discrimination				100143
<i>Citrobacter youngae</i>	32.38	0.52	MAL 5		
<i>Citrobacter werkmanii</i>	31.49	0.35			
<i>Shigella boydii</i> (group C)	19.95	0.37			
100153	Low discrimination				100153
<i>Escherichia vulneris</i>	61.31	0.43	SOR 1		
<i>Citrobacter youngae</i>	23.31	0.50			
<i>Citrobacter freundii</i>	7.06	0.42			
100163	Low discrimination				100163
<i>Yersinia rohdei</i>	55.84	0.59	MAL 1		
<i>Citrobacter freundii</i>	38.75	0.63			
<i>Citrobacter youngae</i>	4.04	0.40			
100173	Low discrimination				100173
<i>Citrobacter freundii</i>	52.41	0.60	MAL 8		
<i>Yersinia rohdei</i>	32.04	0.49			
<i>Citrobacter youngae</i>	5.69	0.38			
100201	Good identification				100201
<i>Shigella dysenteriae</i> (group A)	98.61	0.51	INO 1		
<i>Shigella boydii</i> (group C)	1.05	0.08			
<i>Providencia stuartii</i>	0.19	-0.04			
100203	Low discrimination				100203
<i>Shigella boydii</i> (group C)	58.78	0.39	ONP 10		
<i>Shigella sonnei</i>	27.67	0.24	INO 1		
<i>Shigella flexneri</i> (group B)	3.77	0.18			
100213	Low discrimination				100213
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	56.51	0.51	ADO 97		
<i>Escherichia vulneris</i>	36.43	0.28			
<i>Yersinia kristensenii</i>	3.01	0.11			
100233	Low discrimination				100233
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	66.73	0.39	ADO 97		
<i>Escherichia vulneris</i>	14.96	0.06			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.09	0.15			
100241	Good identification				100241
<i>Shigella dysenteriae</i> (group A)	97.23	0.44	INO 1		
<i>Shigella boydii</i> (group C)	1.81	0.06			
<i>Citrobacter youngae</i>	0.96	0.11			
100243	Low discrimination				100243
<i>Citrobacter youngae</i>	50.35	0.52	INO 5		
<i>Shigella boydii</i> (group C)	31.02	0.37			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.79	0.35			
100253	Low discrimination				100253
<i>Yersinia kristensenii</i>	53.66	0.52	ORN 92		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	18.93	0.57			
<i>Citrobacter youngae</i>	14.15	0.50			
100263	Low discrimination				100263
<i>Yersinia rohdei</i>	72.99	0.59	INO 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.59	0.47			
<i>Citrobacter freundii</i>	5.88	0.43			
100273	Low discrimination				100273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	50.91	0.56	ORN 95		
<i>Yersinia rohdei</i>	28.30	0.49			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.32	0.44			
100313	Good identification				100313
<i>Escherichia vulneris</i>	99.16	0.43	INO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.84	0.20			
100401	Good identification				100401
<i>Shigella dysenteriae</i> (group A)	98.24	0.51	ADO 1		
<i>Shigella boydii</i> (group C)	1.04	0.08			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.56	0.17			
100403	Low discrimination				100403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	49.98	0.58	CEL 92		
<i>Shigella boydii</i> (group C)	30.11	0.39			
<i>Shigella sonnei</i>	14.17	0.24			
100411	Low discrimination				100411
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	84.94	0.39	MAN 99		
<i>Shigella dysenteriae</i> (group A)	12.99	0.10			
<i>Escherichia vulneris</i>	2.07	-0.13			
100412	Good identification				100412
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.81	0.46	TRE 98		
<i>Escherichia vulneris</i>	1.19	-0.13			
100413	Very good identification				100413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.42	0.80			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia vulneris</i>	2.37	0.28			
<i>Shigella sonnei</i>	0.13	-.02			
100423	Low discrimination				100423
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	80.51	0.46	CEL 92		
<i>Yersinia rohdei</i>	8.83	0.18			
<i>Escherichia coli</i>	5.66	0.17			
100433	Very good identification				100433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.35	0.68		1	
<i>Serratia rubidaea</i>	3.42	0.23		99	
<i>Escherichia vulneris</i>	0.81	0.06		1	
100441	Acceptable identification				100441
<i>Shigella dysenteriae</i> (group A)	94.61	0.44	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.35	0.23			
<i>Shigella boydii</i> (group C)	1.76	0.06			
100443	Low discrimination				100443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	67.38	0.64	CEL 92		
<i>Shigella boydii</i> (group C)	16.49	0.37			
<i>Escherichia coli</i>	7.02	0.39			
100451	Good identification				100451
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.59	0.45	MAN 99		
<i>Shigella dysenteriae</i> (group A)	3.41	0.03			
100452	Good identification				100452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.51	TRE 98		
100453	Very good identification				100453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.43	0.86			
<i>Yersinia kristensenii</i>	0.60	0.26			
<i>Citrobacter youngae</i>	0.53	0.35			
100463	Low discrimination				100463
<i>Yersinia rohdei</i>	75.78	0.59	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	12.97	0.52			
<i>Citrobacter freundii</i>	6.11	0.43			
100472	Acceptable identification				100472
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.27	0.39	TRE 98		
<i>Yersinia rohdei</i>	7.74	0.08			
100473	Low discrimination				100473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.91	0.73			
<i>Yersinia rohdei</i>	13.87	0.49			
<i>Citrobacter freundii</i>	2.64	0.41			
100513	Low discrimination				100513
<i>Escherichia vulneris</i>	80.00	0.43	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	17.92	0.49			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	1.27	0.12			
100533	Low discrimination				100533
				VPT	
<i>Serratia rubidaea</i>	84.62	0.47	ESL 94	99	
<i>Escherichia vulneris</i>	7.24	0.22	SCI 95	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	4.66	0.37		1	
100553	Identification to the genus				100553
<i>Klebsiella pneumoniae subsp. ozaenae</i>	80.23	0.55	MAL 3		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	17.09	0.23			
<i>Escherichia vulneris</i>	1.95	0.02			
100603	Very good identification				100603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.27	0.60	CEL 92		
<i>Shigella boydii (group C)</i>	0.49	-.02			
<i>Shigella sonnei</i>	0.23	-.17			
100611	Good identification				100611
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	MAN 99		
100612	Good identification				100612
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.47	TRE 98		
100613	Very good identification				100613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.95	0.82		1	
<i>Serratia odorifera biovar 2</i>	0.04	0.03		99	
<i>Escherichia vulneris</i>	0.02	-.13		1	
100623	Good identification				100623
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.48	CEL 92		
100633	Very good identification				100633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.15	0.70		1	
<i>Serratia rubidaea</i>	0.73	0.10		99	
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	0.12	-.09		1	
100643	Very good identification				100643
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.26	0.66	CEL 92	1	
<i>Citrobacter youngae</i>	0.33	0.11		1	
<i>Serratia odorifera biovar 2</i>	0.22	0.03		99	
100651	Acceptable identification				100651
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	94.54	0.47	MAN 99	1	
<i>Serratia odorifera biovar 2</i>	5.46	0.13		99	
100652	Good identification				100652
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.08	0.53	TRE 98	1	
<i>Serratia odorifera biovar 2</i>	0.93	0.03		99	
100653	Very good identification				100653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.53	0.88		1	
<i>Serratia odorifera biovar 2</i>	1.84	0.44		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.53	0.23		1	
100663	Good identification				100663
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.86	0.53	CEL 92		
<i>Yersinia rohdei</i>	4.53	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.91	0.05			
100672	Good identification				100672
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.90	0.40	TRE 98		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.10	-.09			
100673	Good identification				100673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.52	0.75			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	6.05	0.33			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.24	0.15			
100713	Acceptable identification				100713
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	90.22	0.51	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	5.60	0.08			
<i>Escherichia vulneris</i>	3.33	0.02			
100753	Identification to the genus				100753
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	76.69	0.49	ONP 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	23.17	0.57		1	
<i>Serratia odorifera</i> biovar 2	0.14	0.03		99	
100773	Very good identification				100773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	97.44	0.59	ONP 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.45	0.44		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.05	0.00		99	
101001	Good identification				101001
<i>Shigella dysenteriae</i> (group A)	95.66	0.51	PHE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2.99	0.23			
<i>Shigella boydii</i> (group C)	1.01	0.08			
101003	Low discrimination				101003
<i>Shigella boydii</i> (group C)	61.50	0.39	ONP 10		
<i>Shigella sonnei</i>	28.95	0.24	PHE 1		
<i>Shigella flexneri</i> (group B)	3.94	0.18			
101041	Good identification				101041
<i>Shigella dysenteriae</i> (group A)	98.17	0.44	PHE 1		
<i>Shigella boydii</i> (group C)	1.83	0.06			
101043	Low discrimination				101043
<i>Shigella boydii</i> (group C)	61.17	0.37	ONP 10		
<i>Citrobacter youngae</i>	19.06	0.37	PHE 1		
<i>Escherichia coli</i>	5.00	0.24			
101063	Good identification				101063
<i>Yersinia rohdei</i>	90.09	0.59	PHE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	7.26	0.43			
<i>Citrobacter youngae</i>	1.25	0.25			
101073	Low discrimination				101073
<i>Yersinia rohdei</i>	78.76	0.49	PHE 1		
<i>Citrobacter freundii</i>	14.97	0.41			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.34	0.23			
101113	Good identification				101113
<i>Escherichia vulneris</i>	100.0	0.43	PHE 1		
101413	Good identification				101413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.62	0.39	PHE 1		
<i>Escherichia vulneris</i>	2.38	-.13			
101453	Good identification				101453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.45	PHE 1		
101613	Good identification				101613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	PHE 1		
101653	Good identification				101653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.15	0.47	PHE 1	1	
<i>Serratia odorifera</i> biovar 2	1.85	0.03		99	
102001	Low discrimination				102001
<i>Shigella dysenteriae</i> (group A)	75.04	0.51	ESL 1		
<i>Yersinia pseudotuberculosis</i>	23.76	0.33			
<i>Shigella boydii</i> (group C)	0.80	0.08			
102003	Very good identification				102003
<i>Yersinia pseudotuberculosis</i>	97.72	0.74	URE 95		
<i>Shigella boydii</i> (group C)	1.07	0.39			
<i>Shigella sonnei</i>	0.50	0.24			
102013	Low discrimination				102013
<i>Escherichia vulneris</i>	76.95	0.57			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	15.78	0.62			
<i>Yersinia pseudotuberculosis</i>	6.18	0.33			
102023	Low discrimination				102023
<i>Pantoea agglomerans</i>	70.39	0.47	MAL 99		
<i>Yersinia pseudotuberculosis</i>	22.97	0.33			
<i>Escherichia coli</i>	3.44	0.31			
102033	Low discrimination				102033
<i>Pantoea agglomerans</i>	51.32	0.44	MAL 99		
<i>Escherichia vulneris</i>	23.07	0.35			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	13.60	0.49			
102041	Acceptable identification				102041
<i>Shigella dysenteriae</i> (group A)	90.90	0.44	ESL 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	5.83	0.26			
<i>Shigella boydii</i> (group C)	1.70	0.06			
102043	Low discrimination				102043
<i>Escherichia coli</i>	30.32	0.53	IND 92		
<i>Citrobacter youngae</i>	24.35	0.52			
<i>Yersinia pseudotuberculosis</i>	18.39	0.33			
102053	Low discrimination				102053
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	71.62	0.67	ADO 97		
<i>Citrobacter youngae</i>	16.36	0.50			
<i>Yersinia kristensenii</i>	3.55	0.26			
102063	Low discrimination				102063
<i>Yersinia rohdei</i>	62.78	0.59	ESL 1		
<i>Escherichia coli</i>	14.17	0.49			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.76	0.44			
102073	Low discrimination				102073
<i>Serratia ficaria</i>	69.73	0.57	SCI 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.94	0.54			
<i>Yersinia rohdei</i>	8.53	0.49			
102103	Low discrimination				102103
<i>Pantoea agglomerans</i>	63.85	0.47	SUC 99		
<i>Yersinia pseudotuberculosis</i>	20.83	0.33			
<i>Escherichia vulneris</i>	14.85	0.31			
102113	Very good identification				102113
<i>Escherichia vulneris</i>	96.14	0.72			
<i>Pantoea agglomerans</i>	3.28	0.44			
<i>Leclercia adecarboxylata</i>	0.46	0.30			
102121	Good identification				102121
<i>Pantoea agglomerans</i>	100.0	0.47	MAN 99		
102122	Good identification				102122
<i>Pantoea agglomerans</i>	100.0	0.47	TRE 99		
102123	Very good identification				102123
				VPT	
<i>Pantoea agglomerans</i>	99.96	0.88		64	
<i>Escherichia vulneris</i>	0.02	0.09		1	
<i>Serratia rubidaea</i>	0.01	0.06		99	
102131	Good identification				102131
<i>Pantoea agglomerans</i>	97.23	0.44	MAN 99		
<i>Escherichia vulneris</i>	2.50	0.09			
<i>Leclercia adecarboxylata</i>	0.27	-0.05			
102132	Good identification				102132
<i>Pantoea agglomerans</i>	97.23	0.44	TRE 99		
<i>Escherichia vulneris</i>	2.50	0.09			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	0.27	-0.05			
102133	Very good identification				102133
<i>Pantoea agglomerans</i>	97.02	0.86			
<i>Escherichia vulneris</i>	2.50	0.50			
<i>Leclercia adecarboxylata</i>	0.27	0.36			
102163	Good identification				102163
<i>Pantoea agglomerans</i>	96.21	0.47	SOR 1		
<i>Yersinia rohdei</i>	1.54	0.18			
<i>Citrobacter freundii</i>	1.07	0.21			
102173	Low discrimination				102173
<i>Pantoea agglomerans</i>	86.40	0.44	SOR 1		
<i>Serratia ficaria</i>	4.81	0.16			
<i>Escherichia vulneris</i>	2.22	0.09			
102213	Very good identification				102213
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.46	0.63	ADO 97		
<i>Escherichia vulneris</i>	3.85	0.16			
<i>Yersinia pseudotuberculosis</i>	0.31	-0.09			
102233	Low discrimination				102233
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	44.53	0.51	ADO 97	1	
<i>Cronobacter sakazakii</i>	43.13	0.38		99	
<i>Serratia ficaria</i>	9.35	0.18		75	
102243	Low discrimination				102243
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.92	0.47	ADO 97		
<i>Citrobacter youngae</i>	11.05	0.25	CEL 92		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.71	0.10			
102253	Low discrimination				102253
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	87.93	0.69	ADO 97	1	
<i>Serratia odorifera biovar 2</i>	7.31	0.39		99	
<i>Serratia ficaria</i>	2.48	0.18		75	
102263	Low discrimination				102263
<i>Yersinia enterocolitica ssp. enterocolitica</i>	46.82	0.37	ORN 95		
<i>Serratia ficaria</i>	23.63	0.18			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	18.18	0.35			
102273	Low discrimination				102273
<i>Serratia ficaria</i>	86.79	0.59	SCI 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	7.76	0.57			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	5.21	0.47			
102323	Good identification				102323
<i>Pantoea agglomerans</i>	99.76	0.47	INO 1		
<i>Serratia rubidaea</i>	0.24	-0.06			
102333	Low discrimination				102333

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Pantoea agglomerans</i>	86.58	0.44	INO 1		
<i>Cronobacter sakazakii</i>	5.96	0.25			
<i>Serratia rubidaea</i>	4.12	0.18			
102353	Low discrimination				102353
<i>Klebsiella pneumoniae subsp. ozaenae</i>	84.52	0.38	MAL 3		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	9.79	0.00	ADO 97		
<i>Escherichia vulneris</i>	3.39	-.10			
102402	Acceptable identification				102402
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.55	0.36	CEL 92		
<i>Yersinia pseudotuberculosis</i>	6.45	-.09	TRE 98		
102403	Low discrimination				102403
<i>Klebsiella pneumoniae subsp. ozaenae</i>	87.48	0.71	CEL 92		
<i>Yersinia pseudotuberculosis</i>	12.18	0.33			
<i>Escherichia coli</i>	0.14	0.09			
102411	Good identification				102411
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.52	MAN 99		
102412	Very good identification				102412
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.58	TRE 98		
102413	Very good identification				102413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.39	0.93			
<i>Leclercia adecarboxylata</i>	0.41	0.30			
<i>Escherichia vulneris</i>	0.15	0.16			
102423	Low discrimination				102423
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	88.18	0.58	CEL 92	1	
<i>Serratia rubidaea</i>	9.09	0.23		99	
<i>Pantoea agglomerans</i>	1.52	0.05		64	
102431	Low discrimination				102431
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	85.32	0.39	MAN 99	1	
<i>Serratia rubidaea</i>	11.98	0.06		99	
<i>Leclercia adecarboxylata</i>	2.70	-.05		1	
102432	Acceptable identification				102432
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	92.15	0.46	TRE 98	1	
<i>Serratia rubidaea</i>	6.40	0.06		99	
<i>Leclercia adecarboxylata</i>	1.44	-.05		1	
102433	Low discrimination				102433
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	85.20	0.80		1	
<i>Serratia rubidaea</i>	11.96	0.47		99	
<i>Leclercia adecarboxylata</i>	2.69	0.36		1	
102441	Acceptable identification				102441
<i>Klebsiella pneumoniae subsp. ozaenae</i>	90.79	0.35	CEL 92		
<i>Shigella dysenteriae (group A)</i>	9.21	0.03	MAN 99		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
102442	Good identification					102442
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.42	CEL 92		
102443	Very good identification					102443
<i>Klebsiella pneumoniae subsp. ozaenae</i>		99.12	0.76	CEL 92		
<i>Escherichia coli</i>		0.65	0.26			
<i>Citrobacter youngae</i>		0.10	0.11			
102451	Very good identification					102451
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.57	MAN 99		
102452	Very good identification					102452
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.63	TRE 98		
102453	Excellent identification					102453
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		99.99	0.98		1	
<i>Citrobacter youngae</i>		0.01	0.09		1	
<i>Serratia odorifera biovar 2</i>		0.00	0.00		99	
102463	Very good identification					102463
<i>Klebsiella pneumoniae subsp. ozaenae</i>		96.67	0.64	CEL 92		
<i>Escherichia coli</i>		1.68	0.23			
<i>Yersinia rohdei</i>		1.43	0.18			
102471	Good identification					102471
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.45	MAN 99		
102472	Good identification					102472
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.51	TRE 98		
102473	Very good identification					102473
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		99.40	0.86		1	
<i>Serratia ficaria</i>		0.35	0.16		75	
<i>Serratia rubidaea</i>		0.08	0.06		99	
102503	Low discrimination					102503
<i>Klebsiella pneumoniae subsp. ozaenae</i>		64.42	0.40	MAL 3		
<i>Leclercia adecarboxylata</i>		13.09	0.12	CEL 92		
<i>Pantoea agglomerans</i>		8.98	0.05			
102513	Low discrimination					102513
<i>Leclercia adecarboxylata</i>		54.36	0.53	IND 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>		31.08	0.62			
<i>Escherichia vulneris</i>		8.67	0.31			
102523	Low discrimination					102523
					VPT	
<i>Pantoea agglomerans</i>		50.19	0.47	ADO 1	64	
<i>Serratia rubidaea</i>		47.47	0.47		99	
<i>Leclercia adecarboxylata</i>		1.43	0.18		1	
102533	Low discrimination					102533
					VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia rubidaea</i>	79.40	0.72	SCI 95	99	
<i>Leclercia adecarboxylata</i>	15.16	0.59		1	
<i>Pantoea agglomerans</i>	4.21	0.44		64	
102543	Good identification				102543
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.45	MAL 3		
102553	Very good identification				102553
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.73	0.67	MAL 3		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	2.21	0.15			
<i>Leclercia adecarboxylata</i>	0.92	0.12			
102573	Low discrimination				102573
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	56.45	0.55	MAL 3	1	
<i>Serratia rubidaea</i>	21.84	0.31		99	
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	15.46	0.25		1	
102602	Good identification				102602
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.38	CEL 92		
102603	Very good identification				102603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.89	0.73	CEL 92		
<i>Yersinia pseudotuberculosis</i>	0.12	-.09			
102611	Very good identification				102611
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.53	MAN 99		
102612	Very good identification				102612
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.60	TRE 98		
102613	Excellent identification				102613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.99	0.95		1	
<i>Serratia rubidaea</i>	0.01	-.06		99	
<i>Serratia odorifera biovar 2</i>	0.01	0.00		99	
102623	Very good identification				102623
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.94	0.60	CEL 92	1	
<i>Serratia rubidaea</i>	2.07	0.10		99	
102631	Good identification				102631
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.21	0.41	MAN 99	1	
<i>Serratia rubidaea</i>	2.79	-.06		99	
102632	Good identification				102632
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.60	0.47	TRE 98	1	
<i>Serratia rubidaea</i>	1.40	-.06		99	
102633	Very good identification				102633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.16	0.82		1	
<i>Serratia rubidaea</i>	2.79	0.35		99	
<i>Cronobacter sakazakii</i>	0.03	-.03		99	
102641	Good identification				102641

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	CEL 92		
102642	Good identification				102642
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	CEL 92		
102643	Very good identification				102643
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.96	0.78	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	0.04	0.00		99	
102651	Very good identification				102651
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.05	0.59	MAN 99	1	
<i>Serratia odorifera</i> biovar 2	0.95	0.10		99	
102652	Very good identification				102652
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.85	0.65	TRE 98	1	
<i>Serratia odorifera</i> biovar 2	0.16	0.00		99	
102653	Excellent identification				102653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.63	1.00		1	
<i>Serratia odorifera</i> biovar 2	0.31	0.41		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.06	0.15		1	
102663	Very good identification				102663
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.66	CEL 92		
102671	Good identification				102671
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.47	MAN 99		
102672	Good identification				102672
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.53	TRE 98		
102673	Very good identification				102673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.92	0.88			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.69	0.25			
<i>Serratia ficaria</i>	0.35	0.18			
102703	Good identification				102703
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.37	0.42	MAL 3	1	
<i>Serratia rubidaea</i>	2.63	-.06	CEL 92	99	
102713	Good identification				102713
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.33	0.63	MAL 3	1	
<i>Serratia rubidaea</i>	3.47	0.18		99	
<i>Leclercia adecarboxylata</i>	1.36	0.12		1	
102733	Good identification				102733
				VPT	
<i>Serratia rubidaea</i>	92.24	0.60	SCI 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.34	0.51		1	
<i>Leclercia adecarboxylata</i>	0.71	0.18		1	
102743	Good identification				102743

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.04	0.47	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.96	0.00	CEL 92		
102753	Identification to the genus				102753
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	73.76	0.69	MAL 3	1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	26.16	0.42		1	
<i>Serratia odorifera</i> biovar 2	0.08	0.00		99	
102773	Identification to the genus				102773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	78.74	0.51	ONP 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	18.50	0.57		1	
<i>Serratia rubidaea</i>	1.46	0.18		99	
103123	Very good identification				103123
<i>Pantoea agglomerans</i>	100.0	0.67	PHE 9		
103133	Very good identification				103133
				VPT	
<i>Pantoea agglomerans</i>	99.48	0.65	PHE 9	64	
<i>Escherichia vulneris</i>	0.26	0.09		1	
<i>Cronobacter sakazakii</i>	0.23	0.15		99	
103233	Good identification				103233
				VPT	
<i>Cronobacter sakazakii</i>	98.97	0.38	ORN 91	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.03	0.10	SCI 99	1	
103413	Good identification				103413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.52	PHE 1		
103433	Low discrimination				103433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	85.32	0.39	PHE 1	1	
<i>Serratia rubidaea</i>	11.98	0.06		99	
<i>Leclercia adecarboxylata</i>	2.70	-.05		1	
103443	Good identification				103443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.35	PHE 1		
103453	Very good identification				103453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.57	PHE 1		
103473	Good identification				103473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.45	PHE 1		
103613	Very good identification				103613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.53	PHE 1		
103633	Acceptable identification				103633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.46	0.41	PHE 1	1	
<i>Cronobacter sakazakii</i>	2.83	-.03		99	
<i>Serratia rubidaea</i>	2.71	-.06		99	
103643	Good identification				103643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	PHE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
103653	Very good identification				103653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.69	0.59	PHE 1	VPT 1	
<i>Serratia odorifera</i> biovar 2	0.31	0.00		99	
103673	Good identification				103673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.47	PHE 1		
104001	Good identification				104001
<i>Shigella dysenteriae</i> (group A)	98.57	0.51	SCI 1		
<i>Shigella boydii</i> (group C)	1.04	0.08			
<i>Citrobacter youngae</i>	0.23	0.05			
104003	Low discrimination				104003
<i>Shigella boydii</i> (group C)	36.40	0.39	ONP 10		
<i>Citrobacter youngae</i>	24.35	0.46	SCI 1		
<i>Shigella sonnei</i>	17.13	0.24			
104013	Low discrimination				104013
<i>Citrobacter youngae</i>	31.51	0.44	SOR 99		
<i>Escherichia vulneris</i>	26.78	0.28			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	14.57	0.42			
104023	Low discrimination				104023
<i>Citrobacter freundii</i>	79.65	0.56	SOR 99		
<i>Citrobacter youngae</i>	9.75	0.34			
<i>Pantoea agglomerans</i>	6.28	0.18			
104033	Low discrimination				104033
<i>Citrobacter freundii</i>	53.85	0.54	SOR 99	VPT 1	
<i>Cronobacter sakazakii</i>	10.99	0.28		99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	10.35	0.30		99	
104041	Low discrimination				104041
<i>Shigella dysenteriae</i> (group A)	56.09	0.44	SCI 1		
<i>Citrobacter youngae</i>	29.98	0.46			
<i>Citrobacter freundii</i>	8.05	0.37			
104042	Low discrimination				104042
<i>Citrobacter youngae</i>	60.68	0.46	TRE 99		
<i>Citrobacter freundii</i>	16.28	0.37			
<i>Shigella boydii</i> (group C)	12.08	0.21			
104043	Identification to the genus				104043
<i>Citrobacter youngae</i>	69.24	0.87			
<i>Citrobacter freundii</i>	18.58	0.78			
<i>Citrobacter braakii</i>	9.92	0.71			
104051	Identification to the genus				104051
<i>Citrobacter youngae</i>	59.71	0.44	MAN 99		
<i>Citrobacter braakii</i>	21.23	0.36			
<i>Citrobacter freundii</i>	15.39	0.35			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
104052	Identification to the genus				104052
<i>Citrobacter youngae</i>	60.67	0.44	TRE 99		
<i>Citrobacter braakii</i>	21.57	0.36			
<i>Citrobacter freundii</i>	15.63	0.35			
104053	Identification to the genus				104053
<i>Citrobacter youngae</i>	60.50	0.86			
<i>Citrobacter braakii</i>	21.51	0.77			
<i>Citrobacter freundii</i>	15.59	0.76			
104061	Identification to the genus				104061
<i>Citrobacter freundii</i>	85.66	0.56	MAN 99		
<i>Citrobacter youngae</i>	10.49	0.34			
<i>Yersinia rohdei</i>	2.68	0.18			
104062	Identification to the genus				104062
<i>Citrobacter freundii</i>	86.30	0.56	TRE 99		
<i>Citrobacter youngae</i>	10.57	0.34			
<i>Yersinia rohdei</i>	2.70	0.18			
104063	Identification to the genus				104063
<i>Citrobacter freundii</i>	86.17	0.97			
<i>Citrobacter youngae</i>	10.55	0.76			
<i>Yersinia rohdei</i>	2.70	0.59			
104071	Low discrimination				104071
<i>Citrobacter freundii</i>	76.98	0.54	MAN 99		
<i>Citrobacter youngae</i>	9.82	0.33			
<i>Serratia ficaria</i>	8.36	0.16			
104072	Low discrimination				104072
<i>Citrobacter freundii</i>	76.98	0.54	TRE 99		
<i>Citrobacter youngae</i>	9.82	0.33			
<i>Serratia ficaria</i>	8.36	0.16			
104073	Low discrimination				104073
<i>Citrobacter freundii</i>	76.84	0.95			
<i>Citrobacter youngae</i>	9.80	0.74			
<i>Serratia ficaria</i>	8.34	0.57			
104103	Low discrimination				104103
<i>Citrobacter werkmanii</i>	86.90	0.37	H2S 92		
<i>Pantoea agglomerans</i>	6.54	0.18	URE 92		
<i>Citrobacter youngae</i>	2.01	0.20	SOR 90		
104113	Acceptable identification				104113
<i>Escherichia vulneris</i>	93.62	0.43	SCI 1		
<i>Pantoea agglomerans</i>	3.20	0.16			
<i>Citrobacter youngae</i>	1.02	0.18			
104123	Very good identification				104123

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Pantoea agglomerans</i>	98.35	0.59	ESL 99	64	
<i>Citrobacter freundii</i>	1.10	0.34		1	
<i>Serratia rubidaea</i>	0.29	0.08		99	
104133	Low discrimination				104133
<i>Pantoea agglomerans</i>	85.10	0.57	ESL 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	6.29	0.40			
<i>Serratia rubidaea</i>	4.91	0.33			
104143	Identification to the genus				104143
<i>Citrobacter werkmanii</i>	72.73	0.56	H2S 92		
<i>Citrobacter youngae</i>	18.51	0.61	URE 92		
<i>Citrobacter freundii</i>	8.21	0.56			
104153	Low discrimination				104153
				VPT	
<i>Citrobacter youngae</i>	58.57	0.59	MAL 5	1	
<i>Citrobacter freundii</i>	24.93	0.54		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	7.94	0.35		99	
104163	Good identification				104163
<i>Citrobacter freundii</i>	90.20	0.75	MAL 8		
<i>Citrobacter youngae</i>	6.69	0.49			
<i>Citrobacter werkmanii</i>	1.00	0.15			
104173	Low discrimination				104173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	53.58	0.66	ORN 96	99	
<i>Citrobacter freundii</i>	42.10	0.73		1	
<i>Citrobacter youngae</i>	3.25	0.47		1	
104213	Low discrimination				104213
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.42	0.43	ADO 97	1	
<i>Serratia odorifera</i> biovar 2	38.44	0.33		99	
<i>Citrobacter youngae</i>	5.07	0.18		1	
104233	Low discrimination				104233
				VPT	
<i>Cronobacter sakazakii</i>	70.33	0.38	ORN 91	99	
<i>Serratia ficaria</i>	15.24	0.18	ESL 99	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	7.78	0.31		1	
104243	Low discrimination				104243
				VPT	
<i>Citrobacter youngae</i>	86.09	0.61	INO 5	1	
<i>Serratia odorifera</i> biovar 2	5.40	0.33		99	
<i>Citrobacter freundii</i>	4.43	0.37		1	
104251	Good identification				104251
				VPT	
<i>Serratia odorifera</i> biovar 2	95.08	0.43	LYS 94	99	
<i>Citrobacter youngae</i>	4.10	0.18	MAN 97	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.83	0.08		1	
104253	Low discrimination				104253
				VPT	
<i>Serratia odorifera</i> biovar 2	84.44	0.74	LYS 94	99	
<i>Citrobacter youngae</i>	11.14	0.59		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.24	0.49		1	
104263	Low discrimination				104263
<i>Citrobacter freundii</i>	55.50	0.56	INO 1		
<i>Citrobacter youngae</i>	35.41	0.49			
<i>Serratia ficaria</i>	5.79	0.18			
104273	Low discrimination				104273
<i>Serratia ficaria</i>	83.05	0.59	ESL 99		
<i>Citrobacter freundii</i>	6.32	0.54			
<i>Citrobacter youngae</i>	4.20	0.47			
104373	Low discrimination				104373
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	88.21	0.51	ORN 96	99	
<i>Serratia ficaria</i>	6.06	0.18		75	
<i>Citrobacter freundii</i>	3.97	0.32		1	
104403	Good identification				104403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.05	0.51	CEL 92		
<i>Shigella boydii</i> (group C)	1.38	-.02			
<i>Citrobacter youngae</i>	0.92	0.05			
104412	Good identification				104412
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.38	TRE 98		
104413	Very good identification				104413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.48	0.73		1	
<i>Serratia rubidaea</i>	0.40	0.08		99	
<i>Citrobacter youngae</i>	0.07	0.03		1	
104433	Low discrimination				104433
				VPT	
<i>Serratia rubidaea</i>	60.42	0.49	ESL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	38.01	0.60	MAL 94	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.36	0.20		99	
104443	Low discrimination				104443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	57.82	0.56	CEL 92		
<i>Citrobacter youngae</i>	29.27	0.46			
<i>Citrobacter freundii</i>	7.85	0.37			
104451	Acceptable identification				104451
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.76	0.37	MAN 99	1	
<i>Serratia odorifera</i> biovar 2	4.94	0.03		99	
<i>Citrobacter youngae</i>	3.31	0.03		1	
104452	Good identification				104452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.25	0.43	TRE 98		
<i>Citrobacter youngae</i>	1.75	0.03			
104453	Good identification				104453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.67	0.78		1	
<i>Citrobacter youngae</i>	3.34	0.44		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 2	1.63	0.34		99	
104463	Low discrimination				104463
<i>Citrobacter freundii</i>	71.64	0.56	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	16.30	0.44			
<i>Citrobacter youngae</i>	8.77	0.34			
104473	Low discrimination				104473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	57.03	0.66		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	20.85	0.46		99	
<i>Citrobacter freundii</i>	17.13	0.54		1	
104523	Good identification				104523
				VPT	
<i>Serratia rubidaea</i>	96.44	0.49	ESL 94	99	
<i>Pantoea agglomerans</i>	3.40	0.18	CEL 94	64	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.16	0.07		1	
104533	Very good identification				104533
<i>Serratia rubidaea</i>	99.27	0.74	ESL 94		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.43	0.30			
<i>Pantoea agglomerans</i>	0.18	0.16			
104553	Low discrimination				104553
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	67.70	0.47	MAL 3	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	18.57	0.25		99	
<i>Citrobacter koseri</i>	7.08	0.15		1	
104573	Low discrimination				104573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	84.07	0.56	ORN 96	99	
<i>Serratia rubidaea</i>	10.38	0.33		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.37	0.35		1	
104603	Good identification				104603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.53	CEL 92		
104612	Good identification				104612
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.40	TRE 98		
104613	Very good identification				104613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.32	0.75		1	
<i>Serratia odorifera</i> biovar 2	2.60	0.34		99	
<i>Serratia rubidaea</i>	0.08	-.05		99	
104623	Low discrimination				104623
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	80.73	0.40	CEL 92	1	
<i>Serratia rubidaea</i>	19.27	0.12		99	
104633	Low discrimination				104633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.01	0.62		1	
<i>Serratia rubidaea</i>	24.39	0.37		99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.39	0.05		99	
104643	Low discrimination				104643

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	84.24	0.58	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	13.93	0.34		99	
<i>Citrobacter youngae</i>	1.84	0.20		1	
104651	Low discrimination				104651
				VPT	
<i>Serratia odorifera</i> biovar 2	81.34	0.44	LYS 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	18.66	0.39	MAN 97	1	
104652	Low discrimination				104652
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	58.67	0.45	TRE 98	1	
<i>Serratia odorifera</i> biovar 2	41.33	0.34		99	
104653	Low discrimination				104653
				VPT	
<i>Serratia odorifera</i> biovar 2	58.69	0.75	LYS 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	41.23	0.80		1	
<i>Citrobacter youngae</i>	0.06	0.18		1	
104663	Acceptable identification				104663
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.38	0.46	CEL 92		
<i>Citrobacter freundii</i>	3.43	0.15			
<i>Citrobacter youngae</i>	2.19	0.08			
104673	Low discrimination				104673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	86.93	0.68		1	
<i>Serratia odorifera</i> biovar 2	5.00	0.34		99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	4.59	0.31		99	
104713	Low discrimination				104713
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	70.63	0.43	MAL 3	1	
<i>Serratia rubidaea</i>	29.37	0.20		99	
104723	Good identification				104723
				VPT	
<i>Serratia rubidaea</i>	99.18	0.37	ESL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.82	0.09	CEL 94	1	
104733	Very good identification				104733
				VPT	
<i>Serratia rubidaea</i>	99.10	0.61	ESL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.60	0.31		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.30	0.14		99	
104753	Low discrimination				104753
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	63.19	0.49	MAL 3	1	
<i>Serratia odorifera</i> biovar 2	29.38	0.34		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	4.93	0.08		1	
104773	Low discrimination				104773
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	62.15	0.41	ORN 96	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	12.14	0.37		1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	11.36	0.18		1	
105043	Identification to the genus				105043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	69.40	0.46	PHE 1		
<i>Citrobacter freundii</i>	18.62	0.37			
<i>Citrobacter braakii</i>	9.94	0.30			
105053	Identification to the genus				105053
<i>Citrobacter youngae</i>	61.00	0.44	PHE 1		
<i>Citrobacter braakii</i>	21.69	0.36			
<i>Citrobacter freundii</i>	15.72	0.35			
105063	Identification to the genus				105063
<i>Citrobacter freundii</i>	86.30	0.56	PHE 1		
<i>Citrobacter youngae</i>	10.57	0.34			
<i>Yersinia rohdei</i>	2.70	0.18			
105073	Low discrimination				105073
<i>Citrobacter freundii</i>	76.98	0.54	PHE 1		
<i>Citrobacter youngae</i>	9.82	0.33			
<i>Serratia ficaria</i>	8.36	0.16			
105123	Good identification				105123
<i>Pantoea agglomerans</i>	100.0	0.38	PHE 9		
105133	Acceptable identification				105133
<i>Pantoea agglomerans</i>	93.33	0.36	PHE 9		
<i>Cronobacter sakazakii</i>	5.42	0.15	ESL 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.70	-.01			
105201	Good identification				105201
<i>Providencia stuartii</i>	100.0	0.46	ONP 10		
105221	Good identification				105221
<i>Providencia stuartii</i>	100.0	0.46	ONP 10		
105233	Good identification				105233
				VPT	
<i>Cronobacter sakazakii</i>	98.85	0.38	ORN 91	99	
<i>Providencia stuartii</i>	1.15	0.00	ESL 99	1	
105453	Good identification				105453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.52	0.37	PHE 1		
<i>Citrobacter youngae</i>	3.48	0.03			
106013	Low discrimination				106013
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	56.54	0.54	ADO 97	1	
<i>Cronobacter sakazakii</i>	13.02	0.28		99	
<i>Yokenella regensburgei</i>	9.58	0.18		1	
106023	Very good identification				106023
<i>Pantoea agglomerans</i>	96.22	0.59	MAL 99		
<i>Cronobacter sakazakii</i>	1.98	0.28			
<i>Serratia ficaria</i>	1.05	0.16			
106033	Low discrimination				106033

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Cronobacter sakazakii</i>	51.11	0.70	ORN 91		
<i>Serratia ficaria</i>	27.18	0.57			
<i>Pantoea agglomerans</i>	19.74	0.57			
106043	Low discrimination				106043
<i>Citrobacter youngae</i>	85.17	0.61	ESL 5		
<i>Citrobacter freundii</i>	4.39	0.37			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.99	0.38			
106053	Low discrimination				106053
<i>Serratia ficaria</i>	69.58	0.57	SUC 99		
<i>Citrobacter youngae</i>	16.18	0.59			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	10.66	0.60			
106063	Low discrimination				106063
<i>Serratia ficaria</i>	82.22	0.57	CEL 99		
<i>Citrobacter freundii</i>	9.73	0.56			
<i>Citrobacter youngae</i>	6.21	0.49			
106071	Very good identification				106071
				VPT	
<i>Serratia ficaria</i>	99.66	0.57	MAN 99	75	
<i>Enterobacter cloacae subsp. cloacae</i>	0.15	0.08		99	
<i>Citrobacter freundii</i>	0.09	0.12		1	
106072	Very good identification				106072
				VPT	
<i>Serratia ficaria</i>	99.62	0.57	TRE 99	75	
<i>Enterobacter cloacae subsp. cloacae</i>	0.15	0.08		99	
<i>Citrobacter freundii</i>	0.09	0.12		1	
106073	Excellent identification				106073
				VPT	
<i>Serratia ficaria</i>	99.63	0.98		75	
<i>Enterobacter cloacae subsp. cloacae</i>	0.15	0.49		99	
<i>Citrobacter freundii</i>	0.09	0.54		1	
106103	Very good identification				106103
<i>Pantoea agglomerans</i>	99.68	0.59	SUC 99		
<i>Citrobacter werkmanii</i>	0.14	-.04			
<i>Yersinia pseudotuberculosis</i>	0.08	-.09			
106113	Good identification				106113
				VPT	
<i>Pantoea agglomerans</i>	91.46	0.57	SUC 99	64	
<i>Escherichia vulneris</i>	6.77	0.31		1	
<i>Serratia rubidaea</i>	0.84	0.16		99	
106121	Very good identification				106121
<i>Pantoea agglomerans</i>	99.95	0.59	MAN 99		
<i>Serratia rubidaea</i>	0.05	-.09			
106122	Very good identification				106122
<i>Pantoea agglomerans</i>	99.95	0.59	TRE 99		
<i>Serratia rubidaea</i>	0.05	-.09			
106123	Excellent identification				106123

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Pantoea agglomerans</i>	99.95	1.00			
<i>Serratia rubidaea</i>	0.05	0.33			
<i>Cronobacter sakazakii</i>	0.01	0.15			
106131	Very good identification				106131
<i>Pantoea agglomerans</i>	98.53	0.57	MAN 99		
<i>Serratia rubidaea</i>	0.90	0.16			
<i>Cronobacter sakazakii</i>	0.57	0.15			
106132	Very good identification				106132
<i>Pantoea agglomerans</i>	98.53	0.57	TRE 99		
<i>Serratia rubidaea</i>	0.90	0.16			
<i>Cronobacter sakazakii</i>	0.57	0.15			
106133	Very good identification				106133
<i>Pantoea agglomerans</i>	98.48	0.98			
<i>Serratia rubidaea</i>	0.90	0.57			
<i>Cronobacter sakazakii</i>	0.57	0.56			
106163	Very good identification				106163
<i>Pantoea agglomerans</i>	96.94	0.59	SOR 1		
<i>Citrobacter freundii</i>	1.08	0.34			
<i>Serratia ficaria</i>	1.06	0.16			
106173	Low discrimination				106173
<i>Serratia ficaria</i>	45.67	0.57	MAL 1		
<i>Pantoea agglomerans</i>	33.17	0.57			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	19.95	0.59			
106213	Low discrimination				106213
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	55.40	0.56	ADO 97	1	
<i>Cronobacter sakazakii</i>	31.30	0.38		99	
<i>Serratia ficaria</i>	6.78	0.18		75	
106223	Low discrimination				106223
<i>Cronobacter sakazakii</i>	69.89	0.38	ORN 91		
<i>Serratia ficaria</i>	15.14	0.18	CEL 99		
<i>Pantoea agglomerans</i>	11.45	0.18			
106231	Low discrimination				106231
<i>Cronobacter sakazakii</i>	82.19	0.38	ORN 91		
<i>Serratia ficaria</i>	17.81	0.18	MAN 99		
106232	Low discrimination				106232
				VPT	
<i>Cronobacter sakazakii</i>	81.59	0.38	ORN 91	99	
<i>Serratia ficaria</i>	17.68	0.18	TRE 99	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.74	0.09		1	
106233	Low discrimination				106233
				VPT	
<i>Cronobacter sakazakii</i>	81.66	0.79	ORN 91	99	
<i>Serratia ficaria</i>	17.69	0.59		75	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.37	0.43		1	
106243	Low discrimination				106243
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	29.37	0.40	ADO 97		
<i>Citrobacter youngae</i>	26.97	0.35	CEL 92		
<i>Serratia ficaria</i>	22.26	0.18			
106251	Identification to the genus				106251
				VPT	
<i>Serratia odorifera</i> biovar 2	71.86	0.39	LYS 94	99	
<i>Serratia ficaria</i>	24.40	0.18	MAN 97	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.74	0.20		1	
106253	Low discrimination				106253
				VPT	
<i>Serratia ficaria</i>	47.04	0.59	SUC 99	75	
<i>Serratia odorifera</i> biovar 2	45.23	0.70		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	7.21	0.61		1	
106263	Very good identification				106263
				VPT	
<i>Serratia ficaria</i>	98.60	0.59	CEL 99	75	
<i>Serratia marcescens</i>	0.61	0.18		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.33	0.27		1	
106271	Very good identification				106271
				VPT	
<i>Serratia ficaria</i>	99.88	0.59	MAN 99	75	
<i>Cronobacter sakazakii</i>	0.05	-.03		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.04	0.08		1	
106272	Very good identification				106272
				VPT	
<i>Serratia ficaria</i>	99.88	0.59	TRE 99	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.08	0.14		1	
<i>Cronobacter sakazakii</i>	0.05	-.03		99	
106273	Excellent identification				106273
				VPT	
<i>Serratia ficaria</i>	99.87	1.00		75	
<i>Cronobacter sakazakii</i>	0.05	0.38		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.04	0.49		1	
106323	Very good identification				106323
<i>Pantoea agglomerans</i>	97.57	0.59	INO 1		
<i>Cronobacter sakazakii</i>	1.32	0.25			
<i>Serratia rubidaea</i>	1.11	0.20			
106333	Low discrimination				106333
<i>Cronobacter sakazakii</i>	57.70	0.66	ORN 91		
<i>Pantoea agglomerans</i>	33.84	0.57			
<i>Serratia rubidaea</i>	7.66	0.45			
106373	Good identification				106373
<i>Serratia ficaria</i>	90.96	0.59	MAL 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.74	0.43			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.48	0.19			
106403	Very good identification				106403

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.54	0.63	CEL 92	1	
<i>Serratia rubidaea</i>	1.14	0.08		99	
<i>Yersinia pseudotuberculosis</i>	0.32	-.09		1	
106411	Good identification				106411
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.45	0.44	MAN 99	1	
<i>Serratia rubidaea</i>	1.55	-.09		99	
106412	Good identification				106412
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.23	0.50	TRE 98	1	
<i>Serratia rubidaea</i>	0.77	-.09		99	
106413	Very good identification				106413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.45	0.85		1	
<i>Serratia rubidaea</i>	1.55	0.33		99	
106423	Low discrimination				106423
				VPT	
<i>Serratia rubidaea</i>	79.74	0.49	MAL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	17.45	0.51	CEL 94	1	
<i>Pantoea agglomerans</i>	2.81	0.18		64	
106433	Low discrimination				106433
				VPT	
<i>Serratia rubidaea</i>	85.46	0.74	MAL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	13.73	0.73		1	
<i>Cronobacter sakazakii</i>	0.39	0.28		99	
106443	Very good identification				106443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.34	0.69	CEL 92		
<i>Citrobacter youngae</i>	0.66	0.20			
106451	Good identification				106451
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.11	0.50	MAN 99	1	
<i>Serratia odorifera</i> biovar 2	0.89	0.00		99	
106452	Very good identification				106452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.56	TRE 98		
106453	Very good identification				106453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.42	0.91		1	
<i>Serratia odorifera</i> biovar 2	0.29	0.31		99	
<i>Serratia ficaria</i>	0.20	0.16		75	
106463	Low discrimination				106463
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	86.44	0.56	CEL 92	1	
<i>Serratia ficaria</i>	8.11	0.16		75	
<i>Serratia rubidaea</i>	2.15	0.08		99	
106471	Low discrimination				106471
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	53.18	0.37	MAN 99	1	
<i>Serratia ficaria</i>	42.93	0.16		75	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.08	-.02		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
106472	Low discrimination				106472
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	69.65	0.43	TRE 98	1	
<i>Serratia ficaria</i>	27.83	0.16		75	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.35	-.02		99	
106473	Low discrimination				106473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	53.13	0.78		1	
<i>Serratia ficaria</i>	42.89	0.57		75	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.08	0.39		99	
106513	Low discrimination				106513
				VPT	
<i>Serratia rubidaea</i>	87.51	0.57	SUC 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	10.99	0.54		1	
<i>Pantoea agglomerans</i>	0.98	0.16		64	
106523	Low discrimination				106523
				VPT	
<i>Serratia rubidaea</i>	81.76	0.74	CEL 94	99	
<i>Pantoea agglomerans</i>	18.20	0.59		64	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.04	0.20		1	
106531	Very good identification				106531
<i>Serratia rubidaea</i>	98.90	0.57	MAN 99		
<i>Pantoea agglomerans</i>	1.10	0.16			
106532	Very good identification				106532
				VPT	
<i>Serratia rubidaea</i>	98.83	0.57	TRE 99	99	
<i>Pantoea agglomerans</i>	1.10	0.16		64	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.06	0.07		1	
106533	Very good identification				106533
				VPT	
<i>Serratia rubidaea</i>	98.84	0.98		99	
<i>Pantoea agglomerans</i>	1.10	0.57		64	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.03	0.42		1	
106543	Good identification				106543
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.92	0.38	MAL 3	1	
<i>Serratia rubidaea</i>	3.08	-.09	CEL 92	99	
106553	Good identification				106553
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.22	0.60	MAL 3	1	
<i>Serratia rubidaea</i>	4.04	0.16		99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.74	0.18		99	
106573	Low discrimination				106573
				VPT	
<i>Serratia rubidaea</i>	75.37	0.57	SOR 1	99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	16.70	0.49		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.39	0.47		1	
106603	Very good identification				106603
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.77	0.65	CEL 92	1	
<i>Serratia rubidaea</i>	0.24	-.05		99	

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
106611	Good identification					106611
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		98.66	0.46	MAN 99	1	
<i>Serratia odorifera biovar 2</i>		1.34	0.00		99	
106612	Good identification					106612
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.52	TRE 98		
106613	Very good identification					106613
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		99.22	0.87		1	
<i>Serratia odorifera biovar 2</i>		0.44	0.31		99	
<i>Serratia rubidaea</i>		0.32	0.20		99	
106623	Low discrimination					106623
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		51.47	0.53	CEL 92	1	
<i>Serratia rubidaea</i>		48.11	0.37		99	
<i>Cronobacter sakazakii</i>		0.42	-.03		99	
106632	Low discrimination					106632
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		60.07	0.40	TRE 98	1	
<i>Serratia rubidaea</i>		37.86	0.20		99	
<i>Cronobacter sakazakii</i>		2.08	-.03		99	
106633	Low discrimination					106633
					VPT	
<i>Serratia rubidaea</i>		53.98	0.61	MAL 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		42.39	0.75		1	
<i>Cronobacter sakazakii</i>		2.96	0.38		99	
106642	Good identification					106642
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.36	CEL 92		
106643	Very good identification					106643
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		97.32	0.71	CEL 92	1	
<i>Serratia odorifera biovar 2</i>		2.68	0.31		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
106651	Low discrimination				106651
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	57.93	0.51	MAN 99	1	
<i>Serratia odorifera</i> biovar 2	42.07	0.41		99	
106652	Low discrimination				106652
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	89.49	0.58	TRE 98	1	
<i>Serratia odorifera</i> biovar 2	10.51	0.31		99	
106653	Low discrimination				106653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	80.69	0.92		1	
<i>Serratia odorifera</i> biovar 2	19.14	0.72		99	
<i>Serratia ficaria</i>	0.17	0.18		75	
106663	Low discrimination				106663
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	87.96	0.58	CEL 92	1	
<i>Serratia ficaria</i>	8.25	0.18		75	
<i>Serratia marcescens</i>	3.34	0.14		98	
106671	Low discrimination				106671
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.45	0.39	MAN 99	1	
<i>Serratia ficaria</i>	43.95	0.18		75	
<i>Serratia odorifera</i> biovar 2	1.60	0.00		99	
106672	Low discrimination				106672
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	71.45	0.45	TRE 98		
<i>Serratia ficaria</i>	28.55	0.18			
106673	Low discrimination				106673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.23	0.80		1	
<i>Serratia ficaria</i>	43.78	0.59		75	
<i>Serratia odorifera</i> biovar 2	0.52	0.31		99	
106713	Low discrimination				106713
				VPT	
<i>Serratia rubidaea</i>	61.96	0.45	SUC 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	38.04	0.56		1	
106723	Very good identification				106723
				VPT	
<i>Serratia rubidaea</i>	98.90	0.61	CEL 94	99	
<i>Pantoea agglomerans</i>	0.89	0.18		64	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.21	0.22		1	
106731	Good identification				106731
<i>Serratia rubidaea</i>	100.0	0.45	MAN 99		
106732	Good identification				106732
				VPT	
<i>Serratia rubidaea</i>	99.69	0.45	TRE 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.31	0.09		1	
106733	Very good identification				106733
				VPT	
<i>Serratia rubidaea</i>	99.70	0.86		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.16	0.43		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Cronobacter sakazakii</i>	0.08	0.25		99	
106743	Good identification				106743
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.40	MAL 3		
106753	Low discrimination				106753
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	89.87	0.61	MAL 3	1	
<i>Serratia odorifera biovar 2</i>	6.96	0.31		99	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.87	-.02		98	
106773	Low discrimination				106773
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	34.95	0.39	LYS 98		
<i>Serratia rubidaea</i>	32.17	0.45	URE 95		
<i>Enterobacter aerogenes</i>	14.92	0.30			
107023	Low discrimination				107023
<i>Pantoea agglomerans</i>	82.80	0.38	PHE 9		
<i>Cronobacter sakazakii</i>	17.20	0.28	MAL 99		
107033	Very good identification				107033
<i>Cronobacter sakazakii</i>	95.80	0.70	ORN 91		
<i>Pantoea agglomerans</i>	3.66	0.36			
<i>Serratia ficaria</i>	0.52	0.16			
107073	Very good identification				107073
<i>Serratia ficaria</i>	97.74	0.57	PHE 1		
<i>Cronobacter sakazakii</i>	1.86	0.28			
<i>Enterobacter cloacae subsp. cloacae</i>	0.14	0.08			
107103	Good identification				107103
<i>Pantoea agglomerans</i>	100.0	0.38	PHE 9		
107113	Acceptable identification				107113
				VPT	
<i>Pantoea agglomerans</i>	93.84	0.36	PHE 9	64	
<i>Cronobacter sakazakii</i>	5.45	0.15	SUC 99	99	
<i>Escherichia vulneris</i>	0.71	-.10		1	
107121	Good identification				107121
<i>Pantoea agglomerans</i>	100.0	0.38	PHE 9		
107122	Good identification				107122
<i>Pantoea agglomerans</i>	100.0	0.38	PHE 9		
107123	Very good identification				107123
<i>Pantoea agglomerans</i>	99.95	0.79	PHE 9		
<i>Cronobacter sakazakii</i>	0.05	0.15			
<i>Serratia rubidaea</i>	0.01	-.09			
107131	Acceptable identification				107131
<i>Pantoea agglomerans</i>	94.51	0.36	PHE 9		
<i>Cronobacter sakazakii</i>	5.49	0.15	MAN 99		
107132	Acceptable identification				107132

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Pantoea agglomerans</i>	94.51	0.36	PHE 9		
<i>Cronobacter sakazakii</i>	5.49	0.15	TRE 99		
107133	Good identification				107133
<i>Pantoea agglomerans</i>	94.43	0.77	PHE 9		
<i>Cronobacter sakazakii</i>	5.48	0.56			
<i>Serratia rubidaea</i>	0.09	0.16			
107163	Good identification				107163
<i>Pantoea agglomerans</i>	100.0	0.38	PHE 9		
107173	Low discrimination				107173
<i>Pantoea agglomerans</i>	79.36	0.36	PHE 9		
<i>Serratia ficaria</i>	11.16	0.16	SOR 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	4.87	0.17			
107213	Good identification				107213
				VPT	
<i>Cronobacter sakazakii</i>	98.24	0.38	ORN 91	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.76	0.15	SUC 99	1	
107223	Good identification				107223
<i>Cronobacter sakazakii</i>	98.41	0.38	ORN 91		
<i>Pantoea agglomerans</i>	1.60	-.03	CEL 99		
107231	Good identification				107231
<i>Cronobacter sakazakii</i>	100.0	0.38	ORN 91		
107232	Good identification				107232
<i>Cronobacter sakazakii</i>	100.0	0.38	ORN 91		
107233	Very good identification				107233
<i>Cronobacter sakazakii</i>	99.77	0.79	ORN 91		
<i>Serratia ficaria</i>	0.22	0.18			
<i>Pantoea agglomerans</i>	0.01	-.05			
107273	Very good identification				107273
				VPT	
<i>Serratia ficaria</i>	95.51	0.59	PHE 1	75	
<i>Cronobacter sakazakii</i>	4.45	0.38		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.04	0.08		1	
107323	Low discrimination				107323
<i>Pantoea agglomerans</i>	87.97	0.38	PHE 9		
<i>Cronobacter sakazakii</i>	12.04	0.25	INO 1		
107333	Good identification				107333
<i>Cronobacter sakazakii</i>	94.40	0.66	ORN 91		
<i>Pantoea agglomerans</i>	5.48	0.36			
<i>Serratia rubidaea</i>	0.13	0.04			
107413	Good identification				107413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.45	0.44	PHE 1	1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia rubidaea</i>	1.55	-.09		99	
107453	Good identification				107453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.50	PHE 1		
107473	Low discrimination				107473
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	53.18	0.37	PHE 1	1	
<i>Serratia ficaria</i>	42.93	0.16		75	
<i>Enterobacter cloacae subsp. cloacae</i>	2.08	-.02		99	
107523	Low discrimination				107523
<i>Pantoea agglomerans</i>	68.55	0.38	PHE 9		
<i>Serratia rubidaea</i>	31.45	0.33	ADO 1		
107533	Low discrimination				107533
<i>Serratia rubidaea</i>	89.63	0.57	PHE 1		
<i>Pantoea agglomerans</i>	9.80	0.36			
<i>Cronobacter sakazakii</i>	0.57	0.15			
107613	Good identification				107613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.28	0.46	PHE 1	1	
<i>Cronobacter sakazakii</i>	1.72	-.03		99	
107633	Low discrimination				107633
				VPT	
<i>Cronobacter sakazakii</i>	75.27	0.38	ORN 91	99	
<i>Serratia rubidaea</i>	13.85	0.20	ADO 1	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	10.88	0.33		1	
107653	Low discrimination				107653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	80.83	0.51	PHE 1	1	
<i>Serratia odorifera biovar 2</i>	19.17	0.31		99	
107673	Low discrimination				107673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	54.20	0.39	PHE 1	1	
<i>Serratia ficaria</i>	43.76	0.18		75	
<i>Cronobacter sakazakii</i>	2.04	-.03		99	
107733	Acceptable identification				107733
<i>Serratia rubidaea</i>	92.55	0.45	PHE 1		
<i>Cronobacter sakazakii</i>	7.05	0.25			
<i>Pantoea agglomerans</i>	0.41	-.05			
110000	Very good identification				110000
<i>Shigella dysenteriae (group A)</i>	98.53	0.71	TRE 90		
<i>Shigella boydii (group C)</i>	0.68	0.24			
<i>Shigella flexneri (group B)</i>	0.62	0.26			
110001	Very good identification				110001
<i>Shigella dysenteriae (group A)</i>	99.21	0.91			
<i>Shigella boydii (group C)</i>	0.43	0.40			
<i>Escherichia coli</i>	0.21	0.43			
110002	Low discrimination				110002

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella boydii</i> (group C)	59.90	0.55	ONP 10		
<i>Shigella flexneri</i> (group B)	32.15	0.53			
<i>Escherichia coli</i>	5.18	0.43			
110003	Low discrimination				110003
<i>Shigella boydii</i> (group C)	63.27	0.71	ONP 10		
<i>Escherichia coli</i>	18.34	0.69			
<i>Shigella flexneri</i> (group B)	12.17	0.59			
110011	Good identification				110011
<i>Shigella dysenteriae</i> (group A)	95.61	0.50	CEL 1		
<i>Escherichia hermannii</i>	3.38	0.18			
<i>Escherichia coli</i>	0.41	0.08			
110013	Low discrimination				110013
<i>Escherichia hermannii</i>	86.24	0.59	ORN 99		
<i>Escherichia vulneris</i>	4.80	0.28			
<i>Shigella boydii</i> (group C)	3.44	0.30			
110021	Low discrimination				110021
<i>Shigella dysenteriae</i> (group A)	86.90	0.50	SUC 1		
<i>Escherichia coli</i>	12.21	0.39			
<i>Providencia stuartii</i>	0.52	0.05			
110022	Low discrimination				110022
<i>Escherichia coli</i>	78.78	0.39	SOR 88		
<i>Shigella boydii</i> (group C)	13.81	0.14	TRE 95		
<i>Shigella flexneri</i> (group B)	7.41	0.12			
110023	Low discrimination				110023
<i>Escherichia coli</i>	87.70	0.66	SOR 88		
<i>Shigella boydii</i> (group C)	4.59	0.30			
<i>Escherichia hermannii</i>	2.91	0.26			
110033	Good identification				110033
<i>Escherichia hermannii</i>	92.10	0.57	ORN 99		
<i>Citrobacter farmeri</i>	1.92	0.18			
<i>Citrobacter freundii</i>	1.89	0.35			
110040	Very good identification				110040
<i>Shigella dysenteriae</i> (group A)	96.59	0.63	TRE 90		
<i>Escherichia coli</i>	1.67	0.34			
<i>Shigella boydii</i> (group C)	1.17	0.21			
110041	Very good identification				110041
<i>Shigella dysenteriae</i> (group A)	95.59	0.83			
<i>Escherichia coli</i>	3.48	0.61			
<i>Shigella boydii</i> (group C)	0.73	0.37			
110042	Low discrimination				110042
<i>Shigella boydii</i> (group C)	45.98	0.53	ONP 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	38.64	0.61			
<i>Shigella flexneri</i> (group B)	13.36	0.45			
110043	Low discrimination				110043
<i>Escherichia coli</i>	65.69	0.87			
<i>Shigella boydii</i> (group C)	23.32	0.68			
<i>Citrobacter youngae</i>	3.85	0.63			
110051	Low discrimination				110051
<i>Shigella dysenteriae</i> (group A)	79.36	0.42	CEL 1		
<i>Yersinia kristensenii</i>	7.22	0.19			
<i>Escherichia coli</i>	5.84	0.26			
110053	Low discrimination				110053
<i>Yersinia kristensenii</i>	46.29	0.60	ORN 92		
<i>Citrobacter youngae</i>	16.85	0.61			
<i>Citrobacter braakii</i>	15.87	0.61			
110061	Low discrimination				110061
<i>Escherichia coli</i>	65.27	0.57	MAN 95		
<i>Shigella dysenteriae</i> (group A)	27.15	0.42			
<i>Citrobacter freundii</i>	4.74	0.37			
110062	Low discrimination				110062
<i>Escherichia coli</i>	88.01	0.57	TRE 95		
<i>Citrobacter freundii</i>	6.39	0.37			
<i>Yersinia rohdei</i>	1.63	0.18			
110063	Low discrimination				110063
<i>Escherichia coli</i>	64.32	0.83			
<i>Citrobacter freundii</i>	24.35	0.78			
<i>Yersinia rohdei</i>	6.19	0.59			
110073	Low discrimination				110073
<i>Citrobacter farmeri</i>	37.08	0.59	ORN 99		
<i>Citrobacter freundii</i>	36.51	0.76			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	16.54	0.64			
110101	Good identification				110101
<i>Shigella dysenteriae</i> (group A)	99.36	0.50	MAL 1		
<i>Shigella boydii</i> (group C)	0.43	-0.02			
<i>Escherichia coli</i>	0.21	0.02			
110113	Low discrimination				110113
<i>Escherichia vulneris</i>	86.61	0.43	IND 1		
<i>Leclercia adecarboxylata</i>	10.21	0.30			
<i>Escherichia hermannii</i>	2.78	0.18			
110133	Low discrimination				110133
<i>Leclercia adecarboxylata</i>	64.44	0.36	ESL 99		
<i>Escherichia vulneris</i>	24.48	0.22	ADO 93		
<i>Escherichia hermannii</i>	7.38	0.16			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
110141	Good identification				110141
<i>Shigella dysenteriae</i> (group A)	95.78	0.42	MAL 1		
<i>Escherichia coli</i>	3.49	0.20			
<i>Shigella boydii</i> (group C)	0.73	-.04			
110143	Low discrimination				110143
<i>Escherichia coli</i>	49.52	0.46	MAL 1		
<i>Shigella boydii</i> (group C)	17.58	0.27			
<i>Citrobacter youngae</i>	15.11	0.36			
110163	Low discrimination				110163
<i>Citrobacter freundii</i>	72.07	0.56	MAL 8		
<i>Escherichia coli</i>	22.12	0.42			
<i>Citrobacter youngae</i>	2.69	0.24			
110173	Low discrimination				110173
<i>Citrobacter freundii</i>	80.97	0.54	MAL 8		
<i>Citrobacter farmeri</i>	9.55	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.26	0.23			
110201	Low discrimination				110201
<i>Shigella dysenteriae</i> (group A)	89.30	0.50	INO 1		
<i>Providencia stuartii</i>	10.12	0.31			
<i>Shigella boydii</i> (group C)	0.39	-.02			
110241	Good identification				110241
<i>Shigella dysenteriae</i> (group A)	95.78	0.42	INO 1		
<i>Escherichia coli</i>	3.49	0.20			
<i>Shigella boydii</i> (group C)	0.73	-.04			
110243	Low discrimination				110243
<i>Escherichia coli</i>	53.63	0.46	INO 1		
<i>Shigella boydii</i> (group C)	19.04	0.27			
<i>Citrobacter youngae</i>	16.36	0.36			
110253	Low discrimination				110253
				VPT	
<i>Yersinia kristensenii</i>	60.45	0.44	ORN 92	1	
<i>Serratia odorifera</i> biovar 2	24.83	0.43		99	
<i>Citrobacter youngae</i>	6.57	0.34		1	
110263	Low discrimination				110263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	54.41	0.47	ORN 95		
<i>Escherichia coli</i>	28.56	0.42			
<i>Citrobacter freundii</i>	10.81	0.37			
110273	Low discrimination				110273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	87.72	0.56	ORN 95		
<i>Citrobacter farmeri</i>	4.63	0.18			
<i>Citrobacter freundii</i>	4.56	0.35			
110401	Good identification				110401

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella dysenteriae</i> (group A)	98.48	0.50	ADO 1		
<i>Escherichia coli</i>	1.09	0.16			
<i>Shigella boydii</i> (group C)	0.43	-.02			
110403	Low discrimination				110403
<i>Escherichia coli</i>	52.30	0.43	ADO 5		
<i>Shigella boydii</i> (group C)	34.64	0.30	SOR 88		
<i>Shigella flexneri</i> (group B)	6.66	0.18			
110423	Good identification				110423
<i>Escherichia coli</i>	98.22	0.39	ADO 5		
<i>Leclercia adecarboxylata</i>	1.78	-.05	SOR 88		
110433	Low discrimination				110433
<i>Leclercia adecarboxylata</i>	82.93	0.36	ESL 99		
<i>Escherichia hermannii</i>	9.50	0.16	MAL 93		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.63	0.27			
110441	Low discrimination				110441
<i>Shigella dysenteriae</i> (group A)	83.52	0.42	ADO 1		
<i>Escherichia coli</i>	15.85	0.34			
<i>Shigella boydii</i> (group C)	0.63	-.04			
110443	Good identification				110443
<i>Escherichia coli</i>	90.26	0.61	ADO 5		
<i>Shigella boydii</i> (group C)	6.15	0.27			
<i>Citrobacter youngae</i>	1.01	0.21			
110453	Low discrimination				110453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	57.93	0.45	IND 1		
<i>Yersinia kristensenii</i>	15.08	0.19			
<i>Escherichia coli</i>	12.19	0.26			
110463	Good identification				110463
<i>Escherichia coli</i>	90.30	0.57	ADO 5		
<i>Citrobacter freundii</i>	6.56	0.37			
<i>Yersinia rohdei</i>	1.67	0.18			
110513	Very good identification				110513
<i>Leclercia adecarboxylata</i>	95.48	0.53	ESL 99		
<i>Escherichia fergusonii</i>	3.77	0.27			
<i>Escherichia vulneris</i>	0.62	0.02			
110533	Very good identification				110533
				VPT	
<i>Leclercia adecarboxylata</i>	99.66	0.59	ESL 99	1	
<i>Serratia rubidaea</i>	0.34	0.06		99	
110613	Good identification				110613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.62	0.41	IND 1	1	
<i>Serratia odorifera</i> biovar 2	3.39	0.03		99	
110653	Low discrimination				110653

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 2	64.29	0.44	LYS 94	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	34.42	0.47	SCI 97	1	
<i>Yersinia kristensenii</i>	1.29	0.03		1	
111001	Low discrimination				111001
<i>Shigella dysenteriae</i> (group A)	86.36	0.50	PHE 1		
<i>Providencia stuartii</i>	9.79	0.31			
<i>Morganella morganii</i> subsp. sibonii	3.30	0.23			
111041	Good identification				111041
<i>Shigella dysenteriae</i> (group A)	95.78	0.42	PHE 1		
<i>Escherichia coli</i>	3.49	0.20			
<i>Shigella boydii</i> (group C)	0.73	-.04			
111043	Low discrimination				111043
<i>Escherichia coli</i>	65.86	0.46	PHE 1		
<i>Shigella boydii</i> (group C)	23.38	0.27			
<i>Citrobacter youngae</i>	3.86	0.21			
111063	Low discrimination				111063
<i>Escherichia coli</i>	64.81	0.42	PHE 1		
<i>Citrobacter freundii</i>	24.53	0.37			
<i>Yersinia rohdei</i>	6.24	0.18			
111201	Very good identification				111201
<i>Providencia stuartii</i>	99.53	0.57	ONP 10		
<i>Shigella dysenteriae</i> (group A)	0.47	0.09	SCI 93		
111203	Good identification				111203
<i>Providencia stuartii</i>	100.0	0.38	ONP 10		
111221	Very good identification				111221
<i>Providencia stuartii</i>	100.0	0.57	ONP 10		
111223	Good identification				111223
<i>Providencia stuartii</i>	100.0	0.38	ONP 10		
112001	Acceptable identification				112001
<i>Shigella dysenteriae</i> (group A)	94.26	0.50	ESL 1		
<i>Escherichia coli</i>	4.97	0.30			
<i>Shigella boydii</i> (group C)	0.41	-.02			
112003	Low discrimination				112003
<i>Escherichia coli</i>	60.72	0.57	SOR 88		
<i>Yersinia pseudotuberculosis</i>	23.48	0.33			
<i>Shigella boydii</i> (group C)	8.47	0.30			
112013	Low discrimination				112013
<i>Escherichia hermannii</i>	68.76	0.55	ORN 99		
<i>Leclercia adecarboxylata</i>	28.56	0.48			
<i>Escherichia vulneris</i>	1.43	0.16			
112023	Identification to the genus				112023

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	87.31	0.53	SOR 88		
<i>Escherichia hermannii</i>	7.73	0.22			
<i>Leclercia adecarboxylata</i>	2.49	0.13			
112033	Low discrimination				112033
<i>Escherichia hermannii</i>	49.71	0.54	ORN 99		
<i>Leclercia adecarboxylata</i>	48.98	0.54			
<i>Escherichia coli</i>	0.35	0.18			
112041	Low discrimination				112041
<i>Shigella dysenteriae</i> (group A)	52.38	0.42	ESL 1		
<i>Escherichia coli</i>	47.22	0.48			
<i>Shigella boydii</i> (group C)	0.40	-0.4			
112042	Acceptable identification				112042
<i>Escherichia coli</i>	94.16	0.48	TRE 95		
<i>Shigella boydii</i> (group C)	4.53	0.11			
<i>Shigella flexneri</i> (group B)	1.32	0.04			
112043	Very good identification				112043
<i>Escherichia coli</i>	96.76	0.75			
<i>Shigella boydii</i> (group C)	1.39	0.27			
<i>Citrobacter youngae</i>	1.19	0.36			
112053	Low discrimination				112053
<i>Escherichia coli</i>	38.44	0.40	CEL 2		
<i>Citrobacter youngae</i>	18.99	0.34			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.87	0.28			
112061	Good identification				112061
<i>Escherichia coli</i>	96.15	0.45	MAN 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.23	0.09			
<i>Shigella dysenteriae</i> (group A)	1.62	0.01			
112062	Good identification				112062
<i>Escherichia coli</i>	97.73	0.45	TRE 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.27	0.09			
112063	Good identification				112063
<i>Escherichia coli</i>	92.25	0.71			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.52	0.44			
<i>Citrobacter freundii</i>	1.41	0.37			
112073	Low discrimination				112073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	72.16	0.54	ORN 95		
<i>Escherichia coli</i>	8.20	0.36			
<i>Citrobacter farmeri</i>	4.90	0.18			
112113	Very good identification				112113
<i>Leclercia adecarboxylata</i>	97.63	0.71	ADO 93		
<i>Escherichia vulneris</i>	2.09	0.31			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	0.18	0.14			
112123	Low discrimination				112123
<i>Pantoea agglomerans</i>	82.06	0.47	IND 1		
<i>Leclercia adecarboxylata</i>	17.47	0.36			
<i>Escherichia coli</i>	0.47	0.12			
112131	Good identification				112131
<i>Leclercia adecarboxylata</i>	96.41	0.36	ADO 93		
<i>Pantoea agglomerans</i>	3.59	0.03	MAN 99		
112132	Good identification				112132
<i>Leclercia adecarboxylata</i>	96.41	0.36	ADO 93		
<i>Pantoea agglomerans</i>	3.59	0.03	TRE 99		
112133	Very good identification				112133
<i>Leclercia adecarboxylata</i>	96.21	0.77	ADO 93		
<i>Pantoea agglomerans</i>	3.59	0.44			
<i>Escherichia vulneris</i>	0.09	0.09			
112173	Low discrimination				112173
<i>Leclercia adecarboxylata</i>	89.90	0.36	ADO 93		
<i>Pantoea agglomerans</i>	3.35	0.03	SOR 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	3.16	0.13			
112253	Low discrimination				112253
				VPT	
<i>Serratia odorifera biovar 2</i>	77.79	0.39	LYS 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	9.45	0.28	SCI 97	1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	8.27	0.20		2	
112263	Low discrimination				112263
<i>Yersinia enterocolitica ssp. enterocolitica</i>	71.76	0.37	ORN 95		
<i>Escherichia coli</i>	28.24	0.30			
112273	Low discrimination				112273
<i>Yersinia enterocolitica ssp. enterocolitica</i>	84.16	0.47	ORN 95		
<i>Serratia ficaria</i>	14.16	0.18			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.27	0.16			
112333	Acceptable identification				112333
				VPT	
<i>Leclercia adecarboxylata</i>	93.57	0.36	INO 1	1	
<i>Pantoea agglomerans</i>	3.49	0.03	ADO 93	64	
<i>Cronobacter sakazakii</i>	2.94	0.06		99	
112413	Very good identification				112413
<i>Leclercia adecarboxylata</i>	96.59	0.71	MAL 93		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.42	0.52			
<i>Escherichia fergusonii</i>	0.81	0.31			
112423	Low discrimination				112423
<i>Leclercia adecarboxylata</i>	85.70	0.36	MAL 93		
<i>Escherichia coli</i>	11.92	0.27	CEL 99		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		2.38	0.17			
112431	Good identification					112431
<i>Leclercia adecarboxylata</i>		100.0	0.36	MAL 93		
112432	Good identification					112432
<i>Leclercia adecarboxylata</i>		100.0	0.36	MAL 93		
112433	Very good identification					112433
<i>Leclercia adecarboxylata</i>		99.56	0.77	MAL 93		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		0.32	0.39			
<i>Escherichia hermannii</i>		0.08	0.12			
112443	Low discrimination					112443
<i>Escherichia coli</i>		88.11	0.48	ADO 5		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		11.89	0.35			
112453	Low discrimination					112453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		81.04	0.57	IND 1		
<i>Leclercia adecarboxylata</i>		17.59	0.30			
<i>Escherichia coli</i>		1.07	0.13			
112463	Acceptable identification					112463
<i>Escherichia coli</i>		93.28	0.45	ADO 5		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		4.72	0.23			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		1.07	0.03			
112473	Low discrimination					112473
<i>Leclercia adecarboxylata</i>		60.63	0.36	MAL 93		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		35.98	0.45	SOR 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>		2.13	0.13			
112503	Very good identification					112503
<i>Leclercia adecarboxylata</i>		99.82	0.53	CEL 99		
<i>Escherichia fergusonii</i>		0.18	-.01			
112511	Very good identification					112511
<i>Leclercia adecarboxylata</i>		100.0	0.53	MAN 99		
112512	Very good identification					112512
<i>Leclercia adecarboxylata</i>		100.0	0.53	TRE 99		
112513	Excellent identification					112513
<i>Leclercia adecarboxylata</i>		99.96	0.94			
<i>Escherichia fergusonii</i>		0.03	0.26			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		0.01	0.21			
112523	Very good identification					112523
<i>Leclercia adecarboxylata</i>		99.31	0.59	CEL 99	VPT 1	
<i>Pantoea agglomerans</i>		0.36	0.05		64	
<i>Serratia rubidaea</i>		0.34	0.06		99	
112531	Very good identification					112531

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	100.0	0.59	MAN 99		
112532	Very good identification				112532
<i>Leclercia adecarboxylata</i>	100.0	0.59	TRE 99		
112533	Excellent identification				112533
				VPT	
<i>Leclercia adecarboxylata</i>	99.94	1.00		1	
<i>Serratia rubidaea</i>	0.05	0.31		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.00	0.08		1	
112553	Very good identification				112553
<i>Leclercia adecarboxylata</i>	98.94	0.53	SOR 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.06	0.26			
112573	Very good identification				112573
<i>Leclercia adecarboxylata</i>	99.86	0.59	SOR 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.14	0.14			
112613	Low discrimination				112613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	74.87	0.53	IND 1	1	
<i>Leclercia adecarboxylata</i>	24.69	0.30		1	
<i>Serratia odorifera</i> biovar 2	0.44	0.00		99	
112633	Low discrimination				112633
				VPT	
<i>Leclercia adecarboxylata</i>	71.34	0.36	MAL 93	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	27.86	0.41	INO 1	1	
<i>Serratia rubidaea</i>	0.80	-0.06		99	
112643	Acceptable identification				112643
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.13	0.37	IND 1	1	
<i>Escherichia coli</i>	5.58	0.07	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	3.30	0.00		99	
112653	Low discrimination				112653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.26	0.59	IND 1	1	
<i>Serratia odorifera</i> biovar 2	23.74	0.41		99	
112673	Good identification				112673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.49	0.47	IND 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.98	0.05			
<i>Leclercia adecarboxylata</i>	1.33	-0.05			
112713	Very good identification				112713
<i>Leclercia adecarboxylata</i>	99.30	0.53	INO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.70	0.22			
112733	Very good identification				112733
				VPT	
<i>Leclercia adecarboxylata</i>	98.61	0.59	INO 1	1	
<i>Serratia rubidaea</i>	1.30	0.18		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.09	0.10		1	
113133	Low discrimination				113133

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Leclercia adecarboxylata</i>	72.70	0.36	PHE 1	1	
<i>Pantoea agglomerans</i>	26.54	0.24	ADO 93	64	
<i>Cronobacter sakazakii</i>	0.76	-.04		99	
113433	Good identification				113433
<i>Leclercia adecarboxylata</i>	100.0	0.36	PHE 1		
113513	Very good identification				113513
<i>Leclercia adecarboxylata</i>	100.0	0.53	PHE 1		
113533	Very good identification				113533
<i>Leclercia adecarboxylata</i>	100.0	0.59	PHE 1		
114001	Acceptable identification				114001
<i>Shigella dysenteriae (group A)</i>	92.11	0.50	SCI 1		
<i>Providencia stuartii</i>	7.30	0.28			
<i>Shigella boydii (group C)</i>	0.40	-.02			
114023	Low discrimination				114023
<i>Citrobacter freundii</i>	85.96	0.49	SOR 99		
<i>Escherichia coli</i>	7.74	0.24			
<i>Citrobacter youngae</i>	3.77	0.19			
114033	Low discrimination				114033
				VPT	
<i>Citrobacter freundii</i>	78.25	0.47	SOR 99	1	
<i>Escherichia hermannii</i>	9.63	0.16		1	
<i>Cronobacter sakazakii</i>	4.01	0.10		99	
114041	Low discrimination				114041
<i>Shigella dysenteriae (group A)</i>	77.42	0.42	SCI 1		
<i>Citrobacter youngae</i>	8.93	0.31			
<i>Citrobacter freundii</i>	6.68	0.31			
114043	Identification to the genus				114043
<i>Citrobacter youngae</i>	44.49	0.72			
<i>Citrobacter freundii</i>	33.31	0.72			
<i>Citrobacter braakii</i>	17.79	0.64			
114053	Low discrimination				114053
<i>Citrobacter amalonaticus</i>	36.04	0.58	ORN 94		
<i>Citrobacter youngae</i>	23.26	0.70	URE 88		
<i>Citrobacter braakii</i>	23.08	0.71			
114061	Acceptable identification				114061
<i>Citrobacter freundii</i>	91.48	0.49	MAN 99		
<i>Citrobacter youngae</i>	4.01	0.19			
<i>Escherichia coli</i>	3.18	0.16			
114062	Acceptable identification				114062
<i>Citrobacter freundii</i>	92.71	0.49	TRE 99		
<i>Citrobacter youngae</i>	4.07	0.19			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	3.22	0.16			
114063	Good identification				114063
<i>Citrobacter freundii</i>	94.62	0.90			
<i>Citrobacter youngae</i>	4.15	0.60			
<i>Escherichia coli</i>	0.63	0.42			
114071	Acceptable identification				114071
<i>Citrobacter freundii</i>	90.60	0.47	MAN 99		
<i>Citrobacter youngae</i>	4.14	0.17			
<i>Citrobacter farmeri</i>	2.56	-.02			
114072	Acceptable identification				114072
<i>Citrobacter freundii</i>	90.60	0.47	TRE 99		
<i>Citrobacter youngae</i>	4.14	0.17			
<i>Citrobacter farmeri</i>	2.56	-.02			
114073	Good identification				114073
<i>Citrobacter freundii</i>	90.20	0.88			
<i>Citrobacter youngae</i>	4.12	0.58			
<i>Citrobacter farmeri</i>	2.54	0.39			
114143	Identification to the genus				114143
<i>Citrobacter freundii</i>	47.91	0.50	MAL 8		
<i>Citrobacter youngae</i>	38.72	0.46	SUC 89		
<i>Citrobacter werkmanii</i>	8.71	0.15			
114153	Low discrimination				114153
<i>Citrobacter freundii</i>	32.90	0.48	MAL 8		
<i>Citrobacter youngae</i>	27.69	0.44	SUC 89		
<i>Citrobacter koseri</i>	17.08	0.31			
114163	Very good identification				114163
<i>Citrobacter freundii</i>	97.07	0.69	MAL 8		
<i>Citrobacter youngae</i>	2.58	0.34			
<i>Citrobacter koseri</i>	0.28	0.05			
114173	Identification to the genus				114173
<i>Citrobacter freundii</i>	89.50	0.66	MAL 8		
<i>Citrobacter koseri</i>	5.09	0.30			
<i>Citrobacter youngae</i>	2.48	0.32			
114201	Very good identification				114201
<i>Providencia stuartii</i>	99.33	0.54	ONP 10		
<i>Shigella dysenteriae</i> (group A)	0.67	0.09	PHE 95		
114221	Very good identification				114221
<i>Providencia stuartii</i>	100.0	0.54	ONP 10		
114243	Low discrimination				114243
				VPT	
<i>Citrobacter youngae</i>	63.00	0.46	INO 5	1	
<i>Serratia odorifera</i> biovar 2	22.37	0.33		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	9.06	0.31		1	
114251	Good identification				114251
				VPT	
<i>Serratia odorifera</i> biovar 2	99.25	0.43	LYS 94	99	
<i>Citrobacter youngae</i>	0.75	0.03	MAN 97	1	
114253	Very good identification				114253
				VPT	
<i>Serratia odorifera</i> biovar 2	96.26	0.74	LYS 94	99	
<i>Citrobacter youngae</i>	2.24	0.44		1	
<i>Citrobacter amalonaticus</i>	0.67	0.17		1	
114263	Identification to the genus				114263
<i>Citrobacter freundii</i>	80.13	0.49	INO 1		
<i>Citrobacter youngae</i>	18.32	0.34			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.02	0.05			
114273	Low discrimination				114273
				VPT	
<i>Citrobacter freundii</i>	49.60	0.47	INO 1	1	
<i>Serratia odorifera</i> biovar 2	19.28	0.33		99	
<i>Serratia ficaria</i>	13.37	0.18		75	
114463	Acceptable identification				114463
<i>Citrobacter freundii</i>	90.65	0.49	ADO 1		
<i>Citrobacter youngae</i>	3.98	0.19			
<i>Escherichia coli</i>	3.15	0.16			
114473	Low discrimination				114473
<i>Citrobacter freundii</i>	59.29	0.47	ADO 1		
<i>Citrobacter koseri</i>	29.04	0.30			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.05	0.25			
114553	Very good identification				114553
<i>Citrobacter koseri</i>	99.68	0.56	ORN 99		
<i>Citrobacter freundii</i>	0.12	0.07			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.10	0.06			
114573	Very good identification				114573
				VPT	
<i>Citrobacter koseri</i>	97.82	0.55	ORN 99	1	
<i>Citrobacter freundii</i>	1.11	0.25		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.96	0.15		99	
114651	Good identification				114651
<i>Serratia odorifera</i> biovar 2	100.0	0.44	LYS 94		
114653	Very good identification				114653
				VPT	
<i>Serratia odorifera</i> biovar 2	99.28	0.75	LYS 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.71	0.39		1	
<i>Citrobacter youngae</i>	0.02	0.03		1	
115001	Very good identification				115001
<i>Providencia stuartii</i>	99.08	0.54	ONP 10		
<i>Shigella dysenteriae</i> (group A)	0.66	0.09	INO 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia alcalifaciens</i>	0.25	-.11			
115021	Very good identification				115021
<i>Providencia stuartii</i>	100.0	0.54	ONP 10		
115063	Good identification				115063
<i>Citrobacter freundii</i>	95.19	0.49	PHE 1		
<i>Citrobacter youngae</i>	4.18	0.19			
<i>Escherichia coli</i>	0.64	0.01			
115073	Acceptable identification				115073
<i>Citrobacter freundii</i>	90.60	0.47	PHE 1		
<i>Citrobacter youngae</i>	4.14	0.17			
<i>Citrobacter farmeri</i>	2.56	-.02			
115200	Good identification				115200
<i>Providencia stuartii</i>	99.68	0.46	ONP 10		
<i>Providencia alcalifaciens</i>	0.32	-.17	TRE 98		
115201	Very good identification				115201
<i>Providencia stuartii</i>	100.0	0.80	ONP 10		
115203	Very good identification				115203
<i>Providencia stuartii</i>	100.0	0.61	ONP 10		
115211	Very good identification				115211
<i>Providencia stuartii</i>	100.0	0.54	ONP 10		
115220	Good identification				115220
<i>Providencia stuartii</i>	100.0	0.46	ONP 10		
115221	Very good identification				115221
<i>Providencia stuartii</i>	100.0	0.80	ONP 10		
115223	Very good identification				115223
<i>Providencia stuartii</i>	100.0	0.61	ONP 10		
115231	Very good identification				115231
<i>Providencia stuartii</i>	100.0	0.54	ONP 10		
115241	Good identification				115241
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
115261	Good identification				115261
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
115301	Good identification				115301
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
115321	Good identification				115321
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
115400	Very good identification				115400
<i>Providencia alcalifaciens</i>	100.0	0.59	ONP 1		
115420	Good identification				115420
<i>Providencia alcalifaciens</i>	100.0	0.43	ONP 1		
115601	Very good identification				115601
<i>Providencia stuartii</i>	99.87	0.54	ONP 10		
<i>Providencia alcalifaciens</i>	0.13	-.17	ADO 5		
115602	Good identification				115602
<i>Providencia rettgeri</i>	99.03	0.39	ONP 5		
<i>Providencia stuartii</i>	0.62	0.00	URE 98		
<i>Providencia alcalifaciens</i>	0.35	-.17			
115621	Very good identification				115621
<i>Providencia stuartii</i>	100.0	0.54	ONP 10		
116033	Low discrimination				116033
<i>Cronobacter sakazakii</i>	89.51	0.51	IND 11		
<i>Serratia ficaria</i>	3.89	0.16	ORN 91		
<i>Pantoea agglomerans</i>	2.83	0.16			
116043	Low discrimination				116043
<i>Citrobacter youngae</i>	65.25	0.46	ESL 5		
<i>Escherichia coli</i>	18.79	0.33			
<i>Citrobacter freundii</i>	9.38	0.31			
116053	Low discrimination				116053
				VPT	
<i>Citrobacter amalonaticus</i>	60.49	0.37	ORN 94	1	
<i>Citrobacter youngae</i>	20.77	0.44	URE 88	1	
<i>Serratia odorifera biovar 2</i>	6.01	0.29	ESL 9	99	
116063	Low discrimination				116063
<i>Citrobacter freundii</i>	63.42	0.49	ESL 1		
<i>Citrobacter youngae</i>	14.50	0.34			
<i>Serratia ficaria</i>	10.99	0.16			
116073	Good identification				116073
<i>Serratia ficaria</i>	93.19	0.57	IND 1		
<i>Citrobacter freundii</i>	4.27	0.47			
<i>Citrobacter youngae</i>	1.02	0.32			
116123	Very good identification				116123
				VPT	
<i>Pantoea agglomerans</i>	99.85	0.59	IND 1	64	
<i>Cronobacter sakazakii</i>	0.06	-.04		99	
<i>Leclercia adecarboxylata</i>	0.05	-.05		1	
116133	Low discrimination				116133
				VPT	
<i>Pantoea agglomerans</i>	83.67	0.57	IND 1	64	
<i>Cronobacter sakazakii</i>	5.88	0.37		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	5.67	0.36		1	
116233	Very good identification				116233
<i>Cronobacter sakazakii</i>	98.26	0.61	IND 11		
<i>Serratia ficaria</i>	1.74	0.18	ORN 91		
116251	Good identification				116251
<i>Serratia odorifera biovar 2</i>	100.0	0.39	LYS 94		
116253	Very good identification				116253
				VPT	
<i>Serratia odorifera biovar 2</i>	98.52	0.70	LYS 94	99	
<i>Serratia ficaria</i>	1.04	0.18		75	
<i>Citrobacter youngae</i>	0.18	0.17		1	
116273	Very good identification				116273
<i>Serratia ficaria</i>	97.81	0.59	IND 1		
<i>Serratia odorifera biovar 2</i>	0.95	0.29			
<i>Cronobacter sakazakii</i>	0.56	0.20			
116333	Acceptable identification				116333
<i>Cronobacter sakazakii</i>	94.16	0.47	IND 11		
<i>Pantoea agglomerans</i>	4.51	0.16	ORN 91		
<i>Serratia rubidaea</i>	1.02	0.04			
116413	Low discrimination				116413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	47.26	0.44	IND 1		
<i>Leclercia adecarboxylata</i>	44.44	0.30			
<i>Escherichia fergusonii</i>	7.56	0.17			
116433	Low discrimination				116433
				VPT	
<i>Leclercia adecarboxylata</i>	49.09	0.36	SCI 1	1	
<i>Serratia rubidaea</i>	41.85	0.33	MAL 93	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	6.72	0.32		1	
116453	Low discrimination				116453
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	75.62	0.50	IND 1	1	
<i>Serratia odorifera biovar 2</i>	21.93	0.31		99	
<i>Citrobacter amalonaticus</i>	1.82	-0.04		1	
116473	Low discrimination				116473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	51.10	0.37	IND 1		
<i>Serratia ficaria</i>	41.25	0.16			
<i>Leclercia adecarboxylata</i>	2.03	-0.05			
116513	Very good identification				116513
				VPT	
<i>Leclercia adecarboxylata</i>	97.17	0.53	SCI 1	1	
<i>Serratia rubidaea</i>	1.92	0.16		99	
<i>Escherichia fergusonii</i>	0.67	0.12		1	
116533	Low discrimination				116533
				VPT	
<i>Serratia rubidaea</i>	49.83	0.57	IND 1	99	
<i>Leclercia adecarboxylata</i>	49.57	0.59		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Pantoea agglomerans</i>	0.56	0.16		64	
116613	Low discrimination				116613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	69.42	0.46	IND 1	1	
<i>Serratia odorifera biovar 2</i>	30.58	0.31		99	
116651	Good identification				116651
				VPT	
<i>Serratia odorifera biovar 2</i>	98.63	0.41	LYS 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.37	0.10	MAN 97	1	
116653	Very good identification				116653
				VPT	
<i>Serratia odorifera biovar 2</i>	95.92	0.72	LYS 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	4.08	0.51		1	
116673	Low discrimination				116673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	29.03	0.39	IND 1	1	
<i>Serratia odorifera biovar 2</i>	27.55	0.31		99	
<i>Serratia ficaria</i>	23.44	0.18		75	
116733	Acceptable identification				116733
				VPT	
<i>Serratia rubidaea</i>	94.12	0.45	IND 1	99	
<i>Leclercia adecarboxylata</i>	3.78	0.18		1	
<i>Klebsiella oxytoca</i>	1.21	-.02		95	
116773	Good identification				116773
<i>Klebsiella oxytoca</i>	97.80	0.39	LYS 99		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.84	-.02	URE 90		
<i>Serratia rubidaea</i>	0.78	0.04			
117033	Good identification				117033
<i>Cronobacter sakazakii</i>	99.69	0.51	IND 11		
<i>Pantoea agglomerans</i>	0.31	-.05	ORN 91		
117123	Good identification				117123
<i>Pantoea agglomerans</i>	99.44	0.38	IND 1		
<i>Cronobacter sakazakii</i>	0.56	-.04	PHE 9		
117133	Low discrimination				117133
				VPT	
<i>Pantoea agglomerans</i>	58.24	0.36	IND 1	64	
<i>Cronobacter sakazakii</i>	41.36	0.37	PHE 9	99	
<i>Leclercia adecarboxylata</i>	0.40	-.05		1	
117201	Good identification				117201
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
117221	Good identification				117221
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
117233	Very good identification				117233
<i>Cronobacter sakazakii</i>	100.0	0.61	IND 11		
117333	Good identification				117333

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Cronobacter sakazakii</i>	99.53	0.47	IND 11		
<i>Pantoea agglomerans</i>	0.47	-.05	ORN 91		
120001	Identification to the genus				120001
<i>Shigella sonnei</i>	88.38	0.59	MAN 99		
<i>Shigella dysenteriae</i> (group A)	11.19	0.51			
<i>Escherichia coli</i>	0.18	0.22			
120002	Very good identification				120002
<i>Shigella sonnei</i>	98.59	0.59	TRE 99		
<i>Shigella boydii</i> (group C)	0.75	0.24			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.22	0.13			
120003	Excellent identification				120003
<i>Shigella sonnei</i>	99.78	1.00			
<i>Salmonella</i> serovar <i>paratyphi</i>	0.05	0.33			
<i>Hafnia alvei</i>	0.05	0.57			
120013	Good identification				120013
<i>Shigella sonnei</i>	90.01	0.74	CEL 5		
<i>Escherichia hermannii</i>	6.27	0.59			
<i>Yersinia kristensenii</i>	1.87	0.48			
120023	Low discrimination				120023
<i>Shigella sonnei</i>	88.85	0.59	SUC 1		
<i>Yersinia rohdei</i>	5.78	0.49			
<i>Escherichia coli</i>	2.31	0.44			
120033	Low discrimination				120033
<i>Escherichia hermannii</i>	67.34	0.57	IND 99		
<i>Shigella sonnei</i>	11.94	0.33			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.90	0.49			
120041	Low discrimination				120041
<i>Shigella dysenteriae</i> (group A)	44.26	0.44	ORN 1		
<i>Shigella sonnei</i>	16.65	0.24			
<i>Citrobacter braakii</i>	15.01	0.43			
120043	Low discrimination				120043
<i>Shigella sonnei</i>	37.40	0.65	SOR 2		
<i>Citrobacter braakii</i>	33.73	0.84			
<i>Salmonella</i> serovar <i>paratyphi</i>	17.40	0.59			
120051	Low discrimination				120051
<i>Yersinia kristensenii</i>	70.28	0.48	MAN 99		
<i>Citrobacter braakii</i>	24.22	0.49			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.61	0.29			
120052	Low discrimination				120052
<i>Yersinia kristensenii</i>	70.44	0.48	TRE 99		
<i>Citrobacter braakii</i>	24.27	0.49			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.62	0.29			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
120053	Low discrimination				120053
<i>Yersinia kristensenii</i>	71.86	0.89			
<i>Citrobacter braakii</i>	24.77	0.90			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.83	0.64			
120061	Low discrimination				120061
<i>Yersinia rohdei</i>	57.81	0.49	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	31.36	0.46			
<i>Escherichia coli</i>	8.93	0.36			
120062	Low discrimination				120062
<i>Yersinia rohdei</i>	57.99	0.49	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	31.46	0.46			
<i>Escherichia coli</i>	8.96	0.36			
120063	Identification to the genus				120063
<i>Yersinia rohdei</i>	75.24	0.90			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.20	0.80			
<i>Escherichia coli</i>	2.23	0.62			
120071	Low discrimination				120071
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	76.56	0.55	MAN 98		
<i>Yersinia rohdei</i>	15.68	0.39			
<i>Citrobacter farmeri</i>	4.47	0.18			
120072	Low discrimination				120072
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	76.56	0.55	TRE 98		
<i>Yersinia rohdei</i>	15.68	0.39			
<i>Citrobacter farmeri</i>	4.47	0.18			
120073	Low discrimination				120073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	61.72	0.90			
<i>Yersinia rohdei</i>	25.54	0.80			
<i>Citrobacter farmeri</i>	7.28	0.59			
120103	Very good identification				120103
<i>Shigella sonnei</i>	95.18	0.59	MAL 1		
<i>Hafnia alvei</i>	4.58	0.57			
<i>Escherichia vulneris</i>	0.11	0.02			
120113	Low discrimination				120113
<i>Escherichia vulneris</i>	62.64	0.43	ORN 1		
<i>Shigella sonnei</i>	28.85	0.33			
<i>Hafnia alvei</i>	4.65	0.42			
120153	Low discrimination				120153
<i>Yersinia kristensenii</i>	58.35	0.48	MAL 1		
<i>Citrobacter braakii</i>	20.11	0.49			
<i>Citrobacter sedlakii</i>	15.56	0.31			
120163	Low discrimination				120163

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia rohdei</i>	72.95	0.49	MAL 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	19.59	0.39			
<i>Escherichia coli</i>	2.16	0.21			
120173	Low discrimination				120173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	60.46	0.53	SCI 99	99	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	24.12	0.49		2	
<i>Yersinia rohdei</i>	9.98	0.39		1	
120203	Very good identification				120203
<i>Shigella sonnei</i>	99.76	0.59	INO 1		
<i>Salmonella serovar paratyphi</i>	0.05	-.09			
<i>Hafnia alvei</i>	0.05	0.16			
120233	Low discrimination				120233
				VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	74.51	0.42	SOR 99	2	
<i>Cronobacter sakazakii</i>	10.26	0.18		99	
<i>Escherichia hermannii</i>	9.94	0.16		1	
120243	Low discrimination				120243
<i>Yersinia enterocolitica ssp. enterocolitica</i>	34.85	0.47	SUC 95		
<i>Shigella sonnei</i>	18.23	0.24			
<i>Yersinia kristensenii</i>	17.09	0.33			
120253	Good identification				120253
<i>Yersinia kristensenii</i>	92.22	0.74			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	5.70	0.56			
<i>Citrobacter braakii</i>	1.82	0.49			
120261	Good identification				120261
<i>Yersinia enterocolitica ssp. enterocolitica</i>	95.84	0.38	MAN 98		
<i>Yersinia rohdei</i>	4.16	0.08			
120262	Good identification				120262
<i>Yersinia enterocolitica ssp. enterocolitica</i>	95.84	0.38	TRE 98		
<i>Yersinia rohdei</i>	4.16	0.08			
120263	Good identification				120263
<i>Yersinia enterocolitica ssp. enterocolitica</i>	91.41	0.73			
<i>Yersinia rohdei</i>	8.02	0.49			
<i>Escherichia coli</i>	0.24	0.21			
120271	Good identification				120271
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.10	0.48	MAN 98		
<i>Yersinia rohdei</i>	0.48	-.02			
<i>Yersinia kristensenii</i>	0.42	-.09			
120272	Good identification				120272
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.10	0.48	TRE 98		
<i>Yersinia rohdei</i>	0.48	-.02			
<i>Yersinia kristensenii</i>	0.42	-.09			
120273	Very good identification				120273

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.44	0.83			
<i>Yersinia rohdei</i>	0.95	0.39			
<i>Yersinia kristensenii</i>	0.84	0.33			
120373	Low discrimination				120373
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	50.33	0.38	SCI 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	48.77	0.42		2	
<i>Yersinia rohdei</i>	0.48	-.02		1	
120403	Very good identification				120403
<i>Shigella sonnei</i>	99.30	0.59	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.22	0.27			
<i>Escherichia coli</i>	0.20	0.22			
120433	Low discrimination				120433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.63	0.37	ORN 3	1	
<i>Escherichia hermannii</i>	25.59	0.16		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	6.56	0.07		99	
120453	Low discrimination				120453
<i>Yersinia kristensenii</i>	54.44	0.48	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	23.87	0.55			
<i>Citrobacter braakii</i>	18.76	0.49			
120463	Low discrimination				120463
<i>Yersinia rohdei</i>	68.34	0.49	ADO 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	18.35	0.39			
<i>Escherichia coli</i>	10.56	0.36			
120473	Low discrimination				120473
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	47.27	0.49	ADO 1	2	
<i>Yersinia rohdei</i>	19.56	0.39		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	13.16	0.34		99	
120573	Acceptable identification				120573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	92.97	0.44	SCI 99	99	
<i>Citrobacter koseri</i>	4.01	0.14		1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.12	0.08		2	
120613	Good identification				120613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.92	0.51	ORN 3		
<i>Shigella sonnei</i>	1.65	-.09			
<i>Escherichia fergusonii</i>	0.83	-.02			
120633	Good identification				120633
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.18	0.39	ORN 3		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.82	0.00			
120653	Low discrimination				120653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	73.41	0.57	ORN 3		
<i>Yersinia kristensenii</i>	24.17	0.33			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.49	0.15			
120673	Low discrimination				120673
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	55.77	0.42	ADO 1	2	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	36.05	0.44		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	6.39	0.18		99	
121003	Very good identification				121003
<i>Shigella sonnei</i>	99.82	0.59	PHE 1		
<i>Salmonella</i> serovar <i>paratyphi</i>	0.05	-.09			
<i>Hafnia alvei</i>	0.05	0.16			
121053	Low discrimination				121053
<i>Yersinia kristensenii</i>	72.00	0.48	PHE 1		
<i>Citrobacter braakii</i>	24.81	0.49			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.83	0.23			
121063	Identification to the genus				121063
<i>Yersinia rohdei</i>	75.61	0.49	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.30	0.39			
<i>Escherichia coli</i>	2.24	0.21			
121073	Low discrimination				121073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	61.93	0.49	PHE 1		
<i>Yersinia rohdei</i>	25.63	0.39			
<i>Citrobacter farmeri</i>	7.31	0.18			
121273	Good identification				121273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.20	0.42	PHE 1		
<i>Yersinia rohdei</i>	0.96	-.02			
<i>Yersinia kristensenii</i>	0.85	-.09			
122003	Good identification				122003
<i>Shigella sonnei</i>	93.91	0.59	ESL 1		
<i>Yersinia pseudotuberculosis</i>	3.77	0.33			
<i>Escherichia coli</i>	0.92	0.36			
122013	Low discrimination				122013
<i>Escherichia hermannii</i>	64.78	0.55	IND 99		
<i>Yokenella regensburgei</i>	17.14	0.37			
<i>Shigella sonnei</i>	14.10	0.33			
122033	Low discrimination				122033
				VPT	
<i>Escherichia hermannii</i>	61.39	0.54	IND 99	1	
<i>Cronobacter sakazakii</i>	31.68	0.49		99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.42	0.39		2	
122043	Low discrimination				122043
<i>Escherichia coli</i>	46.23	0.53	IND 92		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	19.59	0.44			
<i>Shigella sonnei</i>	13.17	0.24			
122053	Low discrimination				122053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia kristensenii</i>	43.09	0.48	ESL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	36.19	0.54			
<i>Citrobacter braakii</i>	14.85	0.49			
122061	Low discrimination				122061
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	78.78	0.36	MAN 98		
<i>Escherichia coli</i>	16.82	0.23			
<i>Yersinia rohdei</i>	4.40	0.08			
122062	Low discrimination				122062
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	78.78	0.36	TRE 98		
<i>Escherichia coli</i>	16.82	0.23			
<i>Yersinia rohdei</i>	4.40	0.08			
122063	Low discrimination				122063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	83.07	0.71			
<i>Yersinia rohdei</i>	9.37	0.49			
<i>Escherichia coli</i>	6.88	0.50			
122071	Good identification				122071
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.38	0.46	MAN 98		
<i>Yersinia rohdei</i>	0.62	-.02			
122072	Good identification				122072
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.38	0.46	TRE 98		
<i>Yersinia rohdei</i>	0.62	-.02			
122073	Very good identification				122073
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.55	0.80		2	
<i>Yersinia rohdei</i>	1.21	0.39		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.05	0.36		99	
122123	Good identification				122123
<i>Pantoea agglomerans</i>	99.34	0.47	ORN 1		
<i>Hafnia alvei</i>	0.48	0.18			
<i>Cronobacter sakazakii</i>	0.18	-.06			
122133	Low discrimination				122133
				VPT	
<i>Pantoea agglomerans</i>	72.41	0.44	ORN 1	64	
<i>Cronobacter sakazakii</i>	16.81	0.36		99	
<i>Kluyvera ascorbata</i>	5.00	0.19		1	
122173	Low discrimination				122173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	70.70	0.46	SCI 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	21.94	0.39		2	
<i>Kluyvera ascorbata</i>	5.58	0.15		1	
122233	Very good identification				122233
				VPT	
<i>Cronobacter sakazakii</i>	96.70	0.59	SCI 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.36	0.32		2	
<i>Escherichia hermannii</i>	0.63	0.12		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
122243	Low discrimination				122243
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	88.16	0.37	SUC 95		
<i>Escherichia coli</i>	4.90	0.12			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.24	0.16			
122253	Low discrimination				122253
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	59.20	0.47	SUC 95		
<i>Yersinia kristensenii</i>	29.03	0.33			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	10.90	0.38			
122263	Very good identification				122263
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.41	0.63		2	
<i>Serratia marcescens</i>	3.15	0.24		98	
<i>Yersinia rohdei</i>	0.26	0.08		1	
122271	Good identification				122271
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.38	MAN 98		
122272	Good identification				122272
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.38	TRE 98		
122273	Very good identification				122273
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.65	0.73		2	
<i>Serratia ficaria</i>	0.87	0.18		75	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.44	0.21		99	
122333	Good identification				122333
<i>Cronobacter sakazakii</i>	97.82	0.45	SCI 99		
<i>Pantoea agglomerans</i>	1.42	0.03			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.76	0.04			
122413	Low discrimination				122413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.61	0.62	ORN 3		
<i>Escherichia fergusonii</i>	17.58	0.38			
<i>Escherichia hermannii</i>	1.90	0.14			
122433	Low discrimination				122433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	83.59	0.49	ORN 3	1	
<i>Escherichia hermannii</i>	6.53	0.12		1	
<i>Serratia rubidaea</i>	3.83	0.06		99	
122443	Low discrimination				122443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.43	0.45	ORN 3		
<i>Escherichia coli</i>	18.11	0.27	CEL 92		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.47	0.03			
122453	Very good identification				122453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.54	0.67	ORN 3		
<i>Yersinia kristensenii</i>	0.57	0.07			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.48	0.13			
122473	Low discrimination				122473

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	66.23	0.55	ORN 3	1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	24.35	0.39		2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	8.72	0.26		99	
122553	Acceptable identification				122553
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.02	0.36	ORN 3	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	8.98	0.05	MAL 3	99	
122573	Low discrimination				122573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	72.92	0.36	SCI 99	99	
<i>Enterobacter aerogenes</i>	21.37	0.13		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.71	0.24		1	
122603	Good identification				122603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.42	ORN 3		
122613	Very good identification				122613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.82	0.63	ORN 3		
<i>Escherichia fergusonii</i>	0.18	-.04			
122633	Acceptable identification				122633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	90.23	0.51	ORN 3	1	
<i>Cronobacter sakazakii</i>	8.93	0.18		99	
<i>Serratia rubidaea</i>	0.85	-.06		99	
122643	Good identification				122643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.47	ORN 3		
122653	Very good identification				122653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.65	0.69	ORN 3	1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.17	0.05		2	
<i>Serratia odorifera</i> biovar 2	0.10	0.00		99	
122673	Low discrimination				122673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	77.78	0.57	ORN 3	1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.03	0.32		2	
<i>Enterobacter aerogenes</i>	7.36	0.13		98	
122753	Low discrimination				122753
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.20	0.38	ORN 3	1	
<i>Enterobacter aerogenes</i>	11.63	-.02	MAL 3	98	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	9.18	0.00		1	
122773	Acceptable identification				122773
				VPT	
<i>Enterobacter aerogenes</i>	93.21	0.39	LYS 98	98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.96	0.21	SCI 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	2.23	0.10		1	
123033	Good identification				123033
				VPT	
<i>Cronobacter sakazakii</i>	98.08	0.49	SCI 99	99	
<i>Escherichia hermannii</i>	1.92	0.12		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
123073	Acceptable identification				123073
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	93.32	0.39	PHE 1	2	
<i>Cronobacter sakazakii</i>	5.51	0.08		99	
<i>Yersinia rohdei</i>	1.17	-.02		1	
123133	Low discrimination				123133
<i>Cronobacter sakazakii</i>	70.13	0.36	SCI 99		
<i>Pantoea agglomerans</i>	29.87	0.24			
123233	Very good identification				123233
<i>Cronobacter sakazakii</i>	100.0	0.59	SCI 99		
123333	Good identification				123333
<i>Cronobacter sakazakii</i>	100.0	0.45	SCI 99		
124003	Good identification				124003
<i>Shigella sonnei</i>	90.15	0.59	SCI 1		
<i>Citrobacter braakii</i>	4.98	0.53			
<i>Hafnia alvei</i>	4.34	0.57			
124013	Low discrimination				124013
<i>Yokenella regensburgei</i>	65.11	0.53	LYS 99		
<i>Citrobacter braakii</i>	20.14	0.59			
<i>Shigella sonnei</i>	9.46	0.33			
124033	Low discrimination				124033
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	65.30	0.58	SOR 95	99	
<i>Cronobacter sakazakii</i>	29.23	0.49		99	
<i>Citrobacter braakii</i>	2.41	0.36		1	
124041	Good identification				124041
<i>Citrobacter braakii</i>	97.10	0.53	MAN 99		
<i>Citrobacter youngae</i>	1.58	0.15			
<i>Shigella dysenteriae</i> (group A)	0.96	0.03			
124042	Low discrimination				124042
<i>Citrobacter braakii</i>	87.50	0.53	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	10.75	0.23			
<i>Citrobacter youngae</i>	1.42	0.15			
124043	Very good identification				124043
<i>Citrobacter braakii</i>	97.25	0.94			
<i>Citrobacter youngae</i>	1.58	0.56			
<i>Shigella sonnei</i>	0.36	0.24			
124051	Good identification				124051
				VPT	
<i>Citrobacter braakii</i>	92.06	0.59	MAN 99	1	
<i>Citrobacter amalonaticus</i>	5.33	0.17		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.11	0.13		99	
124052	Good identification				124052
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	92.06	0.59	TRE 99	1	124053
<i>Citrobacter amalonaticus</i>	5.33	0.17		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.11	0.13		99	
124053	Good identification				
				VPT	124053
<i>Citrobacter braakii</i>	91.92	1.00		1	
<i>Citrobacter amalonaticus</i>	5.32	0.58		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.11	0.54		99	
124063	Low discrimination				124063
<i>Citrobacter braakii</i>	64.84	0.71	SUC 7		124071
<i>Yersinia rohdei</i>	10.26	0.49			
<i>Citrobacter freundii</i>	9.92	0.56			
124071	Low discrimination				
				VPT	124071
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	79.17	0.44	MAN 99	99	
<i>Citrobacter braakii</i>	15.25	0.36		1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.93	0.14		2	
124072	Low discrimination				124072
				VPT	124072
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	79.17	0.44	TRE 99	99	
<i>Citrobacter braakii</i>	15.25	0.36		1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.93	0.14		2	
124073	Low discrimination				124073
				VPT	124073
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	79.83	0.85		99	
<i>Citrobacter braakii</i>	15.38	0.77		1	
<i>Citrobacter farmeri</i>	1.25	0.39		1	
124103	Low discrimination				124103
<i>Hafnia alvei</i>	80.66	0.57	LYS 99		124113
<i>Shigella sonnei</i>	16.93	0.18			
<i>Citrobacter werkmanii</i>	1.12	-0.04			
124113	Low discrimination				
				VPT	124113
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	54.46	0.37	SUC 97	99	
<i>Hafnia alvei</i>	21.84	0.42	SOR 95	85	
<i>Yokenella regensburgei</i>	9.42	0.12		1	
124133	Very good identification				124133
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.82	0.68	SOR 95		124143
<i>Cronobacter sakazakii</i>	3.14	0.36			
<i>Pantoea agglomerans</i>	0.55	0.16			
124143	Low discrimination				
<i>Citrobacter braakii</i>	57.36	0.53	MAL 1		124153
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	11.78	0.18			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	10.30	0.18			
124153	Low discrimination				
				VPT	124153
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	59.07	0.63	SUC 97	99	
<i>Citrobacter sedlakii</i>	20.74	0.45		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	16.46	0.59		1	
124163	Good identification				124163
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	90.98	0.53	CEL 99	99	
<i>Citrobacter freundii</i>	3.79	0.34		1	
<i>Citrobacter braakii</i>	2.88	0.30		1	
124171	Very good identification				124171
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.53	MAN 99		
124172	Very good identification				124172
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.53	TRE 99		
124173	Excellent identification				124173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	99.77	0.95		99	
<i>Citrobacter koseri</i>	0.09	0.30		1	
<i>Citrobacter braakii</i>	0.07	0.36		1	
124233	Low discrimination				124233
				VPT	
<i>Cronobacter sakazakii</i>	88.33	0.59	ESL 99	99	
<i>Enterobacter cloacae subsp. cloacae</i>	11.61	0.43		99	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.07	0.00		2	
124243	Identification to the genus				124243
<i>Citrobacter braakii</i>	89.30	0.53	INO 1		
<i>Citrobacter youngae</i>	7.56	0.30			
<i>Salmonella serovar enteritidis</i>	1.13	-0.1			
124253	Low discrimination				124253
				VPT	
<i>Citrobacter braakii</i>	63.46	0.59	INO 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	13.40	0.38		99	
<i>Yersinia kristensenii</i>	10.83	0.33		1	
124273	Good identification				124273
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	93.13	0.69		99	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.74	0.42		2	
<i>Serratia odorifera biovar 1</i>	1.41	0.29		50	
124333	Low discrimination				124333
<i>Enterobacter cloacae subsp. cloacae</i>	64.24	0.53	SOR 95		
<i>Cronobacter sakazakii</i>	35.76	0.45			
124353	Good identification				124353
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.01	0.48	SUC 97	99	
<i>Citrobacter sedlakii</i>	1.93	0.04		1	
<i>Citrobacter braakii</i>	1.53	0.18		1	
124363	Good identification				124363
<i>Enterobacter cloacae subsp. cloacae</i>	97.30	0.38	CEL 99		
<i>Serratia marcescens</i>	2.70	0.02			
124371	Good identification				124371

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.38	MAN 99		
124372	Good identification				124372
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.38	TRE 99		
124373	Very good identification				124373
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.93	0.79			
<i>Enterobacter aerogenes</i>	0.04	-.04			
<i>Cronobacter sakazakii</i>	0.03	0.04			
124413	Low discrimination				124413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	43.98	0.42	ORN 3		
<i>Escherichia fergusonii</i>	21.80	0.25			
<i>Yokenella regensburgei</i>	14.68	0.12			
124433	Acceptable identification				124433
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	92.74	0.49	SOR 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.34	0.29		1	
<i>Serratia rubidaea</i>	1.74	0.08		99	
124443	Acceptable identification				124443
<i>Citrobacter braakii</i>	92.95	0.53	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.98	0.25			
<i>Citrobacter youngae</i>	1.51	0.15			
124453	Low discrimination				124453
				VPT	
<i>Citrobacter braakii</i>	56.35	0.59	ADO 1	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	22.47	0.44		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	10.24	0.47		1	
124473	Very good identification				124473
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	98.08	0.75		99	
<i>Citrobacter koseri</i>	0.81	0.30		1	
<i>Citrobacter braakii</i>	0.57	0.36		1	
124533	Low discrimination				124533
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	86.88	0.58	SOR 95	99	
<i>Serratia rubidaea</i>	8.49	0.33		99	
<i>Citrobacter koseri</i>	4.54	0.30		1	
124553	Low discrimination				124553
				VPT	
<i>Citrobacter koseri</i>	60.56	0.56	IND 99	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	38.52	0.54		99	
<i>Citrobacter sedlakii</i>	0.41	0.04		1	
124563	Low discrimination				124563
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	78.59	0.44	CEL 99	99	
<i>Citrobacter koseri</i>	21.41	0.30		1	
124571	Good identification				124571
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.87	0.44	MAN 99	99	
<i>Citrobacter koseri</i>	4.13	0.14		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
124572	Good identification				124572
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.87	0.44	TRE 99	99	
<i>Citrobacter koseri</i>	4.13	0.14		1	
124573	Very good identification				124573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.82	0.85		99	
<i>Citrobacter koseri</i>	4.13	0.55		1	
<i>Enterobacter aerogenes</i>	0.05	0.04		98	
124613	Good identification				124613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.00	0.43	ORN 3	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	3.00	0.02		99	
124653	Low discrimination				124653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.50	0.49	ORN 3	1	
<i>Serratia odorifera</i> biovar 2	25.33	0.34		99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	17.26	0.28		99	
124673	Good identification				124673
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	92.43	0.59		99	
<i>Serratia odorifera</i> biovar 1	4.19	0.29		50	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.26	0.37		1	
124733	Low discrimination				124733
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	85.80	0.43	SOR 95		
<i>Serratia rubidaea</i>	11.88	0.20			
<i>Cronobacter sakazakii</i>	1.45	0.04			
124753	Low discrimination				124753
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	87.73	0.38	SUC 97	99	
<i>Citrobacter koseri</i>	7.90	0.15		1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.86	0.18		1	
124773	Good identification				124773
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.73	0.69		99	
<i>Enterobacter aerogenes</i>	5.02	0.30		98	
<i>Citrobacter koseri</i>	0.23	0.14		1	
125033	Good identification				125033
<i>Cronobacter sakazakii</i>	97.79	0.49	ESL 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.21	0.17			
125043	Good identification				125043
<i>Citrobacter braakii</i>	98.04	0.53	PHE 1		
<i>Citrobacter youngae</i>	1.59	0.15			
<i>Shigella sonnei</i>	0.37	-0.17			
125053	Good identification				125053
				VPT	
<i>Citrobacter braakii</i>	92.06	0.59	PHE 1	1	
<i>Citrobacter amalonaticus</i>	5.33	0.17		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.11	0.13		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
125073	Low discrimination				125073
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	78.47	0.44	PHE 1	99	
<i>Citrobacter braakii</i>	15.12	0.36		1	
<i>Cronobacter sakazakii</i>	1.85	0.08		99	
125133	Low discrimination				125133
<i>Cronobacter sakazakii</i>	75.43	0.36	ESL 99		
<i>Enterobacter cloacae subsp. cloacae</i>	23.27	0.27			
<i>Pantoea agglomerans</i>	1.30	-.05			
125173	Very good identification				125173
<i>Enterobacter cloacae subsp. cloacae</i>	99.83	0.53	PHE 1		
<i>Cronobacter sakazakii</i>	0.17	-.06			
125233	Very good identification				125233
<i>Cronobacter sakazakii</i>	99.87	0.59	ESL 99		
<i>Enterobacter cloacae subsp. cloacae</i>	0.13	0.02			
125333	Good identification				125333
<i>Cronobacter sakazakii</i>	98.22	0.45	ESL 99		
<i>Enterobacter cloacae subsp. cloacae</i>	1.78	0.12			
125373	Good identification				125373
<i>Enterobacter cloacae subsp. cloacae</i>	97.15	0.38	PHE 1		
<i>Cronobacter sakazakii</i>	2.85	0.04			
125573	Good identification				125573
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	95.87	0.44	PHE 1	99	
<i>Citrobacter koseri</i>	4.13	0.14		1	
126013	Low discrimination				126013
				VPT	
<i>Yokenella regensburgei</i>	86.73	0.59	LYS 99	1	
<i>Cronobacter sakazakii</i>	12.04	0.49		99	
<i>Enterobacter cloacae subsp. cloacae</i>	0.36	0.20		99	
126023	Acceptable identification				126023
<i>Cronobacter sakazakii</i>	92.84	0.49	CEL 99		
<i>Pantoea agglomerans</i>	4.51	0.18			
<i>Serratia marcescens</i>	1.21	0.08			
126031	Good identification				126031
<i>Cronobacter sakazakii</i>	99.04	0.49	MAN 99		
<i>Enterobacter cloacae subsp. cloacae</i>	0.96	0.10			
126032	Good identification				126032
<i>Cronobacter sakazakii</i>	99.04	0.49	TRE 99		
<i>Enterobacter cloacae subsp. cloacae</i>	0.96	0.10			
126033	Very good identification				126033
				VPT	
<i>Cronobacter sakazakii</i>	98.79	0.90		99	
<i>Enterobacter cloacae subsp. cloacae</i>	0.96	0.51		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yokenella regensburgei</i>	0.07	0.18		1	
126043	Low discrimination				126043
				VPT	
<i>Citrobacter braakii</i>	86.41	0.53	ESL 1	1	
<i>Citrobacter youngae</i>	7.32	0.30		1	
<i>Serratia marcescens</i>	2.08	0.08		98	
126053	Low discrimination				126053
				VPT	
<i>Citrobacter braakii</i>	43.86	0.59	ESL 1	1	
<i>Citrobacter amalonaticus</i>	24.86	0.37		1	
<i>Enterobacter cloacae subsp. cloacae</i>	22.49	0.46		99	
126063	Low discrimination				126063
				VPT	
<i>Serratia marcescens</i>	77.54	0.49	LYS 99	98	
<i>Enterobacter cloacae subsp. cloacae</i>	11.05	0.36		99	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	3.43	0.30		2	
126071	Low discrimination				126071
<i>Enterobacter cloacae subsp. cloacae</i>	73.52	0.36	MAN 99		
<i>Serratia ficaria</i>	21.04	0.16			
<i>Cronobacter sakazakii</i>	4.04	0.08			
126072	Low discrimination				126072
<i>Enterobacter cloacae subsp. cloacae</i>	73.52	0.36	TRE 99		
<i>Serratia ficaria</i>	21.04	0.16			
<i>Cronobacter sakazakii</i>	4.04	0.08			
126073	Low discrimination				126073
<i>Enterobacter cloacae subsp. cloacae</i>	73.19	0.77			
<i>Serratia ficaria</i>	20.95	0.57			
<i>Cronobacter sakazakii</i>	4.02	0.49			
126103	Low discrimination				126103
<i>Hafnia alvei</i>	50.74	0.38	LYS 99		
<i>Pantoea agglomerans</i>	47.12	0.18	ESL 10		
<i>Cronobacter sakazakii</i>	2.15	-.06			
126113	Low discrimination				126113
				VPT	
<i>Cronobacter sakazakii</i>	47.08	0.36	SUC 99	99	
<i>Enterobacter cloacae subsp. cloacae</i>	19.06	0.30		99	
<i>Yokenella regensburgei</i>	15.61	0.18		1	
126123	Good identification				126123
<i>Pantoea agglomerans</i>	94.64	0.59	ORN 1		
<i>Cronobacter sakazakii</i>	4.32	0.36			
<i>Enterobacter cloacae subsp. cloacae</i>	0.57	0.20			
126131	Low discrimination				126131
<i>Cronobacter sakazakii</i>	72.55	0.36	MAN 99		
<i>Pantoea agglomerans</i>	12.63	0.16			
<i>Enterobacter cloacae subsp. cloacae</i>	9.59	0.20			
126132	Low discrimination				126132

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Cronobacter sakazakii</i>	72.55	0.36	TRE 99		
<i>Pantoea agglomerans</i>	12.63	0.16			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	9.59	0.20			
126133	Low discrimination				126133
<i>Cronobacter sakazakii</i>	72.47	0.77			
<i>Pantoea agglomerans</i>	12.61	0.57			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	9.58	0.61			
126153	Low discrimination				126153
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	83.81	0.56	SUC 97	99	
<i>Citrobacter sedlakii</i>	14.06	0.31		1	
<i>Kluyvera ascorbata</i>	1.06	0.09		1	
126163	Low discrimination				126163
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	84.48	0.46	CEL 99		
<i>Pantoea agglomerans</i>	7.45	0.18			
<i>Serratia marcescens</i>	6.11	0.18			
126171	Good identification				126171
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.74	0.46	MAN 99	99	
<i>Kluyvera ascorbata</i>	1.87	0.02		1	
<i>Cronobacter sakazakii</i>	0.39	-.06		99	
126172	Good identification				126172
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.74	0.46	TRE 99	99	
<i>Kluyvera ascorbata</i>	1.87	0.02		1	
<i>Cronobacter sakazakii</i>	0.39	-.06		99	
126173	Very good identification				126173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.53	0.87		99	
<i>Kluyvera ascorbata</i>	1.87	0.44		1	
<i>Cronobacter sakazakii</i>	0.39	0.36		99	
126213	Very good identification				126213
				VPT	
<i>Cronobacter sakazakii</i>	96.95	0.59	SUC 99	99	
<i>Yokenella regensburgei</i>	2.35	0.18		1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.53	0.25		1	
126223	Very good identification				126223
<i>Cronobacter sakazakii</i>	98.71	0.59	CEL 99		
<i>Serratia marcescens</i>	1.29	0.18			
126231	Very good identification				126231
<i>Cronobacter sakazakii</i>	100.0	0.59	MAN 99		
126232	Very good identification				126232
<i>Cronobacter sakazakii</i>	100.0	0.59	TRE 99		
126233	Excellent identification				126233
<i>Cronobacter sakazakii</i>	99.91	1.00			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.06	0.35			
<i>Serratia ficaria</i>	0.02	0.18			
126263	Very good identification				126263
<i>Serratia marcescens</i>	95.72	0.59	LYS 99		
<i>Serratia ficaria</i>	1.59	0.18			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.80	0.21			
126273	Low discrimination				126273
<i>Serratia ficaria</i>	42.34	0.59	ORN 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	21.36	0.62			
<i>Cronobacter sakazakii</i>	19.96	0.59			
126313	Good identification				126313
<i>Cronobacter sakazakii</i>	97.67	0.45	SUC 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.33	0.14			
126323	Acceptable identification				126323
<i>Cronobacter sakazakii</i>	92.46	0.45	CEL 99		
<i>Pantoea agglomerans</i>	6.83	0.18			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.72	0.04			
126331	Good identification				126331
<i>Cronobacter sakazakii</i>	99.23	0.45	MAN 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.77	0.04			
126332	Good identification				126332
<i>Cronobacter sakazakii</i>	99.23	0.45	TRE 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.77	0.04			
126333	Very good identification				126333
<i>Cronobacter sakazakii</i>	99.13	0.86			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.77	0.45			
<i>Pantoea agglomerans</i>	0.06	0.16			
126353	Good identification				126353
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.66	0.40	SUC 97		
<i>Cronobacter sakazakii</i>	2.14	0.04			
<i>Enterobacter aerogenes</i>	1.29	-.11			
126373	Low discrimination				126373
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	89.27	0.71			
<i>Cronobacter sakazakii</i>	6.10	0.45			
<i>Enterobacter aerogenes</i>	3.68	0.30			
126413	Low discrimination				126413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.39	0.54	ORN 3		
<i>Yokenella regensburgei</i>	12.77	0.18			
<i>Escherichia fergusonii</i>	7.96	0.23			
126433	Low discrimination				126433
<i>Cronobacter sakazakii</i>	60.79	0.49	ADO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	19.41	0.41			
<i>Serratia rubidaea</i>	13.28	0.33			
126443	Low discrimination				126443
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.22	0.38	ORN 3	1	
<i>Serratia marcescens</i>	10.17	0.04	CEL 92	98	
<i>Citrobacter braakii</i>	6.39	0.12		1	
126453	Low discrimination				126453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.57	0.60	ORN 3	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	18.70	0.36		99	
<i>Citrobacter braakii</i>	1.11	0.18		1	
126463	Acceptable identification				126463
				VPT	
<i>Serratia marcescens</i>	91.63	0.46	LYS 99	98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	6.53	0.26		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.85	0.25		1	
126473	Good identification				126473
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.03	0.67		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.09	0.47		1	
<i>Enterobacter aerogenes</i>	0.84	0.13		98	
126533	Low discrimination				126533
<i>Serratia rubidaea</i>	73.32	0.57	ORN 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	20.52	0.51			
<i>Cronobacter sakazakii</i>	4.70	0.36			
126553	Acceptable identification				126553
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	90.55	0.46	SUC 97	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.97	0.29		1	
<i>Citrobacter koseri</i>	3.36	0.15		1	
126563	Low discrimination				126563
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	82.44	0.36	CEL 99		
<i>Serratia marcescens</i>	11.93	0.14			
<i>Enterobacter aerogenes</i>	4.64	-.02			
126571	Acceptable identification				126571
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.68	0.36	MAN 99		
<i>Enterobacter aerogenes</i>	5.32	-.02			
126572	Acceptable identification				126572
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.68	0.36	TRE 99		
<i>Enterobacter aerogenes</i>	5.32	-.02			
126573	Good identification				126573
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.32	0.77			
<i>Enterobacter aerogenes</i>	5.30	0.39			
<i>Serratia rubidaea</i>	0.18	0.16			
126613	Good identification				126613

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.55	0.56	ORN 3	1	
<i>Cronobacter sakazakii</i>	5.46	0.18		99	
126633	Good identification				126633
				VPT	
<i>Cronobacter sakazakii</i>	91.62	0.59	ADO 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.01	0.43		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.72	0.25		99	
126643	Low discrimination				126643
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.49	0.40	ORN 3	1	
<i>Serratia marcescens</i>	23.51	0.14	CEL 92	98	
126653	Low discrimination				126653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	87.39	0.61	ORN 3	1	
<i>Serratia odorifera</i> biovar 2	6.77	0.31		99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.97	0.21		99	
126663	Very good identification				126663
				VPT	
<i>Serratia marcescens</i>	97.58	0.55	LYS 99	98	
<i>Serratia odorifera</i> biovar 1	0.82	0.14		50	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.80	0.27		1	
126673	Low discrimination				126673
<i>Serratia odorifera</i> biovar 1	45.60	0.55	LYS 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	22.68	0.52			
<i>Enterobacter aerogenes</i>	21.68	0.39			
126733	Low discrimination				126733
<i>Serratia rubidaea</i>	45.42	0.45	ORN 1		
<i>Cronobacter sakazakii</i>	34.97	0.45			
<i>Enterobacter aerogenes</i>	10.43	0.24			
126773	Identification to the genus				126773
<i>Enterobacter aerogenes</i>	85.60	0.65	LYS 98		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	14.14	0.62			
<i>Serratia odorifera</i> biovar 1	0.10	0.14			
127013	Acceptable identification				127013
				VPT	
<i>Cronobacter sakazakii</i>	93.22	0.49	SUC 99	99	
<i>Yokenella regensburgei</i>	6.78	0.18		1	
127023	Good identification				127023
<i>Cronobacter sakazakii</i>	99.52	0.49	CEL 99		
<i>Pantoea agglomerans</i>	0.48	-.03			
127031	Good identification				127031
<i>Cronobacter sakazakii</i>	100.0	0.49	MAN 99		
127032	Good identification				127032
<i>Cronobacter sakazakii</i>	100.0	0.49	TRE 99		
127033	Very good identification				127033

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Cronobacter sakazakii</i>	99.99	0.90			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.01	0.10			
<i>Pantoea agglomerans</i>	0.00	-.05			
127073	Low discrimination				127073
<i>Cronobacter sakazakii</i>	80.88	0.49	SOR 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	14.87	0.36			
<i>Serratia ficaria</i>	4.25	0.16			
127113	Good identification				127113
<i>Cronobacter sakazakii</i>	98.31	0.36	SUC 99		
<i>Pantoea agglomerans</i>	1.69	-.05			
127123	Low discrimination				127123
<i>Pantoea agglomerans</i>	68.44	0.38	ORN 1		
<i>Cronobacter sakazakii</i>	31.56	0.36	PHE 9		
127131	Good identification				127131
<i>Cronobacter sakazakii</i>	98.31	0.36	MAN 99		
<i>Pantoea agglomerans</i>	1.69	-.05			
127132	Good identification				127132
<i>Cronobacter sakazakii</i>	98.31	0.36	TRE 99		
<i>Pantoea agglomerans</i>	1.69	-.05			
127133	Very good identification				127133
<i>Cronobacter sakazakii</i>	98.11	0.77			
<i>Pantoea agglomerans</i>	1.69	0.36			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.13	0.20			
127173	Low discrimination				127173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	70.22	0.46	PHE 1	99	
<i>Cronobacter sakazakii</i>	27.96	0.36		99	
<i>Kluyvera ascorbata</i>	1.34	0.02		1	
127213	Very good identification				127213
<i>Cronobacter sakazakii</i>	100.0	0.59	SUC 99		
127223	Very good identification				127223
<i>Cronobacter sakazakii</i>	100.0	0.59	CEL 99		
127231	Very good identification				127231
<i>Cronobacter sakazakii</i>	100.0	0.59	MAN 99		
127232	Very good identification				127232
<i>Cronobacter sakazakii</i>	100.0	0.59	TRE 99		
127233	Excellent identification				127233
<i>Cronobacter sakazakii</i>	100.0	1.00			
127273	Very good identification				127273
<i>Cronobacter sakazakii</i>	96.14	0.59	SOR 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia ficaria</i>	2.06	0.18			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.04	0.21			
127313	Good identification				127313
<i>Cronobacter sakazakii</i>	100.0	0.45	SUC 99		
127323	Good identification				127323
<i>Cronobacter sakazakii</i>	99.28	0.45	CEL 99		
<i>Pantoea agglomerans</i>	0.73	-.03			
127331	Good identification				127331
<i>Cronobacter sakazakii</i>	100.0	0.45	MAN 99		
127332	Good identification				127332
<i>Cronobacter sakazakii</i>	100.0	0.45	TRE 99		
127333	Very good identification				127333
<i>Cronobacter sakazakii</i>	99.99	0.86			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.01	0.04			
<i>Pantoea agglomerans</i>	0.01	-.05			
127373	Low discrimination				127373
<i>Cronobacter sakazakii</i>	86.67	0.45	SOR 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	12.81	0.30			
<i>Enterobacter aerogenes</i>	0.53	-.11			
127433	Good identification				127433
<i>Cronobacter sakazakii</i>	99.46	0.49	ADO 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.32	0.00			
<i>Serratia rubidaea</i>	0.22	-.09			
127533	Low discrimination				127533
<i>Cronobacter sakazakii</i>	82.05	0.36	ADO 1		
<i>Serratia rubidaea</i>	12.92	0.16			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	3.62	0.10			
127573	Acceptable identification				127573
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	93.61	0.36	PHE 1		
<i>Enterobacter aerogenes</i>	5.26	-.02			
<i>Cronobacter sakazakii</i>	1.13	-.06			
127633	Very good identification				127633
<i>Cronobacter sakazakii</i>	100.0	0.59	ADO 1		
127733	Good identification				127733
<i>Cronobacter sakazakii</i>	98.41	0.45	ADO 1		
<i>Serratia rubidaea</i>	1.29	0.04			
<i>Enterobacter aerogenes</i>	0.30	-.17			
130001	Low discrimination				130001
<i>Shigella dysenteriae</i> (group A)	69.27	0.50	ORN 1		
<i>Escherichia coli</i>	15.81	0.44			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	7.50	0.28			
130002	Low discrimination				130002
<i>Escherichia coli</i>	48.37	0.44	SOR 88		
<i>Escherichia hermannii</i>	22.95	0.28	TRE 95		
<i>Shigella sonnei</i>	20.66	0.18			
130003	Low discrimination				130003
<i>Escherichia hermannii</i>	42.80	0.69	CEL 97		
<i>Shigella sonnei</i>	38.54	0.59			
<i>Escherichia coli</i>	17.31	0.70			
130011	Very good identification				130011
<i>Escherichia hermannii</i>	99.04	0.59	MAN 99		
<i>Shigella dysenteriae</i> (group A)	0.29	0.09			
<i>Escherichia fergusonii</i>	0.27	0.10			
130012	Very good identification				130012
<i>Escherichia hermannii</i>	99.05	0.59	TRE 99		
<i>Escherichia fergusonii</i>	0.55	0.16			
<i>Shigella sonnei</i>	0.15	-0.09			
130013	Excellent identification				130013
<i>Escherichia hermannii</i>	99.35	1.00			
<i>Escherichia fergusonii</i>	0.27	0.51			
<i>Shigella sonnei</i>	0.15	0.33			
130021	Low discrimination				130021
<i>Escherichia coli</i>	59.83	0.40	SOR 88		
<i>Escherichia hermannii</i>	34.84	0.26	MAN 95		
<i>Shigella dysenteriae</i> (group A)	3.97	0.09			
130022	Identification to the genus				130022
<i>Escherichia coli</i>	62.31	0.40	SOR 88		
<i>Escherichia hermannii</i>	36.28	0.26	TRE 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.41	0.05			
130023	Identification to the genus				130023
<i>Escherichia hermannii</i>	73.09	0.67	CEL 97		
<i>Escherichia coli</i>	24.09	0.66			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.41	0.39			
130031	Very good identification				130031
<i>Escherichia hermannii</i>	97.51	0.57	MAN 99		
<i>Citrobacter farmeri</i>	2.03	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.35	0.14			
130032	Very good identification				130032
<i>Escherichia hermannii</i>	97.51	0.57	TRE 99		
<i>Citrobacter farmeri</i>	2.03	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.35	0.14			
130033	Very good identification				130033

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	97.76	0.98			
<i>Citrobacter farmeri</i>	2.04	0.59			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.17	0.49			
130040	Low discrimination				130040
<i>Escherichia coli</i>	64.92	0.35	TRE 95		
<i>Shigella dysenteriae</i> (group A)	35.09	0.22	MAN 95		
130041	Low discrimination				130041
<i>Escherichia coli</i>	75.48	0.61	MAN 95		
<i>Shigella dysenteriae</i> (group A)	19.32	0.42			
<i>Citrobacter braakii</i>	3.95	0.36			
130042	Good identification				130042
<i>Escherichia coli</i>	92.39	0.61	TRE 95		
<i>Citrobacter braakii</i>	4.83	0.36			
<i>Shigella boydii</i> (group C)	1.03	0.11			
130043	Low discrimination				130043
<i>Escherichia coli</i>	74.92	0.88			
<i>Citrobacter braakii</i>	20.41	0.78			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.07	0.54			
130051	Low discrimination				130051
<i>Yersinia kristensenii</i>	54.47	0.41	MAN 99		
<i>Citrobacter braakii</i>	21.57	0.43			
<i>Citrobacter farmeri</i>	7.25	0.18			
130052	Low discrimination				130052
<i>Yersinia kristensenii</i>	54.76	0.41	TRE 99		
<i>Citrobacter braakii</i>	21.69	0.43			
<i>Citrobacter farmeri</i>	7.29	0.18			
130053	Low discrimination				130053
<i>Yersinia kristensenii</i>	58.60	0.82			
<i>Citrobacter braakii</i>	23.21	0.84			
<i>Citrobacter farmeri</i>	7.80	0.59			
130061	Low discrimination				130061
<i>Escherichia coli</i>	72.76	0.58	MAN 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	22.22	0.46			
<i>Citrobacter farmeri</i>	3.89	0.18			
130062	Low discrimination				130062
<i>Escherichia coli</i>	72.97	0.58	TRE 95		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	22.29	0.46			
<i>Citrobacter farmeri</i>	3.90	0.18			
130063	Low discrimination				130063
<i>Escherichia coli</i>	46.83	0.84			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	36.89	0.80			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter farmeri</i>	13.06	0.59			
130071	Low discrimination				130071
<i>Citrobacter farmeri</i>	84.38	0.59	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.60	0.55			
<i>Escherichia hermannii</i>	0.41	0.16			
130072	Low discrimination				130072
<i>Citrobacter farmeri</i>	84.38	0.59	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.60	0.55			
<i>Escherichia hermannii</i>	0.41	0.16			
130073	Good identification				130073
<i>Citrobacter farmeri</i>	91.33	1.00			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	7.82	0.90			
<i>Escherichia hermannii</i>	0.45	0.57			
130113	Identification to the genus				130113
<i>Escherichia hermannii</i>	86.39	0.59	MAL 1		
<i>Escherichia fergusonii</i>	12.55	0.45			
<i>Citrobacter sedlakii</i>	0.34	0.04			
130133	Very good identification				130133
<i>Escherichia hermannii</i>	97.04	0.57	MAL 1		
<i>Citrobacter farmeri</i>	2.02	0.18			
<i>Citrobacter koseri</i>	0.25	0.05			
130143	Low discrimination				130143
<i>Escherichia coli</i>	71.55	0.47	MAL 1		
<i>Citrobacter braakii</i>	19.49	0.36			
<i>Citrobacter sedlakii</i>	3.07	0.04			
130153	Low discrimination				130153
<i>Citrobacter sedlakii</i>	60.19	0.45	URE 99		
<i>Yersinia kristensenii</i>	19.81	0.41			
<i>Citrobacter braakii</i>	7.84	0.43			
130163	Low discrimination				130163
<i>Escherichia coli</i>	45.63	0.43	MAL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	35.94	0.39			
<i>Citrobacter farmeri</i>	12.72	0.18			
130173	Low discrimination				130173
<i>Citrobacter farmeri</i>	89.26	0.59	MAL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	7.64	0.49			
<i>Citrobacter koseri</i>	1.74	0.30			
130213	Very good identification				130213
<i>Escherichia hermannii</i>	97.08	0.59	INO 1		
<i>Yersinia kristensenii</i>	2.19	0.25			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.32	0.15			
130233	Good identification				130233

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	91.09	0.57	INO 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.90	0.42			
<i>Citrobacter farmeri</i>	1.90	0.18			
130243	Low discrimination				130243
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	43.33	0.47	SUC 95		
<i>Escherichia coli</i>	36.95	0.47			
<i>Citrobacter braakii</i>	10.06	0.36			
130253	Identification to the genus				130253
<i>Yersinia kristensenii</i>	84.62	0.66			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	12.20	0.56			
<i>Citrobacter braakii</i>	1.92	0.43			
130261	Acceptable identification				130261
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	92.84	0.38	MAN 98		
<i>Escherichia coli</i>	7.16	0.17			
130262	Acceptable identification				130262
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	92.84	0.38	TRE 98		
<i>Escherichia coli</i>	7.16	0.17			
130263	Very good identification				130263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.15	0.73			
<i>Escherichia coli</i>	2.88	0.43			
<i>Citrobacter farmeri</i>	0.80	0.18			
130271	Low discrimination				130271
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	88.01	0.48	MAN 98		
<i>Citrobacter farmeri</i>	11.99	0.18			
130272	Low discrimination				130272
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	88.01	0.48	TRE 98		
<i>Citrobacter farmeri</i>	11.99	0.18			
130273	Low discrimination				130273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	78.05	0.83			
<i>Citrobacter farmeri</i>	21.49	0.59			
<i>Yersinia kristensenii</i>	0.29	0.25			
130373	Low discrimination				130373
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	77.78	0.42	MAL 1	2	
<i>Citrobacter farmeri</i>	21.41	0.18		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.81	-0.03		99	
130403	Low discrimination				130403
<i>Escherichia fergusonii</i>	60.36	0.47	LYS 95		
<i>Escherichia coli</i>	20.85	0.44	CEL 95		
<i>Escherichia hermannii</i>	9.89	0.28			
130412	Identification to the genus				130412

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	87.87	0.39	LYS 95		
<i>Escherichia hermannii</i>	12.13	0.18	TRE 98		
130413	Identification to the genus				130413
<i>Escherichia fergusonii</i>	78.07	0.74	LYS 95		
<i>Escherichia hermannii</i>	21.77	0.59			
<i>Citrobacter koseri</i>	0.05	0.07			
130423	Identification to the genus				130423
<i>Escherichia coli</i>	61.49	0.40	ADO 5		
<i>Escherichia hermannii</i>	35.81	0.26	SOR 88		
<i>Escherichia fergusonii</i>	2.70	0.06			
130433	Good identification				130433
<i>Escherichia hermannii</i>	93.33	0.57	ADO 1		
<i>Escherichia fergusonii</i>	4.13	0.33			
<i>Citrobacter farmeri</i>	1.95	0.18			
130441	Good identification				130441
<i>Escherichia coli</i>	95.32	0.35	ADO 5		
<i>Shigella dysenteriae (group A)</i>	4.68	0.01	MAN 95		
130442	Good identification				130442
<i>Escherichia coli</i>	100.0	0.35	ADO 5		
130443	Good identification				130443
<i>Escherichia coli</i>	93.42	0.61	ADO 5		
<i>Citrobacter braakii</i>	4.88	0.36			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.50	0.13			
130453	Low discrimination				130453
<i>Yersinia kristensenii</i>	42.58	0.41	ADO 1		
<i>Citrobacter braakii</i>	16.87	0.43			
<i>Citrobacter koseri</i>	12.33	0.31			
130463	Low discrimination				130463
<i>Escherichia coli</i>	81.78	0.58	ADO 5		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	12.36	0.39			
<i>Citrobacter farmeri</i>	4.38	0.18			
130473	Low discrimination				130473
<i>Citrobacter farmeri</i>	89.51	0.59	ADO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	7.66	0.49			
<i>Citrobacter koseri</i>	1.74	0.30			
130503	Good identification				130503
<i>Escherichia fergusonii</i>	97.11	0.42	LYS 95		
<i>Citrobacter koseri</i>	2.26	0.07	CEL 95		
<i>Escherichia coli</i>	0.63	0.02			
130513	Very good identification				130513
<i>Escherichia fergusonii</i>	97.37	0.68	LYS 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter koseri</i>	1.87	0.31			
<i>Escherichia hermannii</i>	0.51	0.18			
130553	Very good identification				130553
<i>Citrobacter koseri</i>	95.92	0.56	SCI 99		
<i>Escherichia fergusonii</i>	3.22	0.27			
<i>Citrobacter sedlakii</i>	0.65	0.04			
130573	Very good identification				130573
<i>Citrobacter koseri</i>	96.31	0.55	SCI 99		
<i>Citrobacter farmeri</i>	3.19	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.27	0.08			
130673	Low discrimination				130673
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	78.41	0.42	ADO 1		
<i>Citrobacter farmeri</i>	21.59	0.18			
131000	Good identification				131000
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.52	ONP 10		
131013	Very good identification				131013
<i>Escherichia hermannii</i>	99.45	0.59	PHE 1		
<i>Escherichia fergusonii</i>	0.27	0.10			
<i>Shigella sonnei</i>	0.15	-0.09			
131033	Very good identification				131033
<i>Escherichia hermannii</i>	97.79	0.57	PHE 1		
<i>Citrobacter farmeri</i>	2.04	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.17	0.08			
131043	Low discrimination				131043
<i>Escherichia coli</i>	75.74	0.47	PHE 1		
<i>Citrobacter braakii</i>	20.63	0.36			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.09	0.13			
131053	Low discrimination				131053
<i>Yersinia kristensenii</i>	58.68	0.41	PHE 1		
<i>Citrobacter braakii</i>	23.24	0.43			
<i>Citrobacter farmeri</i>	7.81	0.18			
131063	Low discrimination				131063
<i>Escherichia coli</i>	47.02	0.43	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	37.04	0.39			
<i>Citrobacter farmeri</i>	13.11	0.18			
131073	Good identification				131073
<i>Citrobacter farmeri</i>	91.35	0.59	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	7.82	0.49			
<i>Escherichia hermannii</i>	0.45	0.16			
131273	Low discrimination				131273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	78.41	0.42	PHE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter farmeri</i>	21.59	0.18			
132003	Identification to the genus				132003
<i>Escherichia hermannii</i>	85.31	0.65	CEL 97		
<i>Escherichia coli</i>	12.94	0.57			
<i>Shigella sonnei</i>	1.16	0.18			
132011	Very good identification				132011
<i>Escherichia hermannii</i>	99.65	0.55	MAN 99		
<i>Escherichia fergusonii</i>	0.35	0.08			
132012	Very good identification				132012
<i>Escherichia hermannii</i>	99.30	0.55	TRE 99		
<i>Escherichia fergusonii</i>	0.70	0.14			
132013	Excellent identification				132013
<i>Escherichia hermannii</i>	99.63	0.96			
<i>Escherichia fergusonii</i>	0.35	0.49			
<i>Escherichia coli</i>	0.01	0.23			
132023	Identification to the genus				132023
<i>Escherichia hermannii</i>	88.25	0.64	CEL 97		
<i>Escherichia coli</i>	10.91	0.54			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.85	0.30			
132031	Very good identification				132031
<i>Escherichia hermannii</i>	99.82	0.54	MAN 99		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.18	0.05			
132032	Very good identification				132032
<i>Escherichia hermannii</i>	99.82	0.54	TRE 99		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.18	0.05			
132033	Excellent identification				132033
				VPT	
<i>Escherichia hermannii</i>	99.78	0.95		1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.09	0.39		2	
<i>Cronobacter sakazakii</i>	0.06	0.30		99	
132041	Good identification				132041
<i>Escherichia coli</i>	97.60	0.49	MAN 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.40	0.09			
<i>Shigella dysenteriae (group A)</i>	1.01	0.01			
132042	Good identification				132042
<i>Escherichia coli</i>	98.59	0.49	TRE 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.41	0.09			
132043	Good identification				132043
<i>Escherichia coli</i>	94.51	0.75			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	3.48	0.44			
<i>Citrobacter braakii</i>	1.04	0.36			
132053	Low discrimination				132053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	55.96	0.55	SOR 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	21.07	0.54			
<i>Yersinia kristensenii</i>	10.75	0.41			
132061	Low discrimination				132061
<i>Escherichia coli</i>	71.06	0.45	MAN 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	28.94	0.36			
132062	Low discrimination				132062
<i>Escherichia coli</i>	71.06	0.45	TRE 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	28.94	0.36			
132063	Low discrimination				132063
<i>Yersinia enterocolitica ssp. enterocolitica</i>	50.61	0.71			
<i>Escherichia coli</i>	48.19	0.72			
<i>Escherichia hermannii</i>	0.54	0.22			
132071	Low discrimination				132071
<i>Yersinia enterocolitica ssp. enterocolitica</i>	80.10	0.46	MAN 98		
<i>Citrobacter farmeri</i>	14.03	0.18			
<i>Escherichia hermannii</i>	4.53	0.12			
132072	Low discrimination				132072
<i>Yersinia enterocolitica ssp. enterocolitica</i>	80.10	0.46	TRE 98		
<i>Citrobacter farmeri</i>	14.03	0.18			
<i>Escherichia hermannii</i>	4.53	0.12			
132073	Low discrimination				132073
<i>Yersinia enterocolitica ssp. enterocolitica</i>	67.68	0.80			
<i>Citrobacter farmeri</i>	23.95	0.59			
<i>Escherichia hermannii</i>	7.74	0.54			
132113	Low discrimination				132113
<i>Escherichia hermannii</i>	79.98	0.55	MAL 1		
<i>Escherichia fergusonii</i>	14.85	0.44			
<i>Leclercia adecarboxylata</i>	4.46	0.30			
132133	Low discrimination				132133
<i>Escherichia hermannii</i>	64.90	0.54	MAL 1		
<i>Kluyvera ascorbata</i>	25.14	0.41			
<i>Leclercia adecarboxylata</i>	8.58	0.36			
132173	Low discrimination				132173
<i>Kluyvera ascorbata</i>	65.61	0.37	LYS 97		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	22.44	0.39	SCI 96		
<i>Citrobacter farmeri</i>	7.94	0.18			
132213	Very good identification				132213
<i>Escherichia hermannii</i>	99.34	0.55	INO 1		
<i>Escherichia fergusonii</i>	0.35	0.08			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.16	0.05			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
132233	Low discrimination				132233
				VPT	
<i>Escherichia hermannii</i>	81.35	0.54	INO 1	1	
<i>Cronobacter sakazakii</i>	15.57	0.40		99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.08	0.32		2	
132243	Low discrimination				132243
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	60.99	0.37	SUC 95		
<i>Escherichia coli</i>	39.01	0.34			
132253	Low discrimination				132253
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	78.26	0.47	SUC 95		
<i>Yersinia kristensenii</i>	16.45	0.25			
<i>Escherichia hermannii</i>	4.90	0.14			
132263	Very good identification				132263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.81	0.63			
<i>Escherichia coli</i>	2.20	0.31			
132271	Good identification				132271
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.38	MAN 98		
132272	Good identification				132272
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.38	TRE 98		
132273	Very good identification				132273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.42	0.73			
<i>Citrobacter farmeri</i>	0.82	0.18			
<i>Serratia odorifera</i> biovar 1	0.44	0.18			
132403	Identification to the genus				132403
<i>Escherichia fergusonii</i>	81.33	0.46	LYS 95		
<i>Escherichia hermannii</i>	10.43	0.24	CEL 95		
<i>Escherichia coli</i>	8.24	0.31			
132412	Acceptable identification				132412
<i>Escherichia fergusonii</i>	90.25	0.38	LYS 95		
<i>Escherichia hermannii</i>	9.75	0.14	TRE 98		
132413	Identification to the genus				132413
<i>Escherichia fergusonii</i>	81.21	0.72	LYS 95		
<i>Escherichia hermannii</i>	17.73	0.55			
<i>Leclercia adecarboxylata</i>	0.99	0.30			
132433	Low discrimination				132433
<i>Escherichia hermannii</i>	84.03	0.54	ADO 1		
<i>Leclercia adecarboxylata</i>	11.11	0.36			
<i>Escherichia fergusonii</i>	4.75	0.31			
132443	Good identification				132443
<i>Escherichia coli</i>	97.98	0.49	ADO 5		
<i>Escherichia fergusonii</i>	1.33	0.05			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.69	0.03			
132463	Low discrimination				132463
<i>Escherichia coli</i>	83.23	0.45	ADO 5		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	16.78	0.30			
132473	Low discrimination				132473
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	64.74	0.39	ADO 1		
<i>Citrobacter farmeri</i>	22.91	0.18			
<i>Escherichia hermannii</i>	7.40	0.12			
132503	Acceptable identification				132503
<i>Escherichia fergusonii</i>	94.55	0.40	LYS 95		
<i>Leclercia adecarboxylata</i>	5.45	0.12	CEL 95		
132513	Low discrimination				132513
<i>Escherichia fergusonii</i>	76.67	0.67	LYS 95		
<i>Leclercia adecarboxylata</i>	23.01	0.53			
<i>Escherichia hermannii</i>	0.31	0.14			
132533	Very good identification				132533
<i>Leclercia adecarboxylata</i>	97.53	0.59	ORN 1		
<i>Escherichia fergusonii</i>	1.69	0.26			
<i>Escherichia hermannii</i>	0.56	0.12			
133013	Very good identification				133013
<i>Escherichia hermannii</i>	99.65	0.55	PHE 1		
<i>Escherichia fergusonii</i>	0.35	0.08			
133033	Good identification				133033
				VPT	
<i>Escherichia hermannii</i>	94.00	0.54	PHE 1	1	
<i>Cronobacter sakazakii</i>	6.00	0.30		99	
133073	Low discrimination				133073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	68.11	0.39	PHE 1		
<i>Citrobacter farmeri</i>	24.11	0.18			
<i>Escherichia hermannii</i>	7.79	0.12			
133233	Acceptable identification				133233
				VPT	
<i>Cronobacter sakazakii</i>	94.99	0.40	IND 11	99	
<i>Escherichia hermannii</i>	5.01	0.12	SCI 99	1	
134003	Low discrimination				134003
<i>Citrobacter braakii</i>	48.59	0.46	SOR 99		
<i>Escherichia hermannii</i>	20.05	0.28			
<i>Shigella sonnei</i>	18.05	0.18			
134013	Low discrimination				134013
<i>Escherichia hermannii</i>	65.90	0.59	SCI 1		
<i>Citrobacter amalonaticus</i>	18.47	0.41			
<i>Citrobacter braakii</i>	10.03	0.53			
134033	Low discrimination				134033

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Escherichia hermannii</i>	74.77	0.57	SCI 1	1	
<i>Citrobacter farmeri</i>	17.14	0.39		1	
<i>Cronobacter sakazakii</i>	3.18	0.30		99	
134041	Low discrimination				134041
<i>Citrobacter braakii</i>	89.39	0.46	MAN 99		
<i>Escherichia coli</i>	5.76	0.20			
<i>Citrobacter amalonaticus</i>	3.38	0.00			
134042	Acceptable identification				134042
<i>Citrobacter braakii</i>	90.73	0.46	TRE 99		
<i>Escherichia coli</i>	5.84	0.20			
<i>Citrobacter amalonaticus</i>	3.43	0.00			
134043	Good identification				134043
<i>Citrobacter braakii</i>	94.32	0.87			
<i>Citrobacter amalonaticus</i>	3.56	0.41			
<i>Escherichia coli</i>	1.17	0.47			
134051	Identification to the genus				134051
<i>Citrobacter amalonaticus</i>	63.98	0.41	URE 88		
<i>Citrobacter braakii</i>	34.75	0.53	MAN 99		
<i>Citrobacter koseri</i>	0.54	0.07			
134052	Identification to the genus				134052
<i>Citrobacter amalonaticus</i>	63.98	0.41	URE 88		
<i>Citrobacter braakii</i>	34.75	0.53	TRE 99		
<i>Citrobacter koseri</i>	0.54	0.07			
134053	Identification to the genus				134053
<i>Citrobacter amalonaticus</i>	63.86	0.82	URE 88		
<i>Citrobacter braakii</i>	34.68	0.94			
<i>Citrobacter koseri</i>	0.54	0.48			
134063	Low discrimination				134063
<i>Citrobacter braakii</i>	56.62	0.64	SUC 7		
<i>Citrobacter farmeri</i>	19.01	0.39			
<i>Citrobacter freundii</i>	8.66	0.49			
134071	Identification to the genus				134071
<i>Citrobacter farmeri</i>	83.79	0.39	SCI 10		
<i>Citrobacter amalonaticus</i>	7.99	0.17	MAN 99		
<i>Citrobacter braakii</i>	5.12	0.30			
134072	Identification to the genus				134072
<i>Citrobacter farmeri</i>	83.79	0.39	SCI 10		
<i>Citrobacter amalonaticus</i>	7.99	0.17	TRE 99		
<i>Citrobacter braakii</i>	5.12	0.30			
134073	Identification to the genus				134073
<i>Citrobacter farmeri</i>	84.26	0.80	SCI 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter amalonaticus</i>	8.04	0.58			
<i>Citrobacter braakii</i>	5.15	0.71			
134113	Low discrimination				134113
<i>Citrobacter koseri</i>	78.27	0.48	ADO 94		
<i>Escherichia fergusonii</i>	9.94	0.31	SOR 94		
<i>Citrobacter sedlakii</i>	6.41	0.18			
134133	Low discrimination				134133
				VPT	
<i>Citrobacter koseri</i>	70.24	0.47	ADO 94	1	
<i>Kluyvera ascorbata</i>	17.31	0.28	SOR 94	1	
<i>Enterobacter cloacae subsp. cloacae</i>	6.44	0.27		99	
134143	Identification to the genus				134143
<i>Citrobacter koseri</i>	69.75	0.48	ADO 94		
<i>Citrobacter braakii</i>	22.31	0.46	CEL 94		
<i>Citrobacter sedlakii</i>	5.71	0.18			
134153	Identification to the genus				134153
<i>Citrobacter koseri</i>	60.97	0.72	ADO 94		
<i>Citrobacter sedlakii</i>	31.55	0.59			
<i>Citrobacter amalonaticus</i>	4.65	0.41			
134163	Acceptable identification				134163
<i>Citrobacter koseri</i>	91.28	0.47	ADO 94		
<i>Citrobacter freundii</i>	3.26	0.28	CEL 94		
<i>Citrobacter braakii</i>	2.48	0.23			
134173	Low discrimination				134173
				VPT	
<i>Citrobacter koseri</i>	83.58	0.71	ADO 94	1	
<i>Enterobacter cloacae subsp. cloacae</i>	9.30	0.53		99	
<i>Citrobacter farmeri</i>	4.81	0.39		1	
134233	Low discrimination				134233
				VPT	
<i>Cronobacter sakazakii</i>	89.76	0.40	IND 11	99	
<i>Escherichia hermannii</i>	7.11	0.16	ESL 99	1	
<i>Citrobacter farmeri</i>	1.63	-0.02		1	
134243	Acceptable identification				134243
<i>Citrobacter braakii</i>	91.33	0.46	INO 1		
<i>Citrobacter amalonaticus</i>	3.45	0.00			
<i>Citrobacter youngae</i>	2.77	0.14			
134253	Low discrimination				134253
				VPT	
<i>Citrobacter amalonaticus</i>	57.06	0.41	URE 88	1	
<i>Citrobacter braakii</i>	30.98	0.53	INO 1	1	
<i>Serratia odorifera biovar 2</i>	5.32	0.33		99	
134273	Low discrimination				134273
<i>Citrobacter farmeri</i>	53.31	0.39	SCI 10		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	17.61	0.42	INO 1		
<i>Serratia odorifera biovar 1</i>	13.60	0.33			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
134373	Low discrimination				134373
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	64.35	0.38	IND 1	99	
<i>Citrobacter koseri</i>	33.12	0.30		1	
<i>Citrobacter farmeri</i>	1.91	-.02		1	
134413	Low discrimination				134413
<i>Escherichia fergusonii</i>	74.69	0.60	LYS 95		
<i>Citrobacter koseri</i>	23.84	0.48			
<i>Escherichia hermannii</i>	1.03	0.18			
134433	Acceptable identification				134433
<i>Citrobacter koseri</i>	91.35	0.47	MAL 94		
<i>Escherichia hermannii</i>	3.63	0.16	SOR 94		
<i>Escherichia fergusonii</i>	3.26	0.18			
134443	Identification to the genus				134443
<i>Citrobacter koseri</i>	73.94	0.48	MAL 94		
<i>Citrobacter braakii</i>	23.65	0.46	CEL 94		
<i>Escherichia coli</i>	1.52	0.20			
134453	Identification to the genus				134453
<i>Citrobacter koseri</i>	89.20	0.72	MAL 94		
<i>Citrobacter amalonaticus</i>	6.81	0.41			
<i>Citrobacter braakii</i>	3.70	0.53			
134463	Acceptable identification				134463
<i>Citrobacter koseri</i>	94.71	0.47	MAL 94		
<i>Citrobacter braakii</i>	2.57	0.23	CEL 94		
<i>Escherichia coli</i>	1.47	0.17			
134473	Good identification				134473
				VPT	
<i>Citrobacter koseri</i>	92.63	0.71	MAL 94	1	
<i>Citrobacter farmeri</i>	5.34	0.39		1	
<i>Enterobacter cloacae subsp. cloacae</i>	1.15	0.34		99	
134503	Acceptable identification				134503
<i>Citrobacter koseri</i>	91.85	0.48	CEL 94		
<i>Escherichia fergusonii</i>	8.16	0.28	SOR 94		
134513	Good identification				134513
<i>Citrobacter koseri</i>	90.28	0.72	SOR 94		
<i>Escherichia fergusonii</i>	9.72	0.54			
134523	Good identification				134523
<i>Citrobacter koseri</i>	100.0	0.47	CEL 94		
134533	Very good identification				134533
				VPT	
<i>Citrobacter koseri</i>	99.66	0.71	SOR 94	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.19	0.17		99	
<i>Escherichia fergusonii</i>	0.12	0.13		1	
134543	Very good identification				134543

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter koseri</i>	99.98	0.72	CEL 94		
<i>Citrobacter braakii</i>	0.02	0.05			
134551	Very good identification				134551
<i>Citrobacter koseri</i>	100.0	0.56	MAN 99		
134552	Very good identification				134552
<i>Citrobacter koseri</i>	100.0	0.56	TRE 99		
134553	Excellent identification				134553
<i>Citrobacter koseri</i>	99.95	0.97			
<i>Citrobacter sedlakii</i>	0.03	0.18			
<i>Escherichia fergusonii</i>	0.01	0.13			
134563	Very good identification				134563
				VPT	
<i>Citrobacter koseri</i>	99.96	0.71	CEL 94	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.04	0.03		99	
134571	Very good identification				134571
				VPT	
<i>Citrobacter koseri</i>	99.76	0.55	MAN 99	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.24	0.03		99	
134572	Very good identification				134572
				VPT	
<i>Citrobacter koseri</i>	99.76	0.55	TRE 99	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.24	0.03		99	
134573	Excellent identification				134573
				VPT	
<i>Citrobacter koseri</i>	99.76	0.96		1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.24	0.44		99	
<i>Citrobacter farmeri</i>	0.00	-.02		1	
134753	Very good identification				134753
				VPT	
<i>Citrobacter koseri</i>	99.89	0.56	INO 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.11	-.03		99	
134773	Very good identification				134773
				VPT	
<i>Citrobacter koseri</i>	95.83	0.55	INO 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	3.96	0.28		99	
<i>Enterobacter aerogenes</i>	0.21	-.11		98	
135043	Good identification				135043
<i>Citrobacter braakii</i>	95.23	0.46	PHE 1		
<i>Citrobacter amalonaticus</i>	3.60	0.00			
<i>Escherichia coli</i>	1.18	0.05			
135053	Identification to the genus				135053
<i>Citrobacter amalonaticus</i>	63.98	0.41	URE 88		
<i>Citrobacter braakii</i>	34.75	0.53	PHE 1		
<i>Citrobacter koseri</i>	0.54	0.07			
135073	Identification to the genus				135073

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter farmeri</i>	84.35	0.39	PHE 1		
<i>Citrobacter amalonaticus</i>	8.05	0.17	SCI 10		
<i>Citrobacter braakii</i>	5.15	0.30			
135201	Good identification				135201
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
135221	Good identification				135221
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
135233	Good identification				135233
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
135553	Very good identification				135553
<i>Citrobacter koseri</i>	100.0	0.56	PHE 1		
135573	Very good identification				135573
				VPT	
<i>Citrobacter koseri</i>	99.76	0.55	PHE 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.24	0.03		99	
136013	Low discrimination				136013
				VPT	
<i>Escherichia hermannii</i>	83.06	0.55	SCI 1	1	
<i>Escherichia fergusonii</i>	5.87	0.35		1	
<i>Cronobacter sakazakii</i>	4.34	0.30		99	
136033	Low discrimination				136033
				VPT	
<i>Cronobacter sakazakii</i>	81.86	0.72	IND 11	99	
<i>Escherichia hermannii</i>	12.96	0.54		1	
<i>Kluyvera ascorbata</i>	5.02	0.41		1	
136043	Low discrimination				136043
<i>Citrobacter braakii</i>	58.23	0.46	ESL 1		
<i>Citrobacter amalonaticus</i>	21.53	0.20			
<i>Escherichia coli</i>	17.82	0.34			
136053	Good identification				136053
<i>Citrobacter amalonaticus</i>	93.93	0.62	URE 88		
<i>Citrobacter braakii</i>	5.21	0.53	ESL 9		
<i>Escherichia hermannii</i>	0.23	0.14			
136073	Low discrimination				136073
<i>Citrobacter farmeri</i>	27.50	0.39	ESL 1		
<i>Citrobacter amalonaticus</i>	25.68	0.37	SCI 10		
<i>Kluyvera ascorbata</i>	20.66	0.37			
136133	Low discrimination				136133
				VPT	
<i>Kluyvera ascorbata</i>	86.62	0.69	LYS 97	1	
<i>Cronobacter sakazakii</i>	12.91	0.58		99	
<i>Pantoea agglomerans</i>	0.18	0.16		64	
136153	Low discrimination				136153
<i>Citrobacter sedlakii</i>	73.53	0.45	URE 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Kluyvera ascorbata</i>	13.04	0.31			
<i>Citrobacter koseri</i>	7.01	0.31			
136173	Good identification				136173
				VPT	
<i>Kluyvera ascorbata</i>	94.33	0.65	LYS 97	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	4.33	0.46		99	
<i>Citrobacter koseri</i>	0.92	0.30		1	
136213	Acceptable identification				136213
				VPT	
<i>Cronobacter sakazakii</i>	93.94	0.40	IND 11	99	
<i>Escherichia hermannii</i>	6.06	0.14	SUC 99	1	
136223	Good identification				136223
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
136231	Good identification				136231
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
136232	Good identification				136232
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
136233	Very good identification				136233
				VPT	
<i>Cronobacter sakazakii</i>	99.84	0.81	IND 11	99	
<i>Serratia odorifera</i> biovar 1	0.09	0.18		50	
<i>Escherichia hermannii</i>	0.05	0.12		1	
136273	Low discrimination				136273
				VPT	
<i>Serratia odorifera</i> biovar 1	85.20	0.59	LYS 99	50	
<i>Cronobacter sakazakii</i>	9.78	0.40		99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.94	0.32		2	
136333	Very good identification				136333
				VPT	
<i>Cronobacter sakazakii</i>	97.73	0.68	IND 11	99	
<i>Kluyvera ascorbata</i>	2.21	0.28		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.06	0.04		99	
136413	Very good identification				136413
<i>Escherichia fergusonii</i>	98.38	0.58	LYS 95		
<i>Escherichia hermannii</i>	1.06	0.14			
<i>Citrobacter koseri</i>	0.37	0.07			
136513	Low discrimination				136513
<i>Escherichia fergusonii</i>	88.65	0.53	LYS 95		
<i>Citrobacter koseri</i>	9.76	0.31			
<i>Leclercia adecarboxylata</i>	1.31	0.12			
136553	Very good identification				136553
<i>Citrobacter koseri</i>	98.37	0.56	ESL 1		
<i>Citrobacter sedlakii</i>	0.67	0.04			
<i>Escherichia fergusonii</i>	0.58	0.12			
136573	Low discrimination				136573
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter koseri</i>	85.30	0.55	ESL 1	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	8.56	0.36		99	
<i>Kluyvera ascorbata</i>	5.65	0.24		1	
136633	Acceptable identification				136633
<i>Cronobacter sakazakii</i>	91.92	0.40	IND 11		
<i>Serratia odorifera</i> biovar 1	8.09	0.18	ADO 1		
136673	Very good identification				136673
<i>Serratia odorifera</i> biovar 1	99.16	0.59	LYS 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.33	0.11			
<i>Enterobacter aerogenes</i>	0.32	-.02			
137033	Very good identification				137033
				VPT	
<i>Cronobacter sakazakii</i>	99.78	0.72	IND 11	99	
<i>Escherichia hermannii</i>	0.16	0.12		1	
<i>Kluyvera ascorbata</i>	0.06	-.01		1	
137133	Good identification				137133
				VPT	
<i>Cronobacter sakazakii</i>	93.53	0.58	IND 11	99	
<i>Kluyvera ascorbata</i>	6.34	0.28		1	
<i>Pantoea agglomerans</i>	0.13	-.05		64	
137213	Good identification				137213
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
137223	Good identification				137223
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
137231	Good identification				137231
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
137232	Good identification				137232
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
137233	Very good identification				137233
<i>Cronobacter sakazakii</i>	100.0	0.81	IND 11		
137273	Acceptable identification				137273
<i>Cronobacter sakazakii</i>	91.92	0.40	IND 11		
<i>Serratia odorifera</i> biovar 1	8.09	0.18	SOR 1		
137333	Very good identification				137333
<i>Cronobacter sakazakii</i>	100.0	0.68	IND 11		
137633	Good identification				137633
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
140001	Low discrimination				140001
<i>Shigella dysenteriae</i> (group A)	71.09	0.51	URE 1		
<i>Yersinia pseudotuberculosis</i>	22.51	0.33			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	5.40	0.31			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
140003	Very good identification				140003
<i>Yersinia pseudotuberculosis</i>	97.49	0.74	ESL 95		
<i>Shigella boydii</i> (group C)	1.07	0.39			
<i>Citrobacter youngae</i>	0.56	0.44			
140023	Low discrimination				140023
<i>Yersinia rohdei</i>	70.33	0.56	SOR 99		
<i>Yersinia pseudotuberculosis</i>	19.14	0.33			
<i>Citrobacter freundii</i>	5.91	0.41			
140033	Low discrimination				140033
<i>Yersinia rohdei</i>	65.28	0.47	SOR 99		
<i>Citrobacter freundii</i>	12.92	0.39			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.01	0.33			
140041	Low discrimination				140041
<i>Shigella dysenteriae</i> (group A)	65.09	0.44	URE 1		
<i>Citrobacter youngae</i>	27.21	0.44			
<i>Citrobacter freundii</i>	1.83	0.22			
140042	Low discrimination				140042
<i>Citrobacter youngae</i>	65.90	0.44	TRE 99		
<i>Shigella boydii</i> (group C)	16.77	0.21			
<i>Citrobacter freundii</i>	4.44	0.22			
140043	Low discrimination				140043
<i>Citrobacter youngae</i>	80.07	0.85			
<i>Citrobacter freundii</i>	5.40	0.64			
<i>Yersinia rohdei</i>	5.25	0.56			
140051	Low discrimination				140051
<i>Yersinia kristensenii</i>	57.42	0.37	ORN 92		
<i>Citrobacter youngae</i>	33.76	0.42	MAN 99		
<i>Citrobacter braakii</i>	3.14	0.22			
140052	Low discrimination				140052
<i>Yersinia kristensenii</i>	58.00	0.37	ORN 92		
<i>Citrobacter youngae</i>	34.10	0.42	TRE 99		
<i>Citrobacter braakii</i>	3.17	0.22			
140053	Low discrimination				140053
<i>Yersinia kristensenii</i>	58.37	0.78	ORN 92		
<i>Citrobacter youngae</i>	34.32	0.83			
<i>Citrobacter braakii</i>	3.19	0.63			
140061	Low discrimination				140061
<i>Yersinia rohdei</i>	85.73	0.56	MAN 99		
<i>Citrobacter freundii</i>	7.20	0.41			
<i>Citrobacter youngae</i>	3.51	0.32			
140062	Low discrimination				140062

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia rohdei</i>	86.00	0.56	TRE 99		
<i>Citrobacter freundii</i>	7.22	0.41			
<i>Citrobacter youngae</i>	3.52	0.32			
140063	Low discrimination				140063
<i>Yersinia rohdei</i>	87.39	0.98			
<i>Citrobacter freundii</i>	7.34	0.82			
<i>Citrobacter youngae</i>	3.58	0.73			
140071	Low discrimination				140071
<i>Yersinia rohdei</i>	60.77	0.47	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.70	0.39			
<i>Citrobacter freundii</i>	12.03	0.39			
140072	Low discrimination				140072
<i>Yersinia rohdei</i>	60.77	0.47	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.70	0.39			
<i>Citrobacter freundii</i>	12.03	0.39			
140073	Low discrimination				140073
<i>Yersinia rohdei</i>	67.66	0.88			
<i>Citrobacter freundii</i>	13.39	0.80			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.41	0.74			
140103	Low discrimination				140103
<i>Citrobacter werkmanii</i>	59.96	0.37	H2S 92		
<i>Yersinia pseudotuberculosis</i>	36.43	0.33	SCI 92		
<i>Citrobacter youngae</i>	1.09	0.18	SOR 90		
140113	Good identification				140113
<i>Escherichia vulneris</i>	97.73	0.43	URE 1		
<i>Citrobacter youngae</i>	0.84	0.16			
<i>Citrobacter werkmanii</i>	0.57	-0.04			
140143	Identification to the genus				140143
<i>Citrobacter werkmanii</i>	81.47	0.56	H2S 92		
<i>Citrobacter youngae</i>	16.22	0.59	SCI 92		
<i>Citrobacter freundii</i>	1.81	0.42			
140153	Low discrimination				140153
<i>Citrobacter youngae</i>	54.43	0.57	MAL 5		
<i>Yersinia kristensenii</i>	17.77	0.37			
<i>Citrobacter sedlakii</i>	16.28	0.31			
140163	Low discrimination				140163
<i>Yersinia rohdei</i>	50.11	0.56	MAL 1		
<i>Citrobacter freundii</i>	36.22	0.60			
<i>Citrobacter youngae</i>	10.69	0.47			
140173	Low discrimination				140173
<i>Citrobacter freundii</i>	47.13	0.58	MAL 8		
<i>Yersinia rohdei</i>	27.66	0.47			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	14.48	0.45			
140243	Low discrimination				140243
<i>Citrobacter youngae</i>	87.16	0.59	INO 5		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.54	0.30			
<i>Yersinia kristensenii</i>	4.11	0.22			
140253	Low discrimination				140253
<i>Yersinia kristensenii</i>	81.48	0.63	ORN 92		
<i>Citrobacter youngae</i>	14.29	0.57			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.73	0.40			
140263	Low discrimination				140263
<i>Yersinia rohdei</i>	47.80	0.56	INO 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	37.99	0.56			
<i>Citrobacter youngae</i>	10.20	0.47			
140273	Low discrimination				140273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	79.19	0.66	ORN 95		
<i>Yersinia rohdei</i>	11.07	0.47			
<i>Citrobacter youngae</i>	5.80	0.45			
140413	Very good identification				140413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.00	0.61	URE 10		
<i>Yersinia pseudotuberculosis</i>	0.44	-.09			
<i>Yersinia kristensenii</i>	0.34	-.04			
140433	Good identification				140433
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.80	0.48	URE 10		
<i>Yersinia rohdei</i>	2.09	0.06			
<i>Leclercia adecarboxylata</i>	1.11	-.05			
140443	Low discrimination				140443
<i>Citrobacter youngae</i>	52.78	0.44	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	34.56	0.44			
<i>Citrobacter freundii</i>	3.56	0.22			
140453	Low discrimination				140453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.99	0.66	URE 10		
<i>Yersinia kristensenii</i>	14.04	0.37			
<i>Citrobacter youngae</i>	8.26	0.42			
140463	Low discrimination				140463
<i>Yersinia rohdei</i>	85.56	0.56	ADO 1		
<i>Citrobacter freundii</i>	7.18	0.41			
<i>Citrobacter youngae</i>	3.50	0.32			
140473	Low discrimination				140473
<i>Yersinia rohdei</i>	42.26	0.47	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	36.75	0.54			
<i>Citrobacter freundii</i>	8.36	0.39			
140553	Low discrimination				140553

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.89	0.35	URE 10		
<i>Citrobacter youngae</i>	14.22	0.16	MAL 3		
<i>Yersinia kristensenii</i>	4.64	-.04			
140603	Good identification				140603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.02	0.41	URE 10		
<i>Yersinia pseudotuberculosis</i>	3.98	-.09	CEL 92		
140613	Very good identification				140613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.62	URE 10		
140633	Good identification				140633
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.50	URE 10		
140643	Acceptable identification				140643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.83	0.46	URE 10		
<i>Citrobacter youngae</i>	6.17	0.18	CEL 92		
140653	Very good identification				140653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.80	0.68	URE 10		
<i>Yersinia kristensenii</i>	2.58	0.22			
<i>Citrobacter youngae</i>	0.45	0.16			
140673	Good identification				140673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.56	0.56	URE 10		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.23	0.25			
<i>Yersinia rohdei</i>	0.87	0.06			
140753	Identification to the genus				140753
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.87	0.37	URE 10		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	23.13	0.08	MAL 3		
141001	Very good identification				141001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	95.13	0.54	ONP 1		
<i>Proteus penneri</i>	3.45	0.18			
<i>Shigella dysenteriae</i> (group A)	0.95	0.10			
141020	Very good identification				141020
<i>Proteus penneri</i>	97.71	0.57	ONP 1		
<i>Proteus vulgaris</i>	2.24	0.33			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.06	-.13			
141021	Very good identification				141021
<i>Proteus penneri</i>	97.49	0.59	ONP 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.73	0.29			
<i>Proteus vulgaris</i>	0.78	0.25			
141043	Low discrimination				141043
<i>Citrobacter youngae</i>	80.65	0.44	PHE 1		
<i>Citrobacter freundii</i>	5.44	0.22			
<i>Yersinia rohdei</i>	5.29	0.15			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
141053	Low discrimination				141053
<i>Yersinia kristensenii</i>	58.48	0.37	ORN 92		
<i>Citrobacter youngae</i>	34.38	0.42	PHE 1		
<i>Citrobacter braakii</i>	3.19	0.22			
141063	Low discrimination				141063
<i>Yersinia rohdei</i>	87.44	0.56	PHE 1		
<i>Citrobacter freundii</i>	7.34	0.41			
<i>Citrobacter youngae</i>	3.58	0.32			
141073	Low discrimination				141073
<i>Yersinia rohdei</i>	67.87	0.47	PHE 1		
<i>Citrobacter freundii</i>	13.43	0.39			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.44	0.33			
142001	Very good identification				142001
<i>Yersinia pseudotuberculosis</i>	99.83	0.59	MAN 99		
<i>Shigella dysenteriae</i> (group A)	0.17	0.10			
142002	Very good identification				142002
<i>Yersinia pseudotuberculosis</i>	100.0	0.59	TRE 99		
142003	Excellent identification				142003
<i>Yersinia pseudotuberculosis</i>	100.0	1.00			
<i>Citrobacter youngae</i>	0.00	0.18			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.00	0.20			
142013	Very good identification				142013
<i>Yersinia pseudotuberculosis</i>	97.60	0.59	CEL 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.46	0.42			
<i>Escherichia vulneris</i>	0.65	0.16			
142023	Very good identification				142023
<i>Yersinia pseudotuberculosis</i>	99.45	0.59	SUC 1		
<i>Yersinia rohdei</i>	0.19	0.15			
<i>Pantoea agglomerans</i>	0.16	0.05			
142043	Low discrimination				142043
<i>Yersinia pseudotuberculosis</i>	85.37	0.59	SOR 1		
<i>Citrobacter youngae</i>	13.25	0.59			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.54	0.28			
142053	Low discrimination				142053
<i>Citrobacter youngae</i>	55.20	0.57	ESL 5		
<i>Yersinia kristensenii</i>	18.02	0.37			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	12.06	0.48			
142063	Low discrimination				142063
<i>Yersinia rohdei</i>	50.66	0.56	ESL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	31.32	0.54			
<i>Citrobacter youngae</i>	10.81	0.47			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
142073	Low discrimination				142073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	73.81	0.64	ORN 95		
<i>Yersinia rohdei</i>	13.27	0.47			
<i>Citrobacter youngae</i>	6.94	0.45			
142103	Very good identification				142103
<i>Yersinia pseudotuberculosis</i>	99.71	0.59	MAL 1		
<i>Pantoea agglomerans</i>	0.16	0.05			
<i>Citrobacter werkmanii</i>	0.09	-.04			
142123	Acceptable identification				142123
<i>Pantoea agglomerans</i>	93.92	0.47	URE 1		
<i>Yersinia pseudotuberculosis</i>	5.88	0.18			
<i>Leclercia adecarboxylata</i>	0.20	-.05			
142133	Low discrimination				142133
<i>Pantoea agglomerans</i>	76.75	0.44	URE 1		
<i>Leclercia adecarboxylata</i>	20.80	0.36			
<i>Escherichia vulneris</i>	1.98	0.09			
142203	Very good identification				142203
<i>Yersinia pseudotuberculosis</i>	99.84	0.59	INO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.16	0.22			
142213	Low discrimination				142213
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	64.38	0.44	URE 10		
<i>Yersinia pseudotuberculosis</i>	35.62	0.18	ADO 97		
142253	Low discrimination				142253
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	60.28	0.49	URE 10		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.38	0.30	ADO 97		
<i>Yersinia kristensenii</i>	13.00	0.22			
142263	Acceptable identification				142263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	91.33	0.47	ORN 95		
<i>Citrobacter youngae</i>	3.87	0.21			
<i>Yersinia rohdei</i>	3.48	0.15			
142273	Low discrimination				142273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	88.35	0.56	ORN 95		
<i>Serratia ficaria</i>	4.96	0.18			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.87	0.37			
142403	Very good identification				142403
<i>Yersinia pseudotuberculosis</i>	95.97	0.59	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.03	0.51			
142412	Good identification				142412
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.38	URE 10		
142413	Good identification				142413

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.56	0.73	URE 10		
<i>Leclercia adecarboxylata</i>	3.47	0.30			
<i>Yersinia pseudotuberculosis</i>	1.98	0.18			
142423	Low discrimination				142423
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	50.12	0.39	URE 10		
<i>Yersinia pseudotuberculosis</i>	48.22	0.18	CEL 92		
<i>Leclercia adecarboxylata</i>	1.66	-.05			
142433	Low discrimination				142433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.32	0.61	URE 10	1	
<i>Leclercia adecarboxylata</i>	21.71	0.36		1	
<i>Serratia rubidaea</i>	1.97	0.13		99	
142443	Low discrimination				142443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	86.99	0.57	URE 10		
<i>Yersinia pseudotuberculosis</i>	11.27	0.18	CEL 92		
<i>Citrobacter youngae</i>	1.75	0.18			
142451	Good identification				142451
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.38	URE 10		
142452	Good identification				142452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.44	URE 10		
142453	Very good identification				142453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.81	0.79	URE 10		
<i>Citrobacter youngae</i>	0.14	0.16			
<i>Yersinia kristensenii</i>	0.05	-.04			
142463	Low discrimination				142463
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	84.50	0.44	URE 10		
<i>Yersinia rohdei</i>	8.47	0.15	CEL 92		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.23	0.13			
142473	Very good identification				142473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.56	0.66	URE 10		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.58	0.23			
<i>Yersinia rohdei</i>	0.28	0.06			
142513	Good identification				142513
				VPT	
<i>Leclercia adecarboxylata</i>	93.70	0.53	IND 99	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.95	0.42		1	
<i>Serratia rubidaea</i>	0.20	-.04		99	
142533	Low discrimination				142533
				VPT	
<i>Leclercia adecarboxylata</i>	89.46	0.59	IND 99	1	
<i>Serratia rubidaea</i>	9.56	0.37		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.73	0.30		1	
142553	Acceptable identification				142553
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.11	0.48	URE 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	7.89	0.12	MAL 3		
142573	Low discrimination				142573
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	42.06	0.35	URE 10	1	
<i>Leclercia adecarboxylata</i>	27.96	0.18	MAL 3	1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	15.42	0.04		98	
142603	Low discrimination				142603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	83.56	0.53	URE 10		
<i>Yersinia pseudotuberculosis</i>	16.45	0.18	CEL 92		
142612	Good identification				142612
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.40	URE 10		
142613	Very good identification				142613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.75	URE 10		
142623	Good identification				142623
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	URE 10		
142633	Very good identification				142633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.24	0.62	URE 10	1	
<i>Serratia rubidaea</i>	0.52	0.00		99	
<i>Leclercia adecarboxylata</i>	0.23	-.05		1	
142643	Very good identification				142643
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.59	URE 10		
142651	Good identification				142651
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.39	URE 10		
142652	Good identification				142652
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.46	URE 10		
142653	Very good identification				142653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.97	0.80	URE 10	1	
<i>Serratia odorifera biovar 2</i>	0.03	0.00		99	
142663	Good identification				142663
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.87	0.46	URE 10		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.13	0.05	CEL 92		
142673	Very good identification				142673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.14	0.68	URE 10	1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	1.30	0.07		98	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.56	0.15		2	
142713	Low discrimination				142713
<i>Klebsiella pneumoniae subsp. ozaenae</i>	88.49	0.44	URE 10		
<i>Leclercia adecarboxylata</i>	11.51	0.12	MAL 3		
142753	Good identification				142753

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.54	0.49	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.08	0.00	MAL 3	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.38	-.11		98	
143003	Very good identification				143003
<i>Yersinia pseudotuberculosis</i>	100.0	0.59	PHE 1		
143453	Good identification				143453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.38	URE 10		
143653	Good identification				143653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.39	URE 10		
144003	Low discrimination				144003
<i>Citrobacter werkmanii</i>	36.47	0.37	H2S 92		
<i>Citrobacter youngae</i>	35.68	0.53	MAL 92		
<i>Yersinia pseudotuberculosis</i>	22.16	0.33	SOR 90		
144013	Low discrimination				144013
<i>Citrobacter youngae</i>	76.34	0.52	SOR 99		
<i>Citrobacter braakii</i>	7.47	0.31			
<i>Citrobacter freundii</i>	6.94	0.33			
144023	Identification to the genus				144023
<i>Citrobacter freundii</i>	71.30	0.54	SOR 99		
<i>Citrobacter youngae</i>	24.73	0.42			
<i>Yersinia rohdei</i>	2.14	0.15			
144033	Low discrimination				144033
				VPT	
<i>Citrobacter freundii</i>	54.02	0.51	SOR 99	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	24.54	0.35		99	
<i>Citrobacter youngae</i>	19.51	0.40		1	
144041	Identification to the genus				144041
<i>Citrobacter youngae</i>	80.93	0.53	MAN 99		
<i>Citrobacter freundii</i>	7.67	0.35			
<i>Citrobacter werkmanii</i>	7.52	0.15			
144042	Identification to the genus				144042
<i>Citrobacter youngae</i>	81.49	0.53	TRE 99		
<i>Citrobacter freundii</i>	7.72	0.35			
<i>Citrobacter werkmanii</i>	7.57	0.15			
144043	Identification to the genus				144043
<i>Citrobacter youngae</i>	81.43	0.95			
<i>Citrobacter freundii</i>	7.71	0.76			
<i>Citrobacter werkmanii</i>	7.57	0.56			
144051	Low discrimination				144051
<i>Citrobacter youngae</i>	79.85	0.52	MAN 99		
<i>Citrobacter braakii</i>	7.82	0.31			
<i>Citrobacter freundii</i>	7.26	0.33			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
144052	Low discrimination				144052
<i>Citrobacter youngae</i>	79.85	0.52	TRE 99		
<i>Citrobacter braakii</i>	7.82	0.31			
<i>Citrobacter freundii</i>	7.26	0.33			
144053	Low discrimination				144053
<i>Citrobacter youngae</i>	79.59	0.93			
<i>Citrobacter braakii</i>	7.79	0.73			
<i>Citrobacter freundii</i>	7.24	0.74			
144061	Identification to the genus				144061
<i>Citrobacter freundii</i>	72.42	0.54	MAN 99		
<i>Citrobacter youngae</i>	25.12	0.42			
<i>Yersinia rohdei</i>	2.18	0.15			
144062	Identification to the genus				144062
<i>Citrobacter freundii</i>	72.42	0.54	TRE 99		
<i>Citrobacter youngae</i>	25.12	0.42			
<i>Yersinia rohdei</i>	2.18	0.15			
144063	Identification to the genus				144063
<i>Citrobacter freundii</i>	72.29	0.95			
<i>Citrobacter youngae</i>	25.08	0.83			
<i>Yersinia rohdei</i>	2.17	0.56			
144071	Low discrimination				144071
				VPT	
<i>Citrobacter freundii</i>	67.74	0.51	MAN 99	1	
<i>Citrobacter youngae</i>	24.47	0.40		1	
<i>Enterobacter cloacae subsp. cloacae</i>	5.91	0.21		99	
144072	Low discrimination				144072
				VPT	
<i>Citrobacter freundii</i>	67.74	0.51	TRE 99	1	
<i>Citrobacter youngae</i>	24.47	0.40		1	
<i>Enterobacter cloacae subsp. cloacae</i>	5.91	0.21		99	
144073	Low discrimination				144073
				VPT	
<i>Citrobacter freundii</i>	67.56	0.92		1	
<i>Citrobacter youngae</i>	24.41	0.81		1	
<i>Enterobacter cloacae subsp. cloacae</i>	5.89	0.62		99	
144103	Very good identification				144103
<i>Citrobacter werkmanii</i>	99.30	0.59	H2S 92		
<i>Citrobacter youngae</i>	0.45	0.27	SOR 90		
<i>Hafnia alvei</i>	0.13	0.22			
144133	Low discrimination				144133
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	86.21	0.45	ORN 96	99	
<i>Pantoea agglomerans</i>	6.35	0.16	SOR 95	64	
<i>Citrobacter freundii</i>	5.50	0.30		1	
144141	Acceptable identification				144141

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter werkmanii</i>	94.61	0.37	H2S 92		
<i>Citrobacter youngae</i>	4.66	0.27	MAN 99		
<i>Citrobacter freundii</i>	0.73	0.13			
144142	Acceptable identification				144142
<i>Citrobacter werkmanii</i>	94.61	0.37	H2S 92		
<i>Citrobacter youngae</i>	4.66	0.27	TRE 99		
<i>Citrobacter freundii</i>	0.73	0.13			
144143	Good identification				144143
<i>Citrobacter werkmanii</i>	94.55	0.78	H2S 92		
<i>Citrobacter youngae</i>	4.66	0.68			
<i>Citrobacter freundii</i>	0.73	0.54			
144153	Low discrimination				144153
<i>Citrobacter youngae</i>	48.57	0.66	MAL 5		
<i>Citrobacter sedlakii</i>	24.92	0.45			
<i>Citrobacter werkmanii</i>	12.17	0.37			
144163	Identification to the genus				144163
<i>Citrobacter freundii</i>	71.44	0.73	MAL 8		
<i>Citrobacter youngae</i>	15.00	0.56			
<i>Citrobacter werkmanii</i>	11.57	0.37			
144173	Low discrimination				144173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	71.01	0.72	ORN 96	99	
<i>Citrobacter freundii</i>	23.61	0.71		1	
<i>Citrobacter youngae</i>	5.16	0.55		1	
144243	Very good identification				144243
<i>Citrobacter youngae</i>	95.76	0.68	INO 5		
<i>Citrobacter freundii</i>	1.74	0.35			
<i>Citrobacter werkmanii</i>	1.71	0.15			
144253	Low discrimination				144253
				VPT	
<i>Citrobacter youngae</i>	89.39	0.66	INO 5	1	
<i>Serratia odorifera</i> biovar 2	3.08	0.33		99	
<i>Yersinia kristensenii</i>	1.81	0.22		1	
144263	Identification to the genus				144263
<i>Citrobacter youngae</i>	62.82	0.56	INO 5		
<i>Citrobacter freundii</i>	34.75	0.54			
<i>Yersinia rohdei</i>	1.05	0.15			
144273	Low discrimination				144273
				VPT	
<i>Citrobacter youngae</i>	39.95	0.55	INO 5	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	32.33	0.46		99	
<i>Citrobacter freundii</i>	21.23	0.51		1	
144343	Identification to the genus				144343
<i>Citrobacter werkmanii</i>	79.09	0.37	H2S 92		
<i>Citrobacter youngae</i>	20.30	0.42	INO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	0.61	0.13			
144353	Low discrimination				144353
				VPT	
<i>Citrobacter youngae</i>	64.32	0.40	MAL 5	1	
<i>Enterobacter cloacae subsp. cloacae</i>	24.40	0.25	INO 5	99	
<i>Citrobacter sedlakii</i>	6.33	0.04		1	
144373	Very good identification				144373
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	95.05	0.56	ORN 96	99	
<i>Citrobacter youngae</i>	2.06	0.28		1	
<i>Citrobacter freundii</i>	1.81	0.30		1	
144413	Very good identification				144413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.66	0.53	URE 10		
<i>Citrobacter youngae</i>	1.34	0.11			
144433	Low discrimination				144433
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	51.84	0.41	URE 10	1	
<i>Enterobacter cloacae subsp. cloacae</i>	30.97	0.26		99	
<i>Serratia rubidaea</i>	15.13	0.14		99	
144443	Low discrimination				144443
<i>Citrobacter youngae</i>	75.43	0.53	ADO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	7.44	0.37			
<i>Citrobacter freundii</i>	7.15	0.35			
144453	Low discrimination				144453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	51.19	0.59	URE 10		
<i>Citrobacter youngae</i>	36.94	0.52			
<i>Citrobacter braakii</i>	3.62	0.31			
144463	Low discrimination				144463
<i>Citrobacter freundii</i>	69.65	0.54	ADO 1		
<i>Citrobacter youngae</i>	24.16	0.42			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.24	0.24			
144473	Low discrimination				144473
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	60.74	0.52	ORN 96	99	
<i>Citrobacter freundii</i>	21.11	0.51		1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	9.94	0.46		1	
144533	Low discrimination				144533
				VPT	
<i>Serratia rubidaea</i>	71.50	0.39	URE 2	99	
<i>Enterobacter cloacae subsp. cloacae</i>	28.02	0.35	ESL 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.48	0.10		1	
144543	Acceptable identification				144543
<i>Citrobacter werkmanii</i>	94.10	0.37	H2S 92		
<i>Citrobacter youngae</i>	4.64	0.27	ADO 1		
<i>Citrobacter freundii</i>	0.73	0.13			
144573	Very good identification				144573

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.44	0.62	ORN 96	99	
<i>Citrobacter freundii</i>	0.98	0.30		1	
<i>Citrobacter koseri</i>	0.79	0.17		1	
144613	Very good identification				144613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.55	URE 10		
144633	Low discrimination				144633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	87.26	0.43	URE 10	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	7.53	0.10		99	
<i>Serratia rubidaea</i>	5.21	0.02		99	
144643	Low discrimination				144643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	69.60	0.39	URE 10		
<i>Citrobacter youngae</i>	30.40	0.27	CEL 92		
144653	Low discrimination				144653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	85.67	0.60	URE 10	1	
<i>Serratia odorifera</i> biovar 2	11.09	0.34		99	
<i>Citrobacter youngae</i>	2.66	0.25		1	
144673	Low discrimination				144673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	50.14	0.48	URE 10	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	44.25	0.36		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	3.07	0.01		98	
144773	Low discrimination				144773
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	75.80	0.46	ORN 96	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	23.32	0.24		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.89	0.17		1	
145043	Identification to the genus				145043
<i>Citrobacter youngae</i>	81.49	0.53	PHE 1		
<i>Citrobacter freundii</i>	7.72	0.35			
<i>Citrobacter werkmanii</i>	7.57	0.15			
145053	Low discrimination				145053
<i>Citrobacter youngae</i>	79.85	0.52	PHE 1		
<i>Citrobacter braakii</i>	7.82	0.31			
<i>Citrobacter freundii</i>	7.26	0.33			
145063	Identification to the genus				145063
<i>Citrobacter freundii</i>	72.42	0.54	PHE 1		
<i>Citrobacter youngae</i>	25.12	0.42			
<i>Yersinia rohdei</i>	2.18	0.15			
145073	Low discrimination				145073
				VPT	
<i>Citrobacter freundii</i>	67.74	0.51	PHE 1	1	
<i>Citrobacter youngae</i>	24.47	0.40		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.91	0.21		99	
145143	Acceptable identification				145143

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Citrobacter werkmanii</i>	94.61	0.37	H2S 92		
<i>Citrobacter youngae</i>	4.66	0.27	PHE 1		
<i>Citrobacter freundii</i>	0.73	0.13			
145201	Good identification				145201
<i>Providencia stuartii</i>	100.0	0.38	ONP 10		
145221	Good identification				145221
<i>Providencia stuartii</i>	100.0	0.38	ONP 10		
146003	Very good identification				146003
<i>Yersinia pseudotuberculosis</i>	99.41	0.59	SCI 1		
<i>Citrobacter youngae</i>	0.44	0.27			
<i>Citrobacter werkmanii</i>	0.09	-0.4			
146043	Good identification				146043
<i>Citrobacter youngae</i>	93.49	0.68	ESL 5		
<i>Yersinia pseudotuberculosis</i>	2.14	0.18			
<i>Citrobacter freundii</i>	1.70	0.35			
146053	Low discrimination				146053
<i>Citrobacter youngae</i>	82.30	0.66	ESL 5		
<i>Citrobacter amalonaticus</i>	8.89	0.30			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.71	0.40			
146063	Low discrimination				146063
<i>Citrobacter youngae</i>	60.11	0.56	ESL 5		
<i>Citrobacter freundii</i>	33.26	0.54			
<i>Serratia ficaria</i>	3.61	0.16			
146073	Low discrimination				146073
				VPT	
<i>Serratia ficaria</i>	66.79	0.57	URE 1	75	
<i>Enterobacter cloacae subsp. cloacae</i>	18.06	0.54		99	
<i>Citrobacter youngae</i>	9.19	0.55		1	
146123	Very good identification				146123
<i>Pantoea agglomerans</i>	99.86	0.59	URE 1		
<i>Serratia rubidaea</i>	0.09	-0.2			
<i>Enterobacter cloacae subsp. cloacae</i>	0.05	-0.3			
146133	Good identification				146133
<i>Pantoea agglomerans</i>	92.28	0.57	URE 1		
<i>Enterobacter cloacae subsp. cloacae</i>	5.42	0.38			
<i>Serratia rubidaea</i>	1.70	0.22			
146143	Identification to the genus				146143
<i>Citrobacter werkmanii</i>	78.83	0.37	H2S 92		
<i>Citrobacter youngae</i>	20.23	0.42	ESL 1		
<i>Citrobacter freundii</i>	0.61	0.13			
146173	Good identification				146173
<i>Enterobacter cloacae subsp. cloacae</i>	94.04	0.64	ORN 96		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2.30	0.19			
<i>Serratia ficaria</i>	1.17	0.16			
146213	Good identification				146213
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.12	0.36	URE 10	1	
<i>Cronobacter sakazakii</i>	4.89	-.03	ADO 97	99	
146233	Low discrimination				146233
				VPT	
<i>Cronobacter sakazakii</i>	76.34	0.38	ORN 91	99	
<i>Serratia ficaria</i>	16.54	0.18	URE 1	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.75	0.24		1	
146243	Acceptable identification				146243
<i>Citrobacter youngae</i>	94.84	0.42	ESL 5		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.16	0.20	INO 5		
146253	Low discrimination				146253
<i>Citrobacter youngae</i>	36.65	0.40	ESL 5		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	28.01	0.42	INO 5		
<i>Serratia ficaria</i>	16.61	0.18			
146273	Good identification				146273
<i>Serratia ficaria</i>	93.00	0.59	URE 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	3.63	0.39			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2.16	0.22			
146373	Low discrimination				146373
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	70.73	0.46	LYS 98		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	26.88	0.49	ADO 90		
<i>Serratia ficaria</i>	2.32	0.18			
146403	Low discrimination				146403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	64.05	0.44	URE 10		
<i>Yersinia pseudotuberculosis</i>	35.95	0.18	CEL 92		
146413	Very good identification				146413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.71	0.66	URE 10	1	
<i>Serratia rubidaea</i>	0.29	-.02		99	
146433	Low discrimination				146433
				VPT	
<i>Serratia rubidaea</i>	51.64	0.39	URE 2	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	45.17	0.53	MAL 94	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.89	0.18		99	
146443	Low discrimination				146443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	88.23	0.49	URE 10		
<i>Citrobacter youngae</i>	11.77	0.27	CEL 92		
146452	Good identification				146452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.36	URE 10		
146453	Very good identification				146453
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.47	0.71	URE 10	1	
<i>Citrobacter youngae</i>	0.94	0.25		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.50	0.13		99	
146463	Low discrimination				146463
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	77.13	0.37	URE 10		
<i>Citrobacter youngae</i>	10.95	0.15	CEL 92		
<i>Citrobacter freundii</i>	6.06	0.12			
146473	Low discrimination				146473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	54.13	0.59	URE 10	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	35.44	0.44		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	5.28	0.16		98	
146523	Acceptable identification				146523
<i>Serratia rubidaea</i>	90.08	0.39	URE 2		
<i>Pantoea agglomerans</i>	9.93	0.18	CEL 94		
146533	Very good identification				146533
<i>Serratia rubidaea</i>	97.63	0.63	URE 2		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.05	0.28			
<i>Pantoea agglomerans</i>	0.54	0.16			
146553	Low discrimination				146553
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	61.38	0.40	URE 10	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	30.14	0.23	MAL 3	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	6.50	-.02		98	
146573	Low discrimination				146573
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	57.91	0.54	ORN 96		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	38.22	0.39			
<i>Serratia rubidaea</i>	2.87	0.22			
146603	Good identification				146603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.45	URE 10		
146613	Very good identification				146613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.67	URE 10		
146633	Low discrimination				146633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	78.25	0.55	URE 10	1	
<i>Serratia rubidaea</i>	18.30	0.26		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2.23	0.01		98	
146643	Good identification				146643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.51	URE 10		
146652	Good identification				146652
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.38	URE 10		
146653	Very good identification				146653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.45	0.73	URE 10	1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 2	2.10	0.31		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.37	0.01		98	
146663	Identification to the genus				146663
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	70.60	0.39	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	25.14	0.07	CEL 92	98	
<i>Serratia marcescens</i>	4.26	-.01		98	
146673	Low discrimination				146673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	56.45	0.42	LYS 98	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	37.21	0.60	MAL 93	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	3.52	0.29		99	
146713	Low discrimination				146713
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.97	0.36	URE 10	1	
<i>Serratia rubidaea</i>	23.03	0.10	MAL 3	99	
146733	Low discrimination				146733
				VPT	
<i>Serratia rubidaea</i>	89.35	0.51	URE 2	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	9.22	0.24		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.75	0.24		1	
146773	Very good identification				146773
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	97.78	0.65	LYS 98		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.38	0.39			
<i>Klebsiella oxytoca</i>	0.55	0.18			
147123	Good identification				147123
<i>Pantoea agglomerans</i>	100.0	0.38	URE 1		
147133	Acceptable identification				147133
<i>Pantoea agglomerans</i>	93.98	0.36	URE 1		
<i>Cronobacter sakazakii</i>	5.46	0.15	PHE 9		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.56	-.03			
147233	Good identification				147233
<i>Cronobacter sakazakii</i>	100.0	0.38	ORN 91		
150001	Acceptable identification				150001
<i>Shigella dysenteriae</i> (group A)	90.25	0.50	URE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	8.39	0.31			
<i>Shigella boydii</i> (group C)	0.39	-.02			
150041	Low discrimination				150041
<i>Shigella dysenteriae</i> (group A)	85.68	0.42	URE 1		
<i>Citrobacter youngae</i>	7.73	0.29			
<i>Escherichia coli</i>	3.12	0.20			
150043	Low discrimination				150043
<i>Citrobacter youngae</i>	67.60	0.70			
<i>Citrobacter freundii</i>	12.72	0.57			
<i>Citrobacter braakii</i>	7.06	0.50			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
150053	Low discrimination				150053
<i>Yersinia kristensenii</i>	70.34	0.71	ORN 92		
<i>Citrobacter youngae</i>	17.03	0.68			
<i>Citrobacter braakii</i>	4.42	0.56			
150063	Low discrimination				150063
<i>Citrobacter freundii</i>	52.12	0.76			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	23.61	0.64			
<i>Yersinia rohdei</i>	12.73	0.56			
150071	Low discrimination				150071
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	60.72	0.39	ORN 95		
<i>Citrobacter freundii</i>	17.38	0.33	MAN 98		
<i>Citrobacter farmeri</i>	16.94	0.15			
150072	Low discrimination				150072
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	60.72	0.39	ORN 95		
<i>Citrobacter freundii</i>	17.38	0.33	TRE 98		
<i>Citrobacter farmeri</i>	16.94	0.15			
150073	Low discrimination				150073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	42.82	0.74	ORN 95		
<i>Citrobacter freundii</i>	24.76	0.74			
<i>Citrobacter farmeri</i>	24.14	0.56			
150133	Good identification				150133
<i>Leclercia adecarboxylata</i>	98.43	0.36	ESL 99		
<i>Citrobacter freundii</i>	1.57	0.11	ADO 93		
150143	Low discrimination				150143
<i>Citrobacter youngae</i>	58.77	0.43	MAL 5		
<i>Citrobacter freundii</i>	18.26	0.35			
<i>Citrobacter werkmanii</i>	16.90	0.15			
150153	Low discrimination				150153
<i>Citrobacter sedlakii</i>	78.95	0.45	ORN 99		
<i>Citrobacter youngae</i>	9.54	0.42			
<i>Yersinia kristensenii</i>	7.56	0.30			
150163	Low discrimination				150163
<i>Citrobacter freundii</i>	83.99	0.54	MAL 8		
<i>Citrobacter youngae</i>	8.88	0.31			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.42	0.23			
150173	Low discrimination				150173
<i>Citrobacter freundii</i>	67.69	0.52	MAL 8		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	13.60	0.33			
<i>Citrobacter farmeri</i>	7.67	0.15			
150243	Low discrimination				150243
<i>Citrobacter youngae</i>	67.52	0.43	INO 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	19.95	0.30			
<i>Yersinia kristensenii</i>	7.73	0.14			
150253	Low discrimination				150253
<i>Yersinia kristensenii</i>	86.22	0.55	ORN 92		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.74	0.40			
<i>Citrobacter youngae</i>	6.23	0.42			
150263	Low discrimination				150263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	89.78	0.56	ORN 95		
<i>Citrobacter freundii</i>	4.67	0.35			
<i>Citrobacter youngae</i>	4.25	0.31			
150273	Very good identification				150273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	95.42	0.66	ORN 95		
<i>Citrobacter freundii</i>	1.30	0.33			
<i>Citrobacter farmeri</i>	1.27	0.15			
150433	Good identification				150433
<i>Leclercia adecarboxylata</i>	99.12	0.36	ESL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.88	0.07	MAL 93		
150513	Very good identification				150513
<i>Leclercia adecarboxylata</i>	99.89	0.53	ESL 99		
<i>Citrobacter koseri</i>	0.11	-.07			
150533	Very good identification				150533
<i>Leclercia adecarboxylata</i>	100.0	0.59	ESL 99		
151000	Very good identification				151000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.64	0.54	ONP 10		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.30	0.13	ORN 95		
<i>Proteus vulgaris</i>	0.06	0.02			
151001	Good identification				151001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	92.49	0.54	ONP 1		
<i>Providencia stuartii</i>	3.64	0.23			
<i>Morganella morganii</i> subsp. <i>morganii</i>	3.12	0.13			
151201	Good identification				151201
<i>Providencia stuartii</i>	98.67	0.50	ONP 10		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.33	0.13	SCI 93		
151221	Good identification				151221
<i>Providencia stuartii</i>	100.0	0.50	ONP 10		
151602	Good identification				151602
<i>Providencia rettgeri</i>	100.0	0.47	ONP 5		
152003	Very good identification				152003
<i>Yersinia pseudotuberculosis</i>	99.70	0.59	IND 1		
<i>Escherichia coli</i>	0.14	0.16			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	0.13	0.07			
152013	Acceptable identification				152013
<i>Leclercia adecarboxylata</i>	90.83	0.48	MAL 93		
<i>Yersinia pseudotuberculosis</i>	6.96	0.18	ADO 93		
<i>Escherichia hermannii</i>	2.21	0.14			
152033	Very good identification				152033
<i>Leclercia adecarboxylata</i>	97.62	0.54	MAL 93		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.38	0.23	ADO 93		
<i>Escherichia hermannii</i>	1.00	0.12			
152043	Low discrimination				152043
<i>Citrobacter youngae</i>	49.43	0.43	ESL 5		
<i>Yersinia pseudotuberculosis</i>	18.24	0.18			
<i>Escherichia coli</i>	18.20	0.33			
152053	Low discrimination				152053
<i>Citrobacter youngae</i>	32.42	0.42	ESL 5		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	27.32	0.38			
<i>Yersinia kristensenii</i>	25.70	0.30			
152063	Low discrimination				152063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	83.31	0.54	ORN 95		
<i>Citrobacter freundii</i>	5.57	0.35			
<i>Citrobacter youngae</i>	5.07	0.31			
152073	Good identification				152073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	94.22	0.64	ORN 95		
<i>Citrobacter freundii</i>	1.65	0.33			
<i>Citrobacter farmeri</i>	1.61	0.15			
152113	Very good identification				152113
<i>Leclercia adecarboxylata</i>	99.96	0.71	ADO 93		
<i>Escherichia vulneris</i>	0.02	-.10			
<i>Citrobacter sedlakii</i>	0.02	-.11			
152123	Good identification				152123
<i>Leclercia adecarboxylata</i>	95.47	0.36	ADO 93		
<i>Pantoea agglomerans</i>	4.53	0.05	CEL 99		
152131	Good identification				152131
<i>Leclercia adecarboxylata</i>	100.0	0.36	ADO 93		
152132	Good identification				152132
<i>Leclercia adecarboxylata</i>	100.0	0.36	ADO 93		
152133	Very good identification				152133
<i>Leclercia adecarboxylata</i>	99.96	0.77	ADO 93		
<i>Pantoea agglomerans</i>	0.04	0.03			
152173	Low discrimination				152173

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	87.59	0.36	ADO 93		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.24	0.23	SOR 1		
<i>Citrobacter freundii</i>	1.39	0.11			
152263	Good identification				152263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.26	0.47	ORN 95		
<i>Citrobacter youngae</i>	0.74	0.05			
152273	Very good identification				152273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.80	0.56	ORN 95		
<i>Citrobacter youngae</i>	0.20	0.03			
152333	Good identification				152333
<i>Leclercia adecarboxylata</i>	100.0	0.36	INO 1		
152413	Very good identification				152413
<i>Leclercia adecarboxylata</i>	99.72	0.71	MAL 93		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.28	0.32			
152423	Good identification				152423
<i>Leclercia adecarboxylata</i>	100.0	0.36	MAL 93		
152431	Good identification				152431
<i>Leclercia adecarboxylata</i>	100.0	0.36	MAL 93		
152432	Good identification				152432
<i>Leclercia adecarboxylata</i>	100.0	0.36	MAL 93		
152433	Very good identification				152433
<i>Leclercia adecarboxylata</i>	99.96	0.77	MAL 93		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.04	0.20			
152473	Low discrimination				152473
<i>Leclercia adecarboxylata</i>	85.37	0.36	MAL 93		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.00	0.23	SOR 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.63	0.25			
152503	Very good identification				152503
<i>Leclercia adecarboxylata</i>	100.0	0.53	CEL 99		
152511	Very good identification				152511
<i>Leclercia adecarboxylata</i>	100.0	0.53	MAN 99		
152512	Very good identification				152512
<i>Leclercia adecarboxylata</i>	100.0	0.53	TRE 99		
152513	Excellent identification				152513
<i>Leclercia adecarboxylata</i>	100.0	0.94			
152523	Very good identification				152523
<i>Leclercia adecarboxylata</i>	100.0	0.59	CEL 99		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
152531	Very good identification					152531
<i>Leclercia adecarboxylata</i>		100.0	0.59	MAN 99		
152532	Very good identification					152532
<i>Leclercia adecarboxylata</i>		100.0	0.59	TRE 99		
152533	Excellent identification					152533
					VPT	
<i>Leclercia adecarboxylata</i>		100.0	1.00		1	
<i>Serratia rubidaea</i>		0.00	-.04		99	
152553	Very good identification					152553
<i>Leclercia adecarboxylata</i>		99.72	0.53	SOR 1		
<i>Citrobacter sedlakii</i>		0.16	-.11			
<i>Klebsiella pneumoniae subsp. ozaenae</i>		0.12	0.06			
152573	Very good identification					152573
					VPT	
<i>Leclercia adecarboxylata</i>		99.69	0.59	SOR 1	1	
<i>Klebsiella oxytoca</i>		0.31	-.02		95	
152633	Good identification					152633
<i>Leclercia adecarboxylata</i>		95.84	0.36	MAL 93		
<i>Klebsiella pneumoniae subsp. ozaenae</i>		4.16	0.21	INO 1		
152653	Good identification					152653
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		97.25	0.39	IND 1	1	
<i>Serratia odorifera biovar 2</i>		2.75	0.00	URE 10	99	
152713	Very good identification					152713
<i>Leclercia adecarboxylata</i>		100.0	0.53	INO 1		
152733	Very good identification					152733
					VPT	
<i>Leclercia adecarboxylata</i>		99.85	0.59	INO 1	1	
<i>Klebsiella oxytoca</i>		0.15	-.09		95	
153133	Good identification					153133
<i>Leclercia adecarboxylata</i>		100.0	0.36	PHE 1		
153433	Good identification					153433
<i>Leclercia adecarboxylata</i>		100.0	0.36	PHE 1		
153513	Very good identification					153513
<i>Leclercia adecarboxylata</i>		100.0	0.53	PHE 1		
153533	Very good identification					153533
<i>Leclercia adecarboxylata</i>		100.0	0.59	PHE 1		
153602	Good identification					153602
<i>Providencia rettgeri</i>		100.0	0.42	ONP 5		
154003	Low discrimination					154003

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	64.72	0.38	SOR 99		
<i>Citrobacter freundii</i>	17.11	0.29			
<i>Citrobacter braakii</i>	7.13	0.19			
154023	Identification to the genus				154023
<i>Citrobacter freundii</i>	87.69	0.47	SOR 99		
<i>Citrobacter youngae</i>	10.90	0.26			
<i>Providencia stuartii</i>	1.41	0.01			
154033	Identification to the genus				154033
<i>Citrobacter freundii</i>	75.46	0.45	SOR 99		
<i>Citrobacter amalonaticus</i>	11.97	0.10			
<i>Citrobacter youngae</i>	9.77	0.24			
154041	Low discrimination				154041
<i>Citrobacter youngae</i>	68.68	0.38	MAN 99		
<i>Citrobacter freundii</i>	18.16	0.29			
<i>Citrobacter braakii</i>	7.56	0.19			
154042	Identification to the genus				154042
<i>Citrobacter youngae</i>	70.59	0.38	TRE 99		
<i>Citrobacter freundii</i>	18.66	0.29			
<i>Citrobacter braakii</i>	7.77	0.19			
154043	Identification to the genus				154043
<i>Citrobacter youngae</i>	70.31	0.79			
<i>Citrobacter freundii</i>	18.59	0.70			
<i>Citrobacter braakii</i>	7.74	0.60			
154053	Identification to the genus				154053
<i>Citrobacter amalonaticus</i>	76.69	0.75	ORN 94		
<i>Citrobacter youngae</i>	15.02	0.77			
<i>Citrobacter braakii</i>	4.11	0.66			
154061	Identification to the genus				154061
<i>Citrobacter freundii</i>	88.95	0.47	MAN 99		
<i>Citrobacter youngae</i>	11.05	0.26			
154062	Identification to the genus				154062
<i>Citrobacter freundii</i>	88.95	0.47	TRE 99		
<i>Citrobacter youngae</i>	11.05	0.26			
154063	Identification to the genus				154063
<i>Citrobacter freundii</i>	88.38	0.88			
<i>Citrobacter youngae</i>	10.98	0.67			
<i>Citrobacter braakii</i>	0.34	0.37			
154071	Identification to the genus				154071
<i>Citrobacter freundii</i>	75.46	0.45	MAN 99		
<i>Citrobacter amalonaticus</i>	11.97	0.10			
<i>Citrobacter youngae</i>	9.77	0.24			
154072	Identification to the genus				154072

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	75.46	0.45	TRE 99		
<i>Citrobacter amalonaticus</i>	11.97	0.10			
<i>Citrobacter youngae</i>	9.77	0.24			
154073	Identification to the genus				154073
<i>Citrobacter freundii</i>	75.07	0.86			
<i>Citrobacter amalonaticus</i>	11.91	0.51			
<i>Citrobacter youngae</i>	9.72	0.65			
154143	Low discrimination				154143
<i>Citrobacter werkmanii</i>	42.01	0.37	H2S 92		
<i>Citrobacter youngae</i>	36.15	0.53	IND 1		
<i>Citrobacter freundii</i>	15.79	0.48			
154153	Low discrimination				154153
<i>Citrobacter sedlakii</i>	83.18	0.59	ORN 99		
<i>Citrobacter youngae</i>	5.86	0.51			
<i>Citrobacter amalonaticus</i>	5.74	0.34			
154163	Good identification				154163
<i>Citrobacter freundii</i>	92.27	0.66	MAL 8		
<i>Citrobacter youngae</i>	6.94	0.41			
<i>Citrobacter koseri</i>	0.48	0.09			
154173	Low discrimination				154173
<i>Citrobacter freundii</i>	76.38	0.64	MAL 8		
<i>Citrobacter koseri</i>	7.96	0.33			
<i>Citrobacter youngae</i>	5.98	0.39			
154201	Good identification				154201
<i>Providencia stuartii</i>	100.0	0.47	ONP 10		
154221	Good identification				154221
<i>Providencia stuartii</i>	100.0	0.47	ONP 10		
154243	Acceptable identification				154243
<i>Citrobacter youngae</i>	92.60	0.53	INO 5		
<i>Citrobacter freundii</i>	4.70	0.29			
<i>Citrobacter braakii</i>	1.96	0.19			
154253	Low discrimination				154253
<i>Citrobacter youngae</i>	43.01	0.51	INO 5	VPT 1	
<i>Citrobacter amalonaticus</i>	42.14	0.34		1	
<i>Serratia odorifera</i> biovar 2	8.39	0.33		99	
154263	Identification to the genus				154263
<i>Citrobacter freundii</i>	58.96	0.47	INO 1		
<i>Citrobacter youngae</i>	38.18	0.41			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.86	0.15			
154273	Low discrimination				154273

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	47.92	0.45	INO 1		
<i>Citrobacter youngae</i>	32.32	0.39			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.88	0.25			
154443	Low discrimination				154443
<i>Citrobacter youngae</i>	65.57	0.38	ADO 1		
<i>Citrobacter freundii</i>	17.33	0.29			
<i>Citrobacter braakii</i>	7.22	0.19			
154463	Identification to the genus				154463
<i>Citrobacter freundii</i>	85.52	0.47	ADO 1		
<i>Citrobacter youngae</i>	10.63	0.26			
<i>Citrobacter koseri</i>	3.85	0.09			
154473	Low discrimination				154473
<i>Citrobacter freundii</i>	43.84	0.45	ADO 1		
<i>Citrobacter koseri</i>	39.32	0.33			
<i>Citrobacter amalonaticus</i>	6.96	0.10			
154553	Very good identification				154553
<i>Citrobacter koseri</i>	97.39	0.59	ORN 99		
<i>Citrobacter sedlakii</i>	2.24	0.18			
<i>Citrobacter youngae</i>	0.16	0.10			
154573	Very good identification				154573
				VPT	
<i>Citrobacter koseri</i>	98.08	0.58	ORN 99	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.24	0.21		99	
<i>Citrobacter freundii</i>	0.61	0.23		1	
154602	Good identification				154602
<i>Providencia rettgeri</i>	100.0	0.39	ONP 5		
155001	Good identification				155001
<i>Providencia stuartii</i>	98.11	0.47	ONP 10		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.90	0.13	INO 95		
155021	Good identification				155021
<i>Providencia stuartii</i>	99.04	0.47	ONP 10		
<i>Proteus vulgaris</i>	0.96	0.10	INO 95		
155043	Identification to the genus				155043
<i>Citrobacter youngae</i>	70.59	0.38	PHE 1		
<i>Citrobacter freundii</i>	18.66	0.29			
<i>Citrobacter braakii</i>	7.77	0.19			
155063	Identification to the genus				155063
<i>Citrobacter freundii</i>	88.95	0.47	PHE 1		
<i>Citrobacter youngae</i>	11.05	0.26			
155073	Identification to the genus				155073
<i>Citrobacter freundii</i>	75.46	0.45	PHE 1		
<i>Citrobacter amalonaticus</i>	11.97	0.10			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	9.77	0.24			
155200	Good identification				155200
<i>Providencia stuartii</i>	98.93	0.38	ONP 10		
<i>Providencia rettgeri</i>	1.08	-.09	TRE 98		
155201	Very good identification				155201
<i>Providencia stuartii</i>	100.0	0.73	ONP 10		
155203	Very good identification				155203
<i>Providencia stuartii</i>	99.80	0.53	ONP 10		
<i>Providencia rettgeri</i>	0.20	-.09	MAN 10		
155211	Good identification				155211
<i>Providencia stuartii</i>	100.0	0.47	ONP 10		
155220	Good identification				155220
<i>Providencia stuartii</i>	100.0	0.38	ONP 10		
155221	Very good identification				155221
<i>Providencia stuartii</i>	100.0	0.73	ONP 10		
155223	Very good identification				155223
<i>Providencia stuartii</i>	100.0	0.53	ONP 10		
155231	Good identification				155231
<i>Providencia stuartii</i>	100.0	0.47	ONP 10		
155402	Very good identification				155402
<i>Providencia rettgeri</i>	99.94	0.54	ONP 5		
<i>Providencia alcalifaciens</i>	0.06	-.17	INO 90		
155422	Good identification				155422
<i>Providencia rettgeri</i>	100.0	0.39	ONP 5		
155601	Good identification				155601
<i>Providencia stuartii</i>	99.58	0.47	ONP 10		
<i>Providencia rettgeri</i>	0.42	-.09	ADO 5		
155602	Very good identification				155602
<i>Providencia rettgeri</i>	100.0	0.74	ONP 5		
155612	Good identification				155612
<i>Providencia rettgeri</i>	100.0	0.43	ONP 5		
155621	Good identification				155621
<i>Providencia stuartii</i>	100.0	0.47	ONP 10		
155622	Very good identification				155622
<i>Providencia rettgeri</i>	100.0	0.58	ONP 5		
156043	Identification to the genus				156043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	86.87	0.53	ESL 5		
<i>Citrobacter amalonaticus</i>	6.89	0.14			
<i>Citrobacter freundii</i>	4.41	0.29			
156053	Identification to the genus				156053
<i>Citrobacter amalonaticus</i>	89.46	0.55	ORN 94		
<i>Citrobacter youngae</i>	9.32	0.51	ESL 9		
<i>Citrobacter braakii</i>	0.49	0.25			
156063	Identification to the genus				156063
<i>Citrobacter freundii</i>	58.91	0.47	ESL 1		
<i>Citrobacter youngae</i>	38.15	0.41			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.22	0.13			
156133	Low discrimination				156133
				VPT	
<i>Leclercia adecarboxylata</i>	85.59	0.36	SCI 1	1	
<i>Pantoea agglomerans</i>	12.76	0.16	ADO 93	64	
<i>Cronobacter sakazakii</i>	0.90	-.04		99	
156153	Acceptable identification				156153
<i>Citrobacter sedlakii</i>	94.85	0.45	ORN 99		
<i>Citrobacter amalonaticus</i>	3.16	0.14			
<i>Citrobacter youngae</i>	1.72	0.25			
156433	Good identification				156433
				VPT	
<i>Leclercia adecarboxylata</i>	96.84	0.36	SCI 1	1	
<i>Serratia rubidaea</i>	1.69	-.02	MAL 93	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.47	0.12		1	
156513	Very good identification				156513
<i>Leclercia adecarboxylata</i>	99.89	0.53	SCI 1		
<i>Citrobacter koseri</i>	0.11	-.07			
156533	Very good identification				156533
				VPT	
<i>Leclercia adecarboxylata</i>	97.93	0.59	SCI 1	1	
<i>Serratia rubidaea</i>	2.01	0.22		99	
<i>Klebsiella oxytoca</i>	0.06	-.17		95	
156773	Very good identification				156773
<i>Klebsiella oxytoca</i>	98.19	0.59	LYS 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.79	0.24			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.03	-.02			
157402	Good identification				157402
<i>Providencia rettgeri</i>	100.0	0.49	ONP 5		
157602	Very good identification				157602
<i>Providencia rettgeri</i>	100.0	0.68	ONP 5		
157612	Good identification				157612
<i>Providencia rettgeri</i>	100.0	0.37	ONP 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
157622	Good identification				157622
<i>Providencia rettgeri</i>	100.0	0.53	ONP 5		
160001	Low discrimination				160001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	57.79	0.36	ONP 1		
<i>Shigella sonnei</i>	34.12	0.18	PHE 93		
<i>Shigella dysenteriae</i> (group A)	4.32	0.10			
160003	Good identification				160003
<i>Shigella sonnei</i>	90.22	0.59	URE 1		
<i>Hafnia alvei</i>	4.34	0.57			
<i>Yersinia pseudotuberculosis</i>	3.62	0.33			
160013	Low discrimination				160013
<i>Yersinia kristensenii</i>	78.70	0.59	SOR 99		
<i>Shigella sonnei</i>	11.41	0.33			
<i>Citrobacter braakii</i>	4.97	0.45			
160023	Low discrimination				160023
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	44.25	0.49	SOR 99		
<i>Yersinia rohdei</i>	41.44	0.47			
<i>Shigella sonnei</i>	8.53	0.18			
160033	Low discrimination				160033
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	81.72	0.59	SOR 99		
<i>Yersinia rohdei</i>	8.50	0.37			
<i>Citrobacter farmeri</i>	2.43	0.15			
160041	Low discrimination				160041
<i>Citrobacter braakii</i>	50.19	0.38	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	24.81	0.29			
<i>Yersinia kristensenii</i>	16.32	0.18			
160042	Low discrimination				160042
<i>Citrobacter braakii</i>	50.97	0.38	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	25.19	0.29			
<i>Yersinia kristensenii</i>	16.57	0.18			
160043	Low discrimination				160043
<i>Citrobacter braakii</i>	58.52	0.80			
<i>Yersinia kristensenii</i>	19.02	0.59			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.32	0.64			
160051	Low discrimination				160051
<i>Yersinia kristensenii</i>	89.86	0.59	MAN 99		
<i>Citrobacter braakii</i>	5.67	0.45			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.14	0.39			
160052	Low discrimination				160052
<i>Yersinia kristensenii</i>	89.86	0.59	TRE 99		
<i>Citrobacter braakii</i>	5.67	0.45			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.14	0.39			
160053	Good identification				160053
<i>Yersinia kristensenii</i>	91.71	1.00			
<i>Citrobacter braakii</i>	5.79	0.86			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.09	0.74			
160061	Identification to the genus				160061
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	67.96	0.55	MAN 98		
<i>Yersinia rohdei</i>	31.50	0.47			
<i>Citrobacter braakii</i>	0.55	0.15			
160062	Identification to the genus				160062
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	67.96	0.55	TRE 98		
<i>Yersinia rohdei</i>	31.50	0.47			
<i>Citrobacter braakii</i>	0.55	0.15			
160063	Identification to the genus				160063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	51.00	0.90			
<i>Yersinia rohdei</i>	47.76	0.88			
<i>Citrobacter braakii</i>	0.83	0.56			
160071	Good identification				160071
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	92.10	0.65	MAN 98		
<i>Yersinia rohdei</i>	4.74	0.37			
<i>Citrobacter farmeri</i>	1.35	0.15			
160072	Good identification				160072
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	92.10	0.65	TRE 98		
<i>Yersinia rohdei</i>	4.74	0.37			
<i>Citrobacter farmeri</i>	1.35	0.15			
160073	Low discrimination				160073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	85.11	1.00			
<i>Yersinia rohdei</i>	8.86	0.78			
<i>Citrobacter farmeri</i>	2.53	0.56			
160103	Low discrimination				160103
<i>Hafnia alvei</i>	80.76	0.57	LYS 99		
<i>Shigella sonnei</i>	16.95	0.18			
<i>Citrobacter werkmanii</i>	1.12	-0.04			
160123	Low discrimination				160123
<i>Hafnia alvei</i>	83.91	0.38	LYS 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.31	0.08	SUC 10		
<i>Yersinia rohdei</i>	7.78	0.06			
160153	Low discrimination				160153
<i>Citrobacter sedlakii</i>	87.60	0.72			
<i>Yersinia kristensenii</i>	11.11	0.59			
<i>Citrobacter braakii</i>	0.70	0.45			
160163	Low discrimination				160163

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	48.92	0.49	MAL 1	2	
<i>Yersinia rohdei</i>	45.81	0.47		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.30	0.18		99	
160173	Low discrimination				160173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	53.24	0.59	SCI 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	34.32	0.59		2	
<i>Citrobacter sedlakii</i>	6.31	0.31		1	
160213	Acceptable identification				160213
<i>Yersinia kristensenii</i>	93.70	0.43	SOR 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.19	0.25			
<i>Shigella sonnei</i>	0.78	-0.09			
160223	Good identification				160223
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.84	0.42	SOR 99		
<i>Yersinia rohdei</i>	2.16	0.06			
160233	Good identification				160233
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.96	0.51	SOR 99	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.10	0.07		99	
<i>Yersinia kristensenii</i>	0.94	0.02		1	
160243	Low discrimination				160243
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	59.50	0.56	SUC 95		
<i>Yersinia kristensenii</i>	32.55	0.43			
<i>Citrobacter braakii</i>	5.73	0.38			
160251	Identification to the genus				160251
<i>Yersinia kristensenii</i>	89.65	0.43	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.03	0.31			
<i>Citrobacter braakii</i>	0.32	0.04			
160252	Identification to the genus				160252
<i>Yersinia kristensenii</i>	89.65	0.43	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.03	0.31			
<i>Citrobacter braakii</i>	0.32	0.04			
160253	Good identification				160253
<i>Yersinia kristensenii</i>	94.37	0.85			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.23	0.66			
<i>Citrobacter braakii</i>	0.34	0.45			
160261	Good identification				160261
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.92	0.48	MAN 98		
<i>Yersinia rohdei</i>	1.08	0.06			
160262	Good identification				160262
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.92	0.48	TRE 98		
<i>Yersinia rohdei</i>	1.08	0.06			
160263	Very good identification				160263

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.73	0.83			
<i>Yersinia rohdei</i>	2.16	0.47			
<i>Citrobacter youngae</i>	0.04	0.16			
160271	Very good identification				160271
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.53	0.58	MAN 98		
<i>Yersinia kristensenii</i>	0.47	0.02			
160272	Very good identification				160272
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.53	0.58	TRE 98		
<i>Yersinia kristensenii</i>	0.47	0.02			
160273	Very good identification				160273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.50	0.92			
<i>Yersinia kristensenii</i>	0.95	0.43			
<i>Yersinia rohdei</i>	0.24	0.37			
160353	Low discrimination				160353
<i>Yersinia kristensenii</i>	65.30	0.43	MAL 1		
<i>Citrobacter sedlakii</i>	29.49	0.31			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.62	0.25			
160363	Good identification				160363
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.02	0.42	MAL 1	2	
<i>Yersinia rohdei</i>	2.12	0.06		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.86	0.02		99	
160373	Low discrimination				160373
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	60.51	0.51	MAL 1	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	38.65	0.43		99	
<i>Yersinia kristensenii</i>	0.58	0.02		1	
160443	Low discrimination				160443
<i>Citrobacter braakii</i>	57.64	0.38	ADO 1		
<i>Yersinia kristensenii</i>	18.74	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.10	0.23			
160453	Good identification				160453
<i>Yersinia kristensenii</i>	90.33	0.59	ADO 1		
<i>Citrobacter braakii</i>	5.70	0.45			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.06	0.33			
160463	Identification to the genus				160463
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	51.08	0.49	ADO 1		
<i>Yersinia rohdei</i>	47.83	0.47			
<i>Citrobacter braakii</i>	0.83	0.15			
160473	Low discrimination				160473
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	74.14	0.59	ADO 1	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	12.78	0.39		99	
<i>Yersinia rohdei</i>	7.72	0.37		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
160573	Acceptable identification				160573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.65	0.49	SCI 99	99	
<i>Citrobacter koseri</i>	3.16	0.17		1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.85	0.18		2	
160653	Low discrimination				160653
<i>Yersinia kristensenii</i>	86.22	0.43	ADO 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	8.69	0.37			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.78	0.25			
160663	Good identification				160663
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.84	0.42	ADO 1		
<i>Yersinia rohdei</i>	2.16	0.06			
160673	Acceptable identification				160673
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	90.54	0.51	ADO 1	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	6.43	0.24		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.17	0.25		1	
161000	Very good identification				161000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.46	0.54	ONP 10		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.54	0.18	IND 95		
161001	Very good identification				161001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	95.33	0.59	ONP 1		
<i>Proteus mirabilis</i>	2.86	0.19			
<i>Morganella morganii</i> subsp. <i>morganii</i>	1.81	0.13			
161043	Low discrimination				161043
<i>Citrobacter braakii</i>	59.03	0.38	PHE 1		
<i>Yersinia kristensenii</i>	19.19	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.44	0.23			
161053	Good identification				161053
<i>Yersinia kristensenii</i>	91.78	0.59	PHE 1		
<i>Citrobacter braakii</i>	5.79	0.45			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.09	0.33			
161063	Identification to the genus				161063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	51.21	0.49	PHE 1		
<i>Yersinia rohdei</i>	47.96	0.47			
<i>Citrobacter braakii</i>	0.83	0.15			
161073	Low discrimination				161073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	85.24	0.59	PHE 1		
<i>Yersinia rohdei</i>	8.87	0.37			
<i>Citrobacter farmeri</i>	2.53	0.15			
161253	Acceptable identification				161253
<i>Yersinia kristensenii</i>	94.43	0.43	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.23	0.25			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	0.34	0.04			
161263	Good identification				161263
<i>Yersinia enterocolitica ssp. enterocolitica</i>	97.84	0.42	PHE 1		
<i>Yersinia rohdei</i>	2.16	0.06			
161273	Good identification				161273
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.05	0.51	PHE 1		
<i>Yersinia kristensenii</i>	0.95	0.02			
162003	Very good identification				162003
<i>Yersinia pseudotuberculosis</i>	97.90	0.59	ORN 1		
<i>Shigella sonnei</i>	1.30	0.18			
<i>Hafnia alvei</i>	0.69	0.38			
162023	Identification to the genus				162023
<i>Yersinia enterocolitica ssp. enterocolitica</i>	66.55	0.39	SOR 99		
<i>Yersinia pseudotuberculosis</i>	29.30	0.18			
<i>Hafnia alvei</i>	2.26	0.18			
162033	Acceptable identification				162033
				VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	91.51	0.49	SOR 99	2	
<i>Escherichia hermannii</i>	3.49	0.12		1	
<i>Enterobacter cloacae subsp. cloacae</i>	3.20	0.15		99	
162043	Low discrimination				162043
<i>Yersinia enterocolitica ssp. enterocolitica</i>	76.66	0.54	SUC 95		
<i>Citrobacter braakii</i>	9.50	0.38			
<i>Yersinia pseudotuberculosis</i>	6.48	0.18			
162053	Low discrimination				162053
<i>Yersinia kristensenii</i>	53.82	0.59	ESL 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	40.51	0.64			
<i>Citrobacter braakii</i>	3.40	0.45			
162061	Good identification				162061
<i>Yersinia enterocolitica ssp. enterocolitica</i>	98.62	0.46	MAN 98		
<i>Yersinia rohdei</i>	1.39	0.06			
162062	Good identification				162062
<i>Yersinia enterocolitica ssp. enterocolitica</i>	98.62	0.46	TRE 98		
<i>Yersinia rohdei</i>	1.39	0.06			
162063	Very good identification				162063
<i>Yersinia enterocolitica ssp. enterocolitica</i>	97.07	0.80			
<i>Yersinia rohdei</i>	2.76	0.47			
<i>Citrobacter youngae</i>	0.06	0.16			
162071	Very good identification				162071
				VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.67	0.55	MAN 98	2	
<i>Enterobacter cloacae subsp. cloacae</i>	0.33	0.00		99	
162072	Very good identification				162072

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.67	0.55	TRE 98	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.33	0.00		99	
162073	Very good identification				162073
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.81	0.90		2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.66	0.42		99	
<i>Yersinia rohdei</i>	0.31	0.37		1	
162153	Very good identification				162153
				VPT	
<i>Citrobacter sedlakii</i>	98.34	0.58		1	
<i>Yersinia kristensenii</i>	0.62	0.18		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.54	0.20		99	
162163	Acceptable identification				162163
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	91.84	0.39	MAL 1	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.55	0.10		99	
<i>Yersinia rohdei</i>	2.61	0.06		1	
162173	Low discrimination				162173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	64.19	0.51	SCI 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	32.18	0.49		2	
<i>Citrobacter sedlakii</i>	3.64	0.16		1	
162233	Low discrimination				162233
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	86.80	0.42	SOR 99	2	
<i>Cronobacter sakazakii</i>	11.96	0.18		99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.25	0.00		99	
162243	Good identification				162243
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.89	0.47	SUC 95		
<i>Yersinia kristensenii</i>	1.62	0.02			
<i>Citrobacter youngae</i>	0.48	0.01			
162253	Identification to the genus				162253
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	64.27	0.56	SUC 95		
<i>Yersinia kristensenii</i>	35.16	0.43			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.44	0.18			
162261	Good identification				162261
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.38	MAN 98		
162262	Good identification				162262
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.38	TRE 98		
162263	Very good identification				162263
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.74	0.73		2	
<i>Serratia marcescens</i>	0.19	0.09		98	
<i>Yersinia rohdei</i>	0.07	0.06		1	
162271	Good identification				162271
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.48	MAN 98		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
162272	Good identification				162272
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.48	TRE 98		
162273	Very good identification				162273
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.69	0.83		2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.28	0.26		99	
<i>Yersinia kristensenii</i>	0.03	0.02		1	
162373	Low discrimination				162373
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	54.91	0.42	MAL 1	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	45.10	0.36		99	
162413	Good identification				162413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.03	0.42	ORN 3		
<i>Escherichia fergusonii</i>	1.97	-0.04	URE 10		
162453	Low discrimination				162453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.07	0.48	ORN 3		
<i>Yersinia kristensenii</i>	13.03	0.18	URE 10		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.80	0.23			
162463	Acceptable identification				162463
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	93.22	0.39	ADO 1		
<i>Yersinia rohdei</i>	2.65	0.06			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.45	0.13			
162473	Low discrimination				162473
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	75.62	0.49	ADO 1	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	16.76	0.32		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	7.62	0.35		1	
162573	Good identification				162573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	98.50	0.42	SCI 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.50	0.08		2	
162613	Good identification				162613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.44	ORN 3		
162653	Acceptable identification				162653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.38	0.49	ORN 3		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.28	0.15	URE 10		
<i>Yersinia kristensenii</i>	2.34	0.02			
162673	Low discrimination				162673
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	72.54	0.42	ADO 1	2	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	20.84	0.37		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	6.62	0.16		99	
163063	Good identification				163063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.24	0.39	PHE 1		
<i>Yersinia rohdei</i>	2.76	0.06			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
163073	Good identification				163073
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.33	0.49	PHE 1	2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.67	0.00		99	
163273	Good identification				163273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.42	PHE 1		
164003	Low discrimination				164003
<i>Hafnia alvei</i>	50.33	0.57	LYS 99		
<i>Citrobacter braakii</i>	35.39	0.48			
<i>Shigella sonnei</i>	10.57	0.18			
164013	Low discrimination				164013
				VPT	
<i>Citrobacter braakii</i>	46.17	0.55	SOR 99	1	
<i>Citrobacter amalonaticus</i>	31.98	0.34		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	8.81	0.33		99	
164023	Low discrimination				164023
				VPT	
<i>Hafnia alvei</i>	37.57	0.38	LYS 99	85	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	30.08	0.23	SUC 10	99	
<i>Citrobacter braakii</i>	17.90	0.25		1	
164033	Very good identification				164033
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.00	0.64	SOR 95	99	
<i>Citrobacter braakii</i>	1.18	0.31		1	
<i>Citrobacter amalonaticus</i>	0.70	0.10		1	
164041	Acceptable identification				164041
<i>Citrobacter braakii</i>	93.18	0.48	MAN 99		
<i>Citrobacter youngae</i>	5.50	0.22			
<i>Citrobacter amalonaticus</i>	1.32	-0.07			
164042	Acceptable identification				164042
<i>Citrobacter braakii</i>	93.18	0.48	TRE 99		
<i>Citrobacter youngae</i>	5.50	0.22			
<i>Citrobacter amalonaticus</i>	1.32	-0.07			
164043	Good identification				164043
<i>Citrobacter braakii</i>	92.57	0.89			
<i>Citrobacter youngae</i>	5.46	0.63			
<i>Citrobacter amalonaticus</i>	1.32	0.34			
164051	Low discrimination				164051
<i>Citrobacter braakii</i>	54.73	0.55	MAN 99		
<i>Citrobacter amalonaticus</i>	37.91	0.34			
<i>Yersinia kristensenii</i>	2.92	0.18			
164052	Low discrimination				164052
<i>Citrobacter braakii</i>	54.73	0.55	TRE 99		
<i>Citrobacter amalonaticus</i>	37.91	0.34			
<i>Yersinia kristensenii</i>	2.92	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
164053	Low discrimination				164053
<i>Citrobacter braakii</i>	54.66	0.96			
<i>Citrobacter amalonaticus</i>	37.86	0.75			
<i>Yersinia kristensenii</i>	2.92	0.59			
164063	Low discrimination				164063
				VPT	
<i>Citrobacter braakii</i>	46.54	0.66	SUC 7	1	
<i>Enterobacter cloacae subsp. cloacae</i>	15.01	0.49		99	
<i>Citrobacter youngae</i>	9.70	0.52		1	
164071	Low discrimination				164071
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	86.44	0.49	MAN 99	99	
<i>Citrobacter braakii</i>	5.50	0.31		1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	3.41	0.24		2	
164072	Low discrimination				164072
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	86.44	0.49	TRE 99	99	
<i>Citrobacter braakii</i>	5.50	0.31		1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	3.41	0.24		2	
164073	Low discrimination				164073
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	87.74	0.90		99	
<i>Citrobacter braakii</i>	5.58	0.73		1	
<i>Citrobacter amalonaticus</i>	3.28	0.51		1	
164103	Low discrimination				164103
<i>Hafnia alvei</i>	83.04	0.57	LYS 99		
<i>Citrobacter werkmanii</i>	13.23	0.17			
<i>Citrobacter sedlakii</i>	2.46	0.04			
164113	Low discrimination				164113
				VPT	
<i>Citrobacter sedlakii</i>	73.76	0.45	SOR 99	1	
<i>Enterobacter cloacae subsp. cloacae</i>	20.54	0.43		99	
<i>Hafnia alvei</i>	4.44	0.42		85	
164133	Very good identification				164133
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	99.71	0.74	SOR 95	99	
<i>Citrobacter sedlakii</i>	0.11	0.04		1	
<i>Citrobacter koseri</i>	0.09	0.09		1	
164143	Low discrimination				164143
<i>Citrobacter sedlakii</i>	53.35	0.45	CEL 99		
<i>Citrobacter werkmanii</i>	26.06	0.37			
<i>Citrobacter braakii</i>	12.78	0.48			
164151	Acceptable identification				164151
				VPT	
<i>Citrobacter sedlakii</i>	94.06	0.45	MAN 99	1	
<i>Enterobacter cloacae subsp. cloacae</i>	5.03	0.28		99	
<i>Citrobacter braakii</i>	0.46	0.14		1	
164152	Acceptable identification				164152
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter sedlakii</i>	94.06	0.45	TRE 99	1	164153
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.03	0.28		99	
<i>Citrobacter braakii</i>	0.46	0.14		1	
164153	Good identification				164153
				VPT	
<i>Citrobacter sedlakii</i>	93.98	0.86		1	164163
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.02	0.69		99	
<i>Citrobacter braakii</i>	0.46	0.55		1	
164163	Good identification				164163
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.63	0.59	CEL 99	99	164171
<i>Citrobacter freundii</i>	1.67	0.32		1	
<i>Citrobacter youngae</i>	1.07	0.25		1	
164171	Very good identification				164171
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.42	0.59	MAN 99	99	164172
<i>Citrobacter sedlakii</i>	0.58	0.04		1	
164172	Very good identification				164172
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.42	0.59	TRE 99	99	164173
<i>Citrobacter sedlakii</i>	0.58	0.04		1	
164173	Excellent identification				164173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.28	1.00		99	164233
<i>Citrobacter sedlakii</i>	0.58	0.45		1	
<i>Citrobacter koseri</i>	0.07	0.33		1	
164233	Good identification				164233
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.19	0.48	SOR 95	99	164243
<i>Cronobacter sakazakii</i>	3.94	0.18		99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.87	0.10		2	
164243	Low discrimination				164243
<i>Citrobacter braakii</i>	72.00	0.48	INO 1		164253
<i>Citrobacter youngae</i>	22.14	0.37			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.52	0.15			
164253	Low discrimination				164253
<i>Citrobacter braakii</i>	28.89	0.55	INO 1		164263
<i>Yersinia kristensenii</i>	26.94	0.43			
<i>Citrobacter amalonaticus</i>	20.01	0.34			
164263	Low discrimination				164263
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	48.01	0.42	SCI 1	2	164273
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	30.67	0.34		99	
<i>Serratia marcescens</i>	7.84	0.17		98	
164273	Good identification				164273
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.66	0.75		99	164333
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.49	0.51		2	
<i>Citrobacter braakii</i>	0.34	0.31		1	
164333	Very good identification				164333

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.70	0.58	SOR 95		
<i>Cronobacter sakazakii</i>	0.30	0.04			
164353	Low discrimination				164353
				VPT	
<i>Citrobacter sedlakii</i>	51.25	0.45	INO 1	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	47.85	0.53		99	
<i>Citrobacter braakii</i>	0.25	0.14		1	
164363	Good identification				164363
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.48	0.43	CEL 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.52	0.00		2	
164371	Good identification				164371
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.43	MAN 99		
164372	Good identification				164372
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.43	TRE 99		
164373	Very good identification				164373
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.95	0.85		99	
<i>Citrobacter sedlakii</i>	0.03	0.04		1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.02	0.10		2	
164433	Very good identification				164433
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.02	0.54	SOR 95	99	
<i>Citrobacter koseri</i>	0.77	0.09		1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.21	0.10		1	
164443	Identification to the genus				164443
<i>Citrobacter braakii</i>	87.69	0.48	ADO 1		
<i>Citrobacter youngae</i>	5.17	0.22			
<i>Citrobacter koseri</i>	3.20	0.10			
164453	Low discrimination				164453
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	36.46	0.49	SUC 97	99	
<i>Citrobacter braakii</i>	30.18	0.55		1	
<i>Citrobacter amalonaticus</i>	20.90	0.34		1	
164463	Low discrimination				164463
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	80.63	0.39	CEL 99	99	
<i>Citrobacter braakii</i>	7.57	0.25		1	
<i>Citrobacter koseri</i>	3.26	0.09		1	
164471	Good identification				164471
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.39	MAN 99		
164472	Good identification				164472
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.39	TRE 99		
164473	Very good identification				164473
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	98.94	0.80		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter koseri</i>	0.63	0.33		1	
<i>Citrobacter braakii</i>	0.19	0.31		1	
164533	Very good identification				164533
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.01	0.64	SOR 95	99	
<i>Citrobacter koseri</i>	3.89	0.33		1	
<i>Serratia rubidaea</i>	0.10	-0.2		99	
164553	Low discrimination				164553
				VPT	
<i>Citrobacter koseri</i>	43.67	0.59	IND 99	1	
<i>Enterobacter cloacae subsp. cloacae</i>	35.84	0.59		99	
<i>Citrobacter sedlakii</i>	20.32	0.45		1	
164563	Low discrimination				164563
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	82.57	0.49	CEL 99	99	
<i>Citrobacter koseri</i>	17.43	0.33		1	
164571	Good identification				164571
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.77	0.49	MAN 99	99	
<i>Citrobacter koseri</i>	3.23	0.17		1	
164572	Good identification				164572
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.77	0.49	TRE 99	99	
<i>Citrobacter koseri</i>	3.23	0.17		1	
164573	Very good identification				164573
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.75	0.90		99	
<i>Citrobacter koseri</i>	3.23	0.58		1	
<i>Citrobacter sedlakii</i>	0.02	0.04		1	
164633	Good identification				164633
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	98.53	0.39	SOR 95	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.47	0.11		1	
164673	Very good identification				164673
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	99.58	0.65		99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.15	0.17		1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.14	0.10		2	
164733	Good identification				164733
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.48	SOR 95		
164753	Acceptable identification				164753
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	90.73	0.44	SUC 97	99	
<i>Citrobacter koseri</i>	6.33	0.18		1	
<i>Citrobacter sedlakii</i>	2.95	0.04		1	
164773	Very good identification				164773
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	99.75	0.75		99	
<i>Citrobacter koseri</i>	0.19	0.17		1	
<i>Enterobacter aerogenes</i>	0.06	-0.4		98	
165043	Acceptable identification				165043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	93.18	0.48	PHE 1		
<i>Citrobacter youngae</i>	5.50	0.22			
<i>Citrobacter amalonaticus</i>	1.32	-0.07			
165053	Low discrimination				165053
<i>Citrobacter braakii</i>	54.73	0.55	PHE 1		
<i>Citrobacter amalonaticus</i>	37.91	0.34			
<i>Yersinia kristensenii</i>	2.92	0.18			
165073	Low discrimination				165073
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	87.95	0.49	PHE 1	99	
<i>Citrobacter braakii</i>	5.59	0.31		1	
<i>Citrobacter amalonaticus</i>	3.29	0.10		1	
165153	Acceptable identification				165153
				VPT	
<i>Citrobacter sedlakii</i>	94.06	0.45	PHE 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	5.03	0.28		99	
<i>Citrobacter braakii</i>	0.46	0.14		1	
165173	Very good identification				165173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	99.42	0.59	PHE 1	99	
<i>Citrobacter sedlakii</i>	0.58	0.04		1	
165373	Good identification				165373
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.43	PHE 1		
165473	Good identification				165473
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.39	PHE 1		
165573	Good identification				165573
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.77	0.49	PHE 1	99	
<i>Citrobacter koseri</i>	3.23	0.17		1	
166033	Low discrimination				166033
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	63.82	0.56	SOR 95	99	
<i>Cronobacter sakazakii</i>	35.89	0.49		99	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.19	0.08		2	
166043	Identification to the genus				166043
<i>Citrobacter braakii</i>	65.74	0.48	ESL 1		
<i>Citrobacter youngae</i>	20.21	0.37			
<i>Citrobacter amalonaticus</i>	9.14	0.14			
166053	Low discrimination				166053
				VPT	
<i>Citrobacter amalonaticus</i>	67.97	0.55	IND 94	1	
<i>Enterobacter cloacae subsp. cloacae</i>	15.57	0.52	ESL 9	99	
<i>Citrobacter braakii</i>	10.02	0.55		1	
166063	Low discrimination				166063
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	42.41	0.42	CEL 99	99	
<i>Serratia marcescens</i>	28.29	0.34		98	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	21.26	0.39		2	
166071	Good identification				166071
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	96.22	0.42	MAN 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.95	0.14		2	
<i>Citrobacter amalonaticus</i>	0.83	-.11		1	
166072	Good identification				166072
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	96.22	0.42	TRE 99	99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.95	0.14		2	
<i>Citrobacter amalonaticus</i>	0.83	-.11		1	
166073	Very good identification				166073
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.23	0.83		99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.48	0.49		2	
<i>Citrobacter amalonaticus</i>	0.84	0.30		1	
166103	Acceptable identification				166103
<i>Hafnia alvei</i>	94.82	0.38	LYS 99		
<i>Citrobacter sedlakii</i>	5.18	-.11	ESL 10		
166133	Very good identification				166133
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.08	0.66	SOR 95		
<i>Cronobacter sakazakii</i>	3.91	0.36			
<i>Pantoea agglomerans</i>	0.68	0.16			
166153	Low discrimination				166153
				VPT	
<i>Citrobacter sedlakii</i>	89.77	0.72		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	10.04	0.61		99	
<i>Citrobacter amalonaticus</i>	0.15	0.14		1	
166163	Good identification				166163
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.04	0.51	CEL 99	99	
<i>Serratia marcescens</i>	0.68	0.03		98	
<i>Citrobacter sedlakii</i>	0.28	-.11		1	
166171	Good identification				166171
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.72	0.51	MAN 99	99	
<i>Citrobacter sedlakii</i>	0.28	-.11		1	
166172	Good identification				166172
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.72	0.51	TRE 99	99	
<i>Citrobacter sedlakii</i>	0.28	-.11		1	
166173	Very good identification				166173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.70	0.92		99	
<i>Citrobacter sedlakii</i>	0.28	0.31		1	
<i>Kluyvera ascorbata</i>	0.01	0.02		1	
166233	Good identification				166233
				VPT	
<i>Cronobacter sakazakii</i>	90.47	0.59	URE 1	99	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	9.46	0.41		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.07	0.00		2	
166253	Low discrimination				166253
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	69.38	0.36	SUC 97	99	
<i>Citrobacter amalonaticus</i>	17.34	0.14		1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.36	0.15		2	
166263	Low discrimination				166263
				VPT	
<i>Serratia marcescens</i>	83.64	0.43	LYS 99	98	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.98	0.32		2	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	7.38	0.26		99	
166273	Good identification				166273
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	92.74	0.67		99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.42	0.42		2	
<i>Serratia odorifera</i> biovar 1	1.76	0.29		50	
166333	Low discrimination				166333
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	58.84	0.51	SOR 95		
<i>Cronobacter sakazakii</i>	41.16	0.45			
166353	Low discrimination				166353
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	66.14	0.46	SUC 97	99	
<i>Citrobacter sedlakii</i>	33.86	0.31		1	
166363	Low discrimination				166363
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	89.53	0.36	CEL 99		
<i>Serratia marcescens</i>	10.47	0.12			
166371	Good identification				166371
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.36	MAN 99		
166372	Good identification				166372
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.36	TRE 99		
166373	Very good identification				166373
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.78	0.77			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.11	0.05			
<i>Cronobacter sakazakii</i>	0.04	0.04			
166433	Good identification				166433
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.72	0.47	SOR 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.93	0.22		1	
<i>Cronobacter sakazakii</i>	1.63	0.08		99	
166453	Low discrimination				166453
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	70.42	0.42	SUC 97	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	17.92	0.40		1	
<i>Citrobacter amalonaticus</i>	9.32	0.14		1	
166473	Very good identification				166473
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.66	0.73		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.20	0.28		1	
<i>Serratia marcescens</i>	0.07	0.04		98	
166533	Very good identification				166533
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	96.11	0.56	SOR 95		
<i>Serratia rubidaea</i>	3.77	0.22			
<i>Cronobacter sakazakii</i>	0.12	-0.06			
166553	Low discrimination				166553
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	76.79	0.52	SUC 97	99	
<i>Citrobacter sedlakii</i>	20.81	0.31		1	
<i>Citrobacter koseri</i>	2.21	0.18		1	
166563	Good identification				166563
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	98.64	0.42	CEL 99		
<i>Serratia marcescens</i>	1.36	-0.01			
166571	Good identification				166571
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.42	MAN 99		
166572	Good identification				166572
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.42	TRE 99		
166573	Very good identification				166573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.82	0.83		99	
<i>Citrobacter koseri</i>	0.08	0.17		1	
<i>Enterobacter aerogenes</i>	0.06	0.04		98	
166613	Acceptable identification				166613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.75	0.36	ORN 3	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.25	0.00	URE 10	99	
166653	Low discrimination				166653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	63.81	0.42	ORN 3	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	36.20	0.26	URE 10	99	
166663	Good identification				166663
				VPT	
<i>Serratia marcescens</i>	95.30	0.40	LYS 99	98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	4.20	0.16		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.49	0.08		1	
166673	Good identification				166673
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	90.82	0.57		99	
<i>Serratia odorifera</i> biovar 1	5.18	0.29		50	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.24	0.29		1	
166733	Acceptable identification				166733
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	91.78	0.41	SOR 95		
<i>Serratia rubidaea</i>	5.11	0.10			
<i>Cronobacter sakazakii</i>	1.95	0.04			
166753	Acceptable identification				166753
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.75	0.36	SUC 97	99	
<i>Enterobacter aerogenes</i>	2.06	-.11		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.72	0.11		1	
166773	Good identification				166773
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	91.21	0.67			
<i>Enterobacter aerogenes</i>	6.07	0.30			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2.73	0.24			
167033	Good identification				167033
<i>Cronobacter sakazakii</i>	98.24	0.49	URE 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.77	0.15			
167073	Acceptable identification				167073
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.93	0.42	PHE 1	99	
<i>Cronobacter sakazakii</i>	2.81	0.08		99	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.44	0.08		2	
167133	Low discrimination				167133
<i>Cronobacter sakazakii</i>	79.19	0.36	URE 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	19.44	0.25			
<i>Pantoea agglomerans</i>	1.36	-.05			
167173	Good identification				167173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	99.51	0.51	PHE 1	99	
<i>Citrobacter sedlakii</i>	0.28	-.11		1	
<i>Cronobacter sakazakii</i>	0.22	-.06		99	
167233	Very good identification				167233
<i>Cronobacter sakazakii</i>	99.89	0.59	URE 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.11	0.00			
167333	Good identification				167333
<i>Cronobacter sakazakii</i>	98.58	0.45	URE 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.42	0.10			
167373	Good identification				167373
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	96.45	0.36	PHE 1		
<i>Cronobacter sakazakii</i>	3.55	0.04			
167573	Good identification				167573
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.42	PHE 1		
170000	Very good identification				170000
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.54	ONP 10		
170001	Low discrimination				170001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	75.37	0.36	ONP 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	18.97	0.13	PHE 93		
<i>Shigella dysenteriae</i> (group A)	4.61	0.09			
170013	Low discrimination				170013

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	65.60	0.59	URE 1		
<i>Yersinia kristensenii</i>	28.13	0.51			
<i>Citrobacter braakii</i>	2.04	0.38			
170023	Low discrimination				170023
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	74.67	0.49	SOR 99		
<i>Escherichia hermannii</i>	13.07	0.26			
<i>Citrobacter farmeri</i>	6.65	0.15			
170033	Low discrimination				170033
<i>Citrobacter farmeri</i>	50.27	0.56	SOR 99		
<i>Escherichia hermannii</i>	32.30	0.57			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	17.12	0.59			
170043	Low discrimination				170043
<i>Citrobacter braakii</i>	52.92	0.73			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	26.28	0.64			
<i>Yersinia kristensenii</i>	14.97	0.51			
170051	Low discrimination				170051
<i>Yersinia kristensenii</i>	78.89	0.51	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.48	0.39			
<i>Citrobacter braakii</i>	5.72	0.38			
170052	Low discrimination				170052
<i>Yersinia kristensenii</i>	78.89	0.51	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.48	0.39			
<i>Citrobacter braakii</i>	5.72	0.38			
170053	Low discrimination				170053
<i>Yersinia kristensenii</i>	82.35	0.92			
<i>Citrobacter braakii</i>	5.97	0.80			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.38	0.74			
170061	Good identification				170061
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	94.01	0.55	MAN 98		
<i>Citrobacter farmeri</i>	4.14	0.15			
<i>Escherichia coli</i>	1.04	0.17			
170062	Good identification				170062
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	94.01	0.55	TRE 98		
<i>Citrobacter farmeri</i>	4.14	0.15			
<i>Escherichia coli</i>	1.04	0.17			
170063	Low discrimination				170063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	89.86	0.90			
<i>Citrobacter farmeri</i>	8.00	0.56			
<i>Yersinia rohdei</i>	0.85	0.47			
170071	Low discrimination				170071
<i>Citrobacter farmeri</i>	59.03	0.56	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	40.60	0.65			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia kristensenii</i>	0.20	0.10			
170072	Low discrimination				170072
<i>Citrobacter farmeri</i>	59.03	0.56	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	40.60	0.65			
<i>Yersinia kristensenii</i>	0.20	0.10			
170073	Low discrimination				170073
<i>Citrobacter farmeri</i>	74.22	0.98			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	25.27	1.00			
<i>Yersinia kristensenii</i>	0.25	0.51			
170113	Good identification				170113
<i>Citrobacter sedlakii</i>	95.27	0.45	SOR 99		
<i>Escherichia hermannii</i>	2.47	0.18			
<i>Yersinia kristensenii</i>	1.06	0.10			
170143	Acceptable identification				170143
<i>Citrobacter sedlakii</i>	92.11	0.45	CEL 99		
<i>Citrobacter braakii</i>	3.62	0.32			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.80	0.23			
170151	Good identification				170151
<i>Citrobacter sedlakii</i>	98.76	0.45	MAN 99		
<i>Yersinia kristensenii</i>	1.10	0.10			
<i>Citrobacter koseri</i>	0.14	-.07			
170152	Good identification				170152
<i>Citrobacter sedlakii</i>	98.76	0.45	TRE 99		
<i>Yersinia kristensenii</i>	1.10	0.10			
<i>Citrobacter koseri</i>	0.14	-.07			
170153	Very good identification				170153
<i>Citrobacter sedlakii</i>	98.54	0.86			
<i>Yersinia kristensenii</i>	1.10	0.51			
<i>Citrobacter koseri</i>	0.14	0.34			
170163	Low discrimination				170163
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	85.55	0.49	MAL 1		
<i>Citrobacter farmeri</i>	7.61	0.15			
<i>Citrobacter sedlakii</i>	2.33	0.04			
170173	Low discrimination				170173
<i>Citrobacter farmeri</i>	58.97	0.56	MAL 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.08	0.59			
<i>Citrobacter sedlakii</i>	18.03	0.45			
170213	Low discrimination				170213
<i>Yersinia kristensenii</i>	79.19	0.36	SOR 99		
<i>Escherichia hermannii</i>	10.57	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	10.24	0.25			
170223	Good identification				170223

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.42	SOR 99		
170233	Low discrimination				170233
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	89.46	0.51	SOR 99		
<i>Citrobacter farmeri</i>	6.19	0.15			
<i>Escherichia hermannii</i>	3.98	0.16			
170243	Identification to the genus				170243
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	77.50	0.56	SUC 95		
<i>Yersinia kristensenii</i>	18.17	0.36			
<i>Citrobacter braakii</i>	3.68	0.32			
170251	Identification to the genus				170251
<i>Yersinia kristensenii</i>	79.30	0.36	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.71	0.31			
170252	Identification to the genus				170252
<i>Yersinia kristensenii</i>	79.30	0.36	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	20.71	0.31			
170253	Identification to the genus				170253
<i>Yersinia kristensenii</i>	87.83	0.77			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.35	0.66			
<i>Citrobacter braakii</i>	0.37	0.38			
170261	Good identification				170261
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.48	MAN 98		
170262	Good identification				170262
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.48	TRE 98		
170263	Very good identification				170263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.73	0.83			
<i>Citrobacter farmeri</i>	0.21	0.15			
<i>Citrobacter braakii</i>	0.02	0.09			
170271	Very good identification				170271
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.50	0.58	MAN 98		
<i>Citrobacter farmeri</i>	3.31	0.15			
<i>Yersinia kristensenii</i>	0.20	-.05			
170272	Very good identification				170272
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.50	0.58	TRE 98		
<i>Citrobacter farmeri</i>	3.31	0.15			
<i>Yersinia kristensenii</i>	0.20	-.05			
170273	Good identification				170273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	93.15	0.92			
<i>Citrobacter farmeri</i>	6.45	0.56			
<i>Yersinia kristensenii</i>	0.38	0.36			
170353	Low discrimination				170353

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter sedlakii</i>	81.91	0.45	INO 1		
<i>Yersinia kristensenii</i>	15.92	0.36			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.06	0.25			
170363	Good identification				170363
<i>Yersinia enterocolitica ssp. enterocolitica</i>	100.0	0.42	MAL 1		
170373	Acceptable identification				170373
<i>Yersinia enterocolitica ssp. enterocolitica</i>	90.83	0.51	MAL 1		
<i>Citrobacter farmeri</i>	6.29	0.15			
<i>Citrobacter sedlakii</i>	1.92	0.04			
170453	Low discrimination				170453
<i>Yersinia kristensenii</i>	74.75	0.51	ADO 1		
<i>Citrobacter koseri</i>	9.31	0.34			
<i>Citrobacter braakii</i>	5.42	0.38			
170463	Low discrimination				170463
<i>Yersinia enterocolitica ssp. enterocolitica</i>	86.99	0.49	ADO 1		
<i>Citrobacter farmeri</i>	7.74	0.15			
<i>Escherichia coli</i>	1.94	0.17			
170473	Low discrimination				170473
<i>Citrobacter farmeri</i>	72.23	0.56	ADO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	24.59	0.59			
<i>Citrobacter koseri</i>	2.69	0.33			
170553	Identification to the genus				170553
<i>Citrobacter koseri</i>	68.00	0.59	SCI 99		
<i>Citrobacter sedlakii</i>	31.65	0.45			
<i>Yersinia kristensenii</i>	0.35	0.10			
170573	Very good identification				170573
<i>Citrobacter koseri</i>	96.94	0.58	SCI 99		
<i>Citrobacter farmeri</i>	1.68	0.15			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.57	0.18			
170653	Identification to the genus				170653
<i>Yersinia kristensenii</i>	88.00	0.36	ADO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	11.37	0.25			
<i>Citrobacter koseri</i>	0.63	-0.07			
170663	Good identification				170663
<i>Yersinia enterocolitica ssp. enterocolitica</i>	100.0	0.42	ADO 1		
170673	Acceptable identification				170673
<i>Yersinia enterocolitica ssp. enterocolitica</i>	93.17	0.51	ADO 1		
<i>Citrobacter farmeri</i>	6.45	0.15			
<i>Yersinia kristensenii</i>	0.38	-0.05			
171000	Very good identification				171000

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.97	0.80	ONP 10		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.03	0.18			
171001	Identification to the genus				171001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	73.53	0.59	ONP 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	26.47	0.39			
171002	Good identification				171002
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
171010	Good identification				171010
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
171020	Good identification				171020
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
171040	Good identification				171040
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
171053	Low discrimination				171053
<i>Yersinia kristensenii</i>	82.42	0.51	PHE 1		
<i>Citrobacter braakii</i>	5.98	0.38			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.39	0.33			
171063	Acceptable identification				171063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	90.03	0.49	PHE 1		
<i>Citrobacter farmeri</i>	8.01	0.15			
<i>Yersinia rohdei</i>	0.85	0.06			
171073	Low discrimination				171073
<i>Citrobacter farmeri</i>	74.25	0.56	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	25.28	0.59			
<i>Yersinia kristensenii</i>	0.25	0.10			
171100	Good identification				171100
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
171153	Good identification				171153
<i>Citrobacter sedlakii</i>	98.76	0.45	PHE 1		
<i>Yersinia kristensenii</i>	1.10	0.10			
<i>Citrobacter koseri</i>	0.14	-.07			
171200	Good identification				171200
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
171253	Identification to the genus				171253
<i>Yersinia kristensenii</i>	88.56	0.36	PHE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.44	0.25			
171263	Good identification				171263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.42	PHE 1		
171273	Acceptable identification				171273

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica ssp. enterocolitica</i>	93.17	0.51	PHE 1		
<i>Citrobacter farmeri</i>	6.45	0.15			
<i>Yersinia kristensenii</i>	0.38	-0.05			
171400	Good identification				171400
<i>Morganella morganii subsp. morganii</i>	100.0	0.39	ONP 10		
172013	Very good identification				172013
<i>Escherichia hermannii</i>	97.10	0.55	URE 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.11	0.23			
<i>Yersinia kristensenii</i>	0.63	0.10			
172023	Low discrimination				172023
<i>Yersinia enterocolitica ssp. enterocolitica</i>	71.76	0.39	SOR 99		
<i>Escherichia hermannii</i>	25.13	0.22			
<i>Escherichia coli</i>	3.11	0.13			
172033	Low discrimination				172033
<i>Escherichia hermannii</i>	77.01	0.54	URE 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	20.41	0.49			
<i>Citrobacter farmeri</i>	1.82	0.15			
172043	Low discrimination				172043
<i>Yersinia enterocolitica ssp. enterocolitica</i>	84.17	0.54	SUC 95		
<i>Escherichia coli</i>	7.69	0.34			
<i>Citrobacter braakii</i>	5.14	0.32			
172053	Low discrimination				172053
<i>Yersinia enterocolitica ssp. enterocolitica</i>	49.64	0.64	SUC 95		
<i>Yersinia kristensenii</i>	28.27	0.51			
<i>Citrobacter amalonaticus</i>	13.40	0.38			
172061	Good identification				172061
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.18	0.46	MAN 98		
<i>Escherichia coli</i>	0.82	0.04			
172062	Good identification				172062
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.18	0.46	TRE 98		
<i>Escherichia coli</i>	0.82	0.04			
172063	Very good identification				172063
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.36	0.80			
<i>Escherichia coli</i>	0.32	0.31			
<i>Citrobacter farmeri</i>	0.27	0.15			
172071	Very good identification				172071
<i>Yersinia enterocolitica ssp. enterocolitica</i>	95.78	0.55	MAN 98		
<i>Citrobacter farmeri</i>	4.22	0.15			
172072	Very good identification				172072
<i>Yersinia enterocolitica ssp. enterocolitica</i>	95.78	0.55	TRE 98		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter farmeri</i>	4.22	0.15			
172073	Good identification				172073
<i>Yersinia enterocolitica ssp. enterocolitica</i>	91.67	0.90			
<i>Citrobacter farmeri</i>	8.16	0.56			
<i>Citrobacter amalonaticus</i>	0.08	0.14			
172133	Low discrimination				172133
<i>Leclercia adecarboxylata</i>	87.92	0.36	ORN 1		
<i>Escherichia hermannii</i>	6.72	0.12	ADO 93		
<i>Kluyvera ascorbata</i>	2.60	-0.01			
172153	Very good identification				172153
<i>Citrobacter sedlakii</i>	99.82	0.72			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.10	0.23			
<i>Yersinia kristensenii</i>	0.06	0.10			
172163	Good identification				172163
<i>Yersinia enterocolitica ssp. enterocolitica</i>	98.36	0.39	MAL 1		
<i>Citrobacter sedlakii</i>	1.64	-0.11			
172173	Low discrimination				172173
<i>Yersinia enterocolitica ssp. enterocolitica</i>	59.68	0.49	MAL 1		
<i>Citrobacter sedlakii</i>	32.92	0.31			
<i>Citrobacter farmeri</i>	5.31	0.15			
172233	Acceptable identification				172233
				VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	90.42	0.42	SOR 99	2	
<i>Escherichia hermannii</i>	8.04	0.12		1	
<i>Cronobacter sakazakii</i>	1.54	-0.01		99	
172243	Good identification				172243
<i>Yersinia enterocolitica ssp. enterocolitica</i>	99.29	0.47	SUC 95		
<i>Yersinia kristensenii</i>	0.71	-0.05			
172253	Identification to the genus				172253
<i>Yersinia enterocolitica ssp. enterocolitica</i>	80.43	0.56	SUC 95		
<i>Yersinia kristensenii</i>	18.86	0.36			
<i>Citrobacter amalonaticus</i>	0.51	-0.03			
172261	Good identification				172261
<i>Yersinia enterocolitica ssp. enterocolitica</i>	100.0	0.38	MAN 98		
172262	Good identification				172262
<i>Yersinia enterocolitica ssp. enterocolitica</i>	100.0	0.38	TRE 98		
172263	Very good identification				172263
<i>Yersinia enterocolitica ssp. enterocolitica</i>	100.0	0.73			
172271	Good identification				172271
<i>Yersinia enterocolitica ssp. enterocolitica</i>	100.0	0.48	MAN 98		
172272	Good identification				172272

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.48	TRE 98		
172273	Very good identification				172273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	99.78	0.83			
<i>Citrobacter farmeri</i>	0.21	0.15			
<i>Yersinia kristensenii</i>	0.01	-.05			
172373	Good identification				172373
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.72	0.42	MAL 1		
<i>Citrobacter sedlakii</i>	1.28	-.11			
172433	Acceptable identification				172433
<i>Leclercia adecarboxylata</i>	91.19	0.36	ORN 1		
<i>Escherichia hermannii</i>	6.97	0.12	MAL 93		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.85	0.08			
172463	Good identification				172463
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	98.36	0.39	ADO 1		
<i>Escherichia coli</i>	1.64	0.04			
172473	Acceptable identification				172473
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	91.40	0.49	ADO 1		
<i>Citrobacter farmeri</i>	8.14	0.15			
<i>Leclercia adecarboxylata</i>	0.46	-.05			
172513	Very good identification				172513
<i>Leclercia adecarboxylata</i>	96.49	0.53	ORN 1		
<i>Escherichia fergusonii</i>	3.25	0.26			
<i>Citrobacter sedlakii</i>	0.16	-.11			
172533	Very good identification				172533
<i>Leclercia adecarboxylata</i>	100.0	0.59	ORN 1		
172673	Good identification				172673
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.42	ADO 1		
173000	Good identification				173000
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
173063	Good identification				173063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.39	PHE 1		
173073	Acceptable identification				173073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	91.83	0.49	PHE 1		
<i>Citrobacter farmeri</i>	8.17	0.15			
173273	Good identification				173273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.42	PHE 1		
174003	Identification to the genus				174003
<i>Citrobacter braakii</i>	65.27	0.42	SOR 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter amalonaticus</i>	29.49	0.18			
<i>Citrobacter koseri</i>	1.95	0.02			
174013	Good identification				174013
<i>Citrobacter amalonaticus</i>	93.15	0.59	SOR 99		
<i>Citrobacter braakii</i>	4.23	0.48			
<i>Citrobacter koseri</i>	0.98	0.26			
174033	Low discrimination				174033
<i>Citrobacter farmeri</i>	43.70	0.37	SCI 10		
<i>Citrobacter amalonaticus</i>	40.52	0.34	SOR 99		
<i>Citrobacter koseri</i>	5.90	0.25			
174041	Identification to the genus				174041
<i>Citrobacter braakii</i>	67.89	0.42	MAN 99		
<i>Citrobacter amalonaticus</i>	30.68	0.18			
<i>Citrobacter youngae</i>	1.44	0.07			
174042	Identification to the genus				174042
<i>Citrobacter braakii</i>	67.89	0.42	TRE 99		
<i>Citrobacter amalonaticus</i>	30.68	0.18			
<i>Citrobacter youngae</i>	1.44	0.07			
174043	Identification to the genus				174043
<i>Citrobacter braakii</i>	67.25	0.83			
<i>Citrobacter amalonaticus</i>	30.39	0.59			
<i>Citrobacter youngae</i>	1.42	0.48			
174051	Good identification				174051
<i>Citrobacter amalonaticus</i>	94.38	0.59	MAN 99		
<i>Citrobacter braakii</i>	4.28	0.48			
<i>Citrobacter sedlakii</i>	0.88	0.18			
174052	Good identification				174052
<i>Citrobacter amalonaticus</i>	94.38	0.59	TRE 99		
<i>Citrobacter braakii</i>	4.28	0.48			
<i>Citrobacter sedlakii</i>	0.88	0.18			
174053	Good identification				174053
<i>Citrobacter amalonaticus</i>	94.36	1.00			
<i>Citrobacter braakii</i>	4.28	0.89			
<i>Citrobacter sedlakii</i>	0.88	0.59			
174063	Low discrimination				174063
<i>Citrobacter braakii</i>	39.10	0.60	SUC 7		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	16.51	0.49			
<i>Citrobacter farmeri</i>	16.16	0.37			
174071	Low discrimination				174071
<i>Citrobacter farmeri</i>	48.07	0.37	SCI 10		
<i>Citrobacter amalonaticus</i>	44.57	0.34	MAN 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.01	0.24			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
174072	Low discrimination				174072
<i>Citrobacter farmeri</i>	48.07	0.37	SCI 10		
<i>Citrobacter amalonaticus</i>	44.57	0.34	TRE 99		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	3.01	0.24			
174073	Identification to the genus				174073
<i>Citrobacter farmeri</i>	48.73	0.78	SCI 10		
<i>Citrobacter amalonaticus</i>	45.18	0.75			
<i>Citrobacter braakii</i>	2.42	0.66			
174113	Identification to the genus				174113
<i>Citrobacter sedlakii</i>	84.07	0.59	SOR 99		
<i>Citrobacter koseri</i>	14.92	0.51			
<i>Citrobacter amalonaticus</i>	0.92	0.18			
174133	Low discrimination				174133
				VPT	
<i>Citrobacter koseri</i>	83.91	0.50	ADO 94	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	9.93	0.33	SOR 94	99	
<i>Citrobacter sedlakii</i>	5.39	0.18		1	
174143	Identification to the genus				174143
<i>Citrobacter sedlakii</i>	82.19	0.59	CEL 99		
<i>Citrobacter koseri</i>	14.59	0.51			
<i>Citrobacter braakii</i>	1.99	0.42			
174151	Very good identification				174151
<i>Citrobacter sedlakii</i>	96.20	0.59	MAN 99		
<i>Citrobacter koseri</i>	2.70	0.34			
<i>Citrobacter amalonaticus</i>	1.05	0.18			
174152	Very good identification				174152
<i>Citrobacter sedlakii</i>	96.20	0.59	TRE 99		
<i>Citrobacter koseri</i>	2.70	0.34			
<i>Citrobacter amalonaticus</i>	1.05	0.18			
174153	Very good identification				174153
<i>Citrobacter sedlakii</i>	96.18	1.00			
<i>Citrobacter koseri</i>	2.70	0.75			
<i>Citrobacter amalonaticus</i>	1.05	0.59			
174163	Low discrimination				174163
				VPT	
<i>Citrobacter koseri</i>	87.99	0.50	ADO 94	1	
<i>Citrobacter sedlakii</i>	5.65	0.18	CEL 94	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.00	0.18		99	
174173	Low discrimination				174173
				VPT	
<i>Citrobacter koseri</i>	62.08	0.74	ADO 94	1	
<i>Citrobacter sedlakii</i>	25.17	0.59		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	8.91	0.59		99	
174243	Low discrimination				174243

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	60.62	0.42	INO 1		
<i>Citrobacter amalonaticus</i>	27.39	0.18			
<i>Citrobacter youngae</i>	6.68	0.22			
174253	Good identification				174253
<i>Citrobacter amalonaticus</i>	90.80	0.59	INO 1		
<i>Citrobacter braakii</i>	4.12	0.48			
<i>Yersinia kristensenii</i>	3.34	0.36			
174263	Low discrimination				174263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	88.26	0.42	SCI 1		
<i>Citrobacter braakii</i>	4.93	0.19			
<i>Citrobacter farmeri</i>	2.04	-.04			
174273	Low discrimination				174273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	36.22	0.51	SCI 1		
<i>Citrobacter farmeri</i>	27.58	0.37			
<i>Citrobacter amalonaticus</i>	25.57	0.34			
174353	Very good identification				174353
<i>Citrobacter sedlakii</i>	95.98	0.59	INO 1		
<i>Citrobacter koseri</i>	2.70	0.34			
<i>Citrobacter amalonaticus</i>	1.05	0.18			
174373	Low discrimination				174373
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	62.52	0.43	IND 1	99	
<i>Citrobacter koseri</i>	24.93	0.33		1	
<i>Citrobacter sedlakii</i>	10.11	0.18		1	
174413	Acceptable identification				174413
<i>Citrobacter koseri</i>	92.05	0.51	MAL 94		
<i>Citrobacter amalonaticus</i>	5.67	0.18	SOR 94		
<i>Escherichia fergusonii</i>	2.02	0.18			
174433	Good identification				174433
				VPT	
<i>Citrobacter koseri</i>	97.81	0.50	MAL 94	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.29	0.13	SOR 94	99	
<i>Citrobacter farmeri</i>	0.47	-.04		1	
174443	Identification to the genus				174443
<i>Citrobacter koseri</i>	83.29	0.51	MAL 94		
<i>Citrobacter braakii</i>	11.34	0.42	CEL 94		
<i>Citrobacter amalonaticus</i>	5.13	0.18			
174453	Identification to the genus				174453
<i>Citrobacter koseri</i>	70.83	0.75	MAL 94		
<i>Citrobacter amalonaticus</i>	27.55	0.59			
<i>Citrobacter braakii</i>	1.25	0.48			
174463	Good identification				174463
<i>Citrobacter koseri</i>	97.05	0.50	MAL 94		
<i>Citrobacter braakii</i>	1.12	0.19	CEL 94		

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.47	0.08			
174473	Good identification				174473
<i>Citrobacter koseri</i>	92.88	0.74	MAL 94		
<i>Citrobacter farmeri</i>	2.80	0.37			
<i>Citrobacter amalonaticus</i>	2.60	0.34			
174503	Good identification				174503
<i>Citrobacter koseri</i>	100.0	0.51	CEL 94		
174513	Very good identification				174513
<i>Citrobacter koseri</i>	99.56	0.75	SOR 94		
<i>Citrobacter sedlakii</i>	0.36	0.18			
<i>Escherichia fergusonii</i>	0.08	0.13			
174523	Good identification				174523
<i>Citrobacter koseri</i>	100.0	0.50	CEL 94		
174533	Very good identification				174533
				VPT	
<i>Citrobacter koseri</i>	99.75	0.74	SOR 94	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.25	0.23		99	
174543	Very good identification				174543
<i>Citrobacter koseri</i>	99.64	0.75	CEL 94		
<i>Citrobacter sedlakii</i>	0.36	0.18			
174551	Very good identification				174551
<i>Citrobacter koseri</i>	97.76	0.59	MAN 99		
<i>Citrobacter sedlakii</i>	2.24	0.18			
174552	Very good identification				174552
<i>Citrobacter koseri</i>	97.76	0.59	TRE 99		
<i>Citrobacter sedlakii</i>	2.24	0.18			
174553	Very good identification				174553
<i>Citrobacter koseri</i>	97.72	1.00			
<i>Citrobacter sedlakii</i>	2.24	0.59			
<i>Citrobacter amalonaticus</i>	0.03	0.18			
174563	Very good identification				174563
				VPT	
<i>Citrobacter koseri</i>	99.95	0.74	CEL 94	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.05	0.08		99	
174571	Very good identification				174571
				VPT	
<i>Citrobacter koseri</i>	99.70	0.58	MAN 99	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.30	0.08		99	
174572	Very good identification				174572
				VPT	
<i>Citrobacter koseri</i>	99.70	0.58	TRE 99	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.30	0.08		99	
174573	Excellent identification				174573
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter koseri</i>	99.67	0.99		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.30	0.49		99	
<i>Citrobacter sedlakii</i>	0.03	0.18		1	
174753	Very good identification				174753
				VPT	
<i>Citrobacter koseri</i>	97.62	0.59	INO 1	1	
<i>Citrobacter sedlakii</i>	2.24	0.18		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.14	0.03		99	
174773	Good identification				174773
				VPT	
<i>Citrobacter koseri</i>	94.94	0.58	INO 1	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.07	0.34		99	
175000	Good identification				175000
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.39	ONP 10		
175043	Identification to the genus				175043
<i>Citrobacter braakii</i>	67.89	0.42	PHE 1		
<i>Citrobacter amalonaticus</i>	30.68	0.18			
<i>Citrobacter youngae</i>	1.44	0.07			
175053	Good identification				175053
<i>Citrobacter amalonaticus</i>	94.38	0.59	PHE 1		
<i>Citrobacter braakii</i>	4.28	0.48			
<i>Citrobacter sedlakii</i>	0.88	0.18			
175073	Identification to the genus				175073
<i>Citrobacter farmeri</i>	48.81	0.37	PHE 1		
<i>Citrobacter amalonaticus</i>	45.25	0.34	SCI 10		
<i>Citrobacter braakii</i>	2.42	0.25			
175153	Very good identification				175153
<i>Citrobacter sedlakii</i>	96.20	0.59	PHE 1		
<i>Citrobacter koseri</i>	2.70	0.34			
<i>Citrobacter amalonaticus</i>	1.05	0.18			
175553	Very good identification				175553
<i>Citrobacter koseri</i>	97.76	0.59	PHE 1		
<i>Citrobacter sedlakii</i>	2.24	0.18			
175573	Very good identification				175573
				VPT	
<i>Citrobacter koseri</i>	99.70	0.58	PHE 1	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.30	0.08		99	
176013	Acceptable identification				176013
<i>Citrobacter amalonaticus</i>	94.60	0.38	ESL 9		
<i>Escherichia hermannii</i>	3.13	0.14	SOR 99		
<i>Citrobacter sedlakii</i>	1.83	0.04			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
176043	Identification to the genus				176043
<i>Citrobacter amalonaticus</i>	77.96	0.38	ESL 9		
<i>Citrobacter braakii</i>	17.62	0.42	CEL 99		
<i>Citrobacter youngae</i>	1.94	0.22			
176051	Good identification				176051
<i>Citrobacter amalonaticus</i>	97.66	0.38	ESL 9		
<i>Citrobacter sedlakii</i>	1.89	0.04	MAN 99		
<i>Citrobacter braakii</i>	0.45	0.07			
176052	Good identification				176052
<i>Citrobacter amalonaticus</i>	97.66	0.38	ESL 9		
<i>Citrobacter sedlakii</i>	1.89	0.04	TRE 99		
<i>Citrobacter braakii</i>	0.45	0.07			
176053	Very good identification				176053
<i>Citrobacter amalonaticus</i>	97.55	0.79	ESL 9		
<i>Citrobacter sedlakii</i>	1.89	0.45			
<i>Citrobacter braakii</i>	0.45	0.48			
176063	Low discrimination				176063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	69.14	0.39	SCI 1		
<i>Citrobacter amalonaticus</i>	18.62	0.14			
<i>Citrobacter braakii</i>	4.96	0.19			
176073	Low discrimination				176073
<i>Citrobacter amalonaticus</i>	76.29	0.55	ESL 9		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.58	0.49	SUC 6		
<i>Citrobacter farmeri</i>	8.40	0.37			
176113	Good identification				176113
<i>Citrobacter sedlakii</i>	98.36	0.45	SOR 99		
<i>Citrobacter koseri</i>	0.86	0.10			
<i>Citrobacter amalonaticus</i>	0.52	-.03			
176143	Good identification				176143
<i>Citrobacter sedlakii</i>	98.62	0.45	CEL 99		
<i>Citrobacter koseri</i>	0.86	0.10			
<i>Citrobacter amalonaticus</i>	0.52	-.03			
176151	Good identification				176151
<i>Citrobacter sedlakii</i>	99.34	0.45	MAN 99		
<i>Citrobacter amalonaticus</i>	0.52	-.03			
<i>Citrobacter koseri</i>	0.14	-.07			
176152	Good identification				176152
<i>Citrobacter sedlakii</i>	99.34	0.45	TRE 99		
<i>Citrobacter amalonaticus</i>	0.52	-.03			
<i>Citrobacter koseri</i>	0.14	-.07			
176153	Very good identification				176153

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter sedlakii</i>	99.31	0.86			
<i>Citrobacter amalonaticus</i>	0.52	0.38			
<i>Citrobacter koseri</i>	0.14	0.34			
176173	Low discrimination				176173
				VPT	
<i>Citrobacter sedlakii</i>	50.23	0.45	SUC 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	37.20	0.51		99	
<i>Citrobacter koseri</i>	6.11	0.33		1	
176233	Good identification				176233
				VPT	
<i>Cronobacter sakazakii</i>	98.57	0.40	IND 11	99	
<i>Enterobacter cloacae subsp. cloacae</i>	0.84	0.00	URE 1	99	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.59	0.00		2	
176253	Good identification				176253
<i>Citrobacter amalonaticus</i>	95.81	0.38	ESL 9		
<i>Citrobacter sedlakii</i>	1.85	0.04	INO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.54	0.15			
176273	Low discrimination				176273
				VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	43.56	0.42	SCI 1	2	
<i>Serratia odorifera biovar 1</i>	33.65	0.33		50	
<i>Enterobacter cloacae subsp. cloacae</i>	11.93	0.26		99	
176353	Good identification				176353
				VPT	
<i>Citrobacter sedlakii</i>	98.94	0.45	INO 1	1	
<i>Citrobacter amalonaticus</i>	0.52	-.03		1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.40	0.05		99	
176373	Acceptable identification				176373
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	91.78	0.36	IND 1	99	
<i>Citrobacter sedlakii</i>	7.09	0.04		1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.13	0.00		2	
176453	Identification to the genus				176453
<i>Citrobacter amalonaticus</i>	77.43	0.38	ESL 9		
<i>Citrobacter koseri</i>	20.34	0.34	ADO 1		
<i>Citrobacter sedlakii</i>	1.50	0.04			
176553	Identification to the genus				176553
				VPT	
<i>Citrobacter koseri</i>	67.96	0.59	ESL 1	1	
<i>Citrobacter sedlakii</i>	31.63	0.45		1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.24	0.10		99	
176573	Low discrimination				176573
				VPT	
<i>Citrobacter koseri</i>	88.06	0.58	ESL 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	11.41	0.42		99	
<i>Citrobacter sedlakii</i>	0.47	0.04		1	
177053	Good identification				177053
<i>Citrobacter amalonaticus</i>	97.66	0.38	PHE 1		
<i>Citrobacter sedlakii</i>	1.89	0.04	ESL 9		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	0.45	0.07			
177153	Good identification				177153
<i>Citrobacter sedlakii</i>	99.34	0.45	PHE 1		
<i>Citrobacter amalonaticus</i>	0.52	-.03			
<i>Citrobacter koseri</i>	0.14	-.07			
177233	Good identification				177233
<i>Cronobacter sakazakii</i>	100.0	0.40	IND 11		
200000	Identification to the genus				200000
<i>Shigella dysenteriae</i> (group A)	77.50	0.39	H2S 1		
<i>Shigella flexneri</i> (group B)	16.84	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	5.03	0.12			
200001	Good identification				200001
<i>Shigella dysenteriae</i> (group A)	91.07	0.59	H2S 1		
<i>Shigella flexneri</i> (group B)	4.47	0.33			
<i>Shigella boydii</i> (group C)	3.72	0.28			
200002	Identification to the genus				200002
<i>Shigella flexneri</i> (group B)	65.31	0.53	H2S 1		
<i>Shigella boydii</i> (group C)	33.19	0.43			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	1.09	0.13			
200003	Low discrimination				200003
<i>Shigella boydii</i> (group C)	53.75	0.59	H2S 1		
<i>Shigella flexneri</i> (group B)	37.90	0.59			
<i>Salmonella</i> serovar <i>paratyphi</i>	3.94	0.28			
200041	Low discrimination				200041
<i>Shigella dysenteriae</i> (group A)	73.20	0.51	H2S 1		
<i>Salmonella</i> serovar <i>typhi</i>	13.39	0.24			
<i>Shigella boydii</i> (group C)	5.26	0.25			
200042	Low discrimination				200042
<i>Shigella flexneri</i> (group B)	34.82	0.45	H2S 1		
<i>Shigella boydii</i> (group C)	32.68	0.41			
<i>Salmonella</i> serovar <i>typhi</i>	14.57	0.24			
200043	Low discrimination				200043
<i>Salmonella</i> serovar <i>typhi</i>	65.21	0.65	LYS 98		
<i>Salmonella</i> serovar <i>paratyphi</i>	15.48	0.54			
<i>Shigella boydii</i> (group C)	8.37	0.56			
200053	Low discrimination				200053
<i>Citrobacter youngae</i>	56.73	0.62	ONP 90		
<i>Citrobacter braakii</i>	13.20	0.50			
<i>Citrobacter freundii</i>	9.89	0.49			
200063	Low discrimination				200063
<i>Citrobacter freundii</i>	51.72	0.70	ONP 88		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia rohdei</i>	33.03	0.59			
<i>Citrobacter youngae</i>	9.36	0.52			
200073	Low discrimination				200073
<i>Citrobacter freundii</i>	67.85	0.68	ONP 88		
<i>Yersinia rohdei</i>	18.38	0.49			
<i>Citrobacter youngae</i>	12.79	0.50			
200153	Identification to the genus				200153
<i>Citrobacter youngae</i>	71.89	0.36	ONP 90		
<i>Citrobacter freundii</i>	20.71	0.27	MAL 5		
<i>Citrobacter braakii</i>	3.21	0.09			
200163	Low discrimination				200163
<i>Citrobacter freundii</i>	83.86	0.48	ONP 88		
<i>Citrobacter youngae</i>	9.19	0.26	MAL 8		
<i>Yersinia rohdei</i>	6.22	0.18			
200173	Identification to the genus				200173
<i>Citrobacter freundii</i>	86.19	0.46	ONP 88		
<i>Citrobacter youngae</i>	9.83	0.24	MAL 8		
<i>Yersinia rohdei</i>	2.71	0.08			
200253	Low discrimination				200253
<i>Citrobacter youngae</i>	82.24	0.36	ONP 90		
<i>Yersinia kristensenii</i>	6.54	0.03	INO 5		
<i>Citrobacter braakii</i>	3.67	0.09			
200753	Good identification				200753
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	100.0	0.49	H2S 1		
200773	Very good identification				200773
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	100.0	0.59	H2S 1		
201000	Low discrimination				201000
<i>Proteus vulgaris</i>	85.92	0.43	URE 95		
<i>Morganella morganii subsp. morganii</i>	6.86	0.07	SUC 97		
<i>Proteus penneri</i>	5.31	0.09			
201001	Low discrimination				201001
<i>Morganella morganii subsp. sibonii</i>	51.99	0.39	H2S 6		
<i>Proteus vulgaris</i>	23.48	0.35	URE 97		
<i>Proteus mirabilis</i>	14.19	0.19			
201020	Identification to the genus				201020
<i>Proteus vulgaris</i>	84.09	0.74	URE 95		
<i>Proteus penneri</i>	15.91	0.50			
201021	Identification to the genus				201021
<i>Proteus vulgaris</i>	64.63	0.66	URE 95		
<i>Proteus penneri</i>	34.88	0.51			
<i>Morganella morganii subsp. sibonii</i>	0.28	0.15			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
202053	Low discrimination				202053
<i>Citrobacter youngae</i>	84.03	0.36	ONP 90		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	4.50	0.14	ESL 5		
<i>Citrobacter braakii</i>	3.75	0.09			
202413	Good identification				202413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.39	H2S 1		
202453	Good identification				202453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.55	0.45	H2S 1		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	1.45	-.11			
202613	Good identification				202613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	H2S 1		
202653	Identification to the genus				202653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	81.39	0.47	H2S 1		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	18.61	0.15			
202753	Good identification				202753
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	99.29	0.42	H2S 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.71	0.16			
202773	Good identification				202773
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	100.0	0.51	H2S 1		
203000	Good identification				203000
<i>Proteus vulgaris</i>	100.0	0.43	URE 95		
203001	Good identification				203001
<i>Proteus vulgaris</i>	97.81	0.35	URE 95		
<i>Morganella morganii subsp. sibonii</i>	2.19	-.02	SUC 97		
203020	Very good identification				203020
<i>Proteus vulgaris</i>	99.81	0.74	URE 95		
<i>Proteus penneri</i>	0.19	0.09			
203021	Very good identification				203021
<i>Proteus vulgaris</i>	99.46	0.66	URE 95		
<i>Proteus penneri</i>	0.54	0.10			
204023	Identification to the genus				204023
<i>Citrobacter freundii</i>	88.59	0.41	ONP 88		
<i>Citrobacter youngae</i>	11.41	0.20	SOR 99		
204033	Identification to the genus				204033
<i>Citrobacter freundii</i>	88.18	0.39	ONP 88		
<i>Citrobacter youngae</i>	11.82	0.19	SOR 99		
204043	Low discrimination				204043
<i>Citrobacter youngae</i>	66.94	0.73	ONP 90		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	17.08	0.64			
<i>Citrobacter braakii</i>	6.62	0.53			
204053	Identification to the genus				204053
<i>Citrobacter youngae</i>	66.36	0.71	ONP 90		
<i>Citrobacter braakii</i>	16.28	0.59			
<i>Citrobacter freundii</i>	16.26	0.61			
204061	Identification to the genus				204061
<i>Citrobacter freundii</i>	88.59	0.41	ONP 88		
<i>Citrobacter youngae</i>	11.41	0.20	MAN 99		
204062	Identification to the genus				204062
<i>Citrobacter freundii</i>	88.59	0.41	ONP 88		
<i>Citrobacter youngae</i>	11.41	0.20	TRE 99		
204063	Identification to the genus				204063
<i>Citrobacter freundii</i>	88.15	0.82	ONP 88		
<i>Citrobacter youngae</i>	11.35	0.61			
<i>Citrobacter braakii</i>	0.32	0.30			
204071	Identification to the genus				204071
<i>Citrobacter freundii</i>	88.18	0.39	ONP 88		
<i>Citrobacter youngae</i>	11.82	0.19	MAN 99		
204072	Identification to the genus				204072
<i>Citrobacter freundii</i>	88.18	0.39	ONP 88		
<i>Citrobacter youngae</i>	11.82	0.19	TRE 99		
204073	Identification to the genus				204073
<i>Citrobacter freundii</i>	87.41	0.80	ONP 88		
<i>Citrobacter youngae</i>	11.72	0.60			
<i>Citrobacter braakii</i>	0.81	0.36			
204143	Low discrimination				204143
<i>Citrobacter werkmanii</i>	55.94	0.37	ONP 99		
<i>Citrobacter youngae</i>	25.29	0.47	URE 92		
<i>Citrobacter freundii</i>	10.66	0.42			
204153	Identification to the genus				204153
<i>Citrobacter youngae</i>	67.60	0.45	ONP 90		
<i>Citrobacter freundii</i>	27.37	0.40	MAL 5		
<i>Citrobacter braakii</i>	3.18	0.18			
204163	Good identification				204163
<i>Citrobacter freundii</i>	92.21	0.60	ONP 88		
<i>Citrobacter youngae</i>	7.19	0.35	MAL 8		
<i>Citrobacter werkmanii</i>	0.60	-0.04			
204173	Good identification				204173
<i>Citrobacter freundii</i>	92.49	0.58	ONP 88		
<i>Citrobacter youngae</i>	7.51	0.33	MAL 8		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
204243	Low discrimination				204243
<i>Citrobacter youngae</i>	58.04	0.47	ONP 90		
<i>Salmonella serovar enteritidis</i>	37.58	0.29	INO 5		
<i>Citrobacter freundii</i>	2.84	0.22			
204253	Identification to the genus				204253
<i>Citrobacter youngae</i>	88.05	0.45	ONP 90		
<i>Citrobacter braakii</i>	4.14	0.18	INO 5		
<i>Citrobacter freundii</i>	4.14	0.20			
204263	Identification to the genus				204263
<i>Citrobacter freundii</i>	59.26	0.41	ONP 88		
<i>Citrobacter youngae</i>	39.76	0.35	INO 1		
<i>Salmonella serovar enteritidis</i>	0.98	-.13			
204273	Identification to the genus				204273
<i>Citrobacter freundii</i>	58.87	0.39	ONP 88		
<i>Citrobacter youngae</i>	41.13	0.33	INO 1		
204463	Identification to the genus				204463
<i>Citrobacter freundii</i>	88.59	0.41	ONP 88		
<i>Citrobacter youngae</i>	11.41	0.20	ADO 1		
204473	Identification to the genus				204473
<i>Citrobacter freundii</i>	84.97	0.39	ONP 88		
<i>Citrobacter youngae</i>	11.39	0.19	ADO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.64	0.12			
205020	Very good identification				205020
<i>Proteus vulgaris</i>	98.93	0.58	URE 95		
<i>Proteus penneri</i>	1.07	0.09			
205021	Acceptable identification				205021
<i>Proteus vulgaris</i>	93.45	0.51	URE 95		
<i>Proteus mirabilis</i>	3.24	0.09			
<i>Proteus penneri</i>	2.89	0.10			
205063	Identification to the genus				205063
<i>Citrobacter freundii</i>	88.59	0.41	ONP 88		
<i>Citrobacter youngae</i>	11.41	0.20	PHE 1		
205073	Identification to the genus				205073
<i>Citrobacter freundii</i>	88.18	0.39	ONP 88		
<i>Citrobacter youngae</i>	11.82	0.19	PHE 1		
206043	Low discrimination				206043
<i>Citrobacter youngae</i>	87.82	0.47	ONP 90		
<i>Salmonella serovar enteritidis</i>	5.56	0.08	ESL 5		
<i>Citrobacter freundii</i>	4.30	0.22			
206053	Acceptable identification				206053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	90.73	0.45	ONP 90		
<i>Citrobacter braakii</i>	4.27	0.18	ESL 5		
<i>Citrobacter freundii</i>	4.27	0.20			
206063	Identification to the genus				206063
<i>Citrobacter freundii</i>	59.85	0.41	ONP 88		
<i>Citrobacter youngae</i>	40.15	0.35	ESL 1		
206073	Low discrimination				206073
<i>Citrobacter freundii</i>	44.41	0.39	ONP 88		
<i>Citrobacter youngae</i>	31.02	0.33	ESL 1		
<i>Serratia ficaria</i>	24.57	0.16			
206453	Good identification				206453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.27	0.37	H2S 1		
<i>Citrobacter youngae</i>	3.73	0.04			
206653	Good identification				206653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.39	H2S 1		
207020	Very good identification				207020
<i>Proteus vulgaris</i>	100.0	0.58	URE 95		
207021	Good identification				207021
<i>Proteus vulgaris</i>	100.0	0.51	URE 95		
210000	Low discrimination				210000
<i>Shigella dysenteriae (group A)</i>	54.93	0.38	H2S 1		
<i>Edwardsiella tarda</i>	24.17	0.18	TRE 90		
<i>Shigella flexneri (group B)</i>	14.59	0.26			
210001	Good identification				210001
<i>Shigella dysenteriae (group A)</i>	92.22	0.57	H2S 1		
<i>Shigella flexneri (group B)</i>	5.53	0.33			
<i>Shigella boydii (group C)</i>	1.54	0.18			
210002	Identification to the genus				210002
<i>Shigella flexneri (group B)</i>	85.37	0.53	H2S 1		
<i>Shigella boydii (group C)</i>	14.46	0.34			
<i>Shigella dysenteriae (group A)</i>	0.17	-0.04			
210003	Identification to the genus				210003
<i>Shigella flexneri (group B)</i>	67.12	0.59	H2S 1		
<i>Shigella boydii (group C)</i>	31.73	0.49			
<i>Shigella dysenteriae (group A)</i>	0.60	0.16			
210041	Acceptable identification				210041
<i>Shigella dysenteriae (group A)</i>	91.12	0.50	H2S 1		
<i>Shigella flexneri (group B)</i>	5.20	0.25			
<i>Shigella boydii (group C)</i>	2.67	0.16			
210042	Identification to the genus				210042

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella flexneri</i> (group B)	74.78	0.45	H2S 1		
<i>Shigella boydii</i> (group C)	23.39	0.31			
<i>Escherichia coli</i>	0.73	0.10			
210043	Low discrimination				210043
<i>Shigella flexneri</i> (group B)	35.63	0.51	H2S 1		
<i>Shigella boydii</i> (group C)	31.11	0.47			
<i>Citrobacter youngae</i>	11.65	0.48			
210053	Low discrimination				210053
<i>Citrobacter youngae</i>	43.69	0.47	ONP 90		
<i>Citrobacter braakii</i>	28.37	0.43			
<i>Citrobacter freundii</i>	21.26	0.43			
210063	Low discrimination				210063
<i>Citrobacter freundii</i>	87.43	0.64	ONP 88		
<i>Citrobacter youngae</i>	5.67	0.37			
<i>Escherichia coli</i>	3.96	0.32			
210073	Good identification				210073
<i>Citrobacter freundii</i>	92.12	0.61	ONP 88		
<i>Citrobacter youngae</i>	6.22	0.35			
<i>Citrobacter braakii</i>	1.14	0.20			
210163	Good identification				210163
<i>Citrobacter freundii</i>	96.22	0.42	ONP 88		
<i>Citrobacter youngae</i>	3.78	0.10	MAL 8		
210173	Good identification				210173
<i>Citrobacter freundii</i>	96.07	0.40	ONP 88		
<i>Citrobacter youngae</i>	3.93	0.08	MAL 8		
211001	Low discrimination				211001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	62.18	0.39	H2S 6		
<i>Proteus vulgaris</i>	28.09	0.35	URE 97		
<i>Shigella dysenteriae</i> (group A)	6.07	0.16			
211020	Very good identification				211020
<i>Proteus vulgaris</i>	99.76	0.74	URE 95		
<i>Proteus penneri</i>	0.19	0.09			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.05	-0.08			
211021	Very good identification				211021
<i>Proteus vulgaris</i>	98.74	0.66	URE 95		
<i>Proteus penneri</i>	0.54	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.43	0.15			
211201	Good identification				211201
<i>Providencia stuartii</i>	98.77	0.36	H2S 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.23	-0.02	SCI 93		
211221	Low discrimination				211221

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	84.62	0.36	H2S 1		
<i>Proteus vulgaris</i>	15.38	0.25	SCI 93		
213000	Good identification				213000
<i>Proteus vulgaris</i>	98.49	0.43	URE 95		
<i>Morganella morganii</i> subsp. <i>morganii</i>	1.51	-.08	SUC 97		
213001	Good identification				213001
<i>Proteus vulgaris</i>	97.81	0.35	URE 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2.19	-.02	SUC 97		
213020	Very good identification				213020
<i>Proteus vulgaris</i>	100.0	0.74	URE 95		
213021	Very good identification				213021
<i>Proteus vulgaris</i>	100.0	0.66	URE 95		
214043	Identification to the genus				214043
<i>Citrobacter youngae</i>	49.65	0.58	ONP 90		
<i>Citrobacter freundii</i>	35.36	0.57			
<i>Citrobacter braakii</i>	13.70	0.47			
214053	Identification to the genus				214053
<i>Citrobacter youngae</i>	41.78	0.56	ONP 90		
<i>Citrobacter braakii</i>	28.60	0.53			
<i>Citrobacter freundii</i>	28.57	0.55			
214063	Very good identification				214063
<i>Citrobacter freundii</i>	95.26	0.76	ONP 88		
<i>Citrobacter youngae</i>	4.40	0.46			
<i>Citrobacter braakii</i>	0.34	0.24			
214073	Good identification				214073
<i>Citrobacter freundii</i>	94.58	0.74	ONP 88		
<i>Citrobacter youngae</i>	4.54	0.44			
<i>Citrobacter braakii</i>	0.88	0.30			
214143	Identification to the genus				214143
<i>Citrobacter freundii</i>	49.94	0.35	ONP 88		
<i>Citrobacter youngae</i>	42.44	0.31	MAL 8		
<i>Citrobacter werkmanii</i>	5.37	-.04	SUC 89		
214163	Very good identification				214163
<i>Citrobacter freundii</i>	97.28	0.54	ONP 88		
<i>Citrobacter youngae</i>	2.72	0.20	MAL 8		
214173	Good identification				214173
<i>Citrobacter freundii</i>	97.17	0.52	ONP 88		
<i>Citrobacter youngae</i>	2.83	0.18	MAL 8		
215020	Very good identification				215020
<i>Proteus vulgaris</i>	97.58	0.58	URE 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia alcalifaciens</i>	2.23	0.09			
<i>Providencia stuartii</i>	0.19	-.02			
215021	Low discrimination				215021
<i>Proteus vulgaris</i>	81.95	0.51	URE 95		
<i>Providencia stuartii</i>	18.05	0.33			
215201	Very good identification				215201
<i>Providencia stuartii</i>	100.0	0.59	H2S 1		
215203	Good identification				215203
<i>Providencia stuartii</i>	100.0	0.39	H2S 1		
215221	Very good identification				215221
<i>Providencia stuartii</i>	99.76	0.59	H2S 1		
<i>Proteus vulgaris</i>	0.24	0.10			
215223	Good identification				215223
<i>Providencia stuartii</i>	100.0	0.39	H2S 1		
215400	Very good identification				215400
<i>Providencia alcalifaciens</i>	100.0	0.59	H2S 1		
215420	Good identification				215420
<i>Providencia alcalifaciens</i>	99.11	0.43	H2S 1		
<i>Proteus vulgaris</i>	0.89	0.17			
217020	Very good identification				217020
<i>Proteus vulgaris</i>	100.0	0.58	URE 95		
217021	Good identification				217021
<i>Proteus vulgaris</i>	100.0	0.51	URE 95		
220002	Very good identification				220002
<i>Salmonella enterica subsp. enterica</i>	96.27	0.54	LYS 95		
<i>Salmonella serovar paratyphi</i>	2.36	0.13	SOR 90		
<i>Shigella flexneri (group B)</i>	0.59	0.12			
220003	Low discrimination				220003
<i>Salmonella serovar paratyphi</i>	81.09	0.54	H2S 10		
<i>Shigella sonnei</i>	16.56	0.39	SOR 95		
<i>Shigella boydii (group C)</i>	0.59	0.18			
220040	Good identification				220040
<i>Salmonella enterica subsp. enterica</i>	97.50	0.39	LYS 95		
<i>Salmonella serovar paratyphi</i>	2.50	-.02	MAN 98		
220041	Good identification				220041
<i>Salmonella serovar paratyphi</i>	95.07	0.39	H2S 10		
<i>Citrobacter braakii</i>	2.39	0.25	MAN 99		
<i>Shigella dysenteriae (group A)</i>	1.16	0.10			
220042	Good identification				220042

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>enterica</i>	94.87	0.74	LYS 95		
<i>Salmonella</i> serovar <i>paratyphi</i>	4.92	0.39			
<i>Citrobacter braakii</i>	0.12	0.25			
220043	Very good identification				220043
<i>Salmonella</i> serovar <i>paratyphi</i>	96.29	0.80	H2S 10		
<i>Citrobacter braakii</i>	2.42	0.66			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.59	0.39			
220053	Low discrimination				220053
<i>Salmonella</i> serovar <i>paratyphi</i>	47.82	0.54	H2S 10		
<i>Citrobacter braakii</i>	46.27	0.73	CEL 5		
<i>Yersinia kristensenii</i>	4.08	0.41			
220063	Low discrimination				220063
<i>Salmonella</i> serovar <i>paratyphi</i>	53.15	0.39	H2S 10		
<i>Yersinia rohdei</i>	33.13	0.49	SUC 1		
<i>Citrobacter braakii</i>	9.94	0.43			
220073	Low discrimination				220073
<i>Citrobacter braakii</i>	53.64	0.50	SUC 7		
<i>Yersinia rohdei</i>	29.37	0.39			
<i>Salmonella</i> serovar <i>paratyphi</i>	7.44	0.13			
220143	Identification to the genus				220143
<i>Salmonella</i> serovar <i>paratyphi</i>	88.38	0.39	H2S 10		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.72	0.18	MAL 1		
<i>Citrobacter braakii</i>	2.22	0.25			
220243	Identification to the genus				220243
<i>Salmonella</i> serovar <i>paratyphi</i>	73.44	0.39	H2S 10		
<i>Salmonella</i> serovar <i>enteritidis</i>	24.17	0.33	INO 1		
<i>Citrobacter braakii</i>	1.84	0.25			
220443	Good identification				220443
<i>Salmonella</i> serovar <i>paratyphi</i>	96.05	0.39	H2S 10		
<i>Citrobacter braakii</i>	2.41	0.25	ADO 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	0.59	-.02			
221001	Good identification				221001
<i>Proteus mirabilis</i>	93.77	0.60	URE 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	6.17	0.44			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.06	-.08			
221021	Acceptable identification				221021
<i>Proteus mirabilis</i>	93.33	0.44	URE 98		
<i>Proteus vulgaris</i>	2.89	0.25			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2.22	0.20			
221043	Good identification				221043
<i>Salmonella</i> serovar <i>paratyphi</i>	96.58	0.39	H2S 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	2.42	0.25	PHE 1		
<i>Salmonella serovar enteritidis</i>	0.60	-.02			
222043	Acceptable identification				222043
<i>Salmonella serovar paratyphi</i>	93.72	0.39	H2S 10		
<i>Salmonella serovar enteritidis</i>	3.01	0.13	ESL 1		
<i>Citrobacter braakii</i>	2.35	0.25			
224002	Good identification				224002
<i>Salmonella enterica subsp. enterica</i>	99.14	0.44	LYS 95		
<i>Salmonella serovar enteritidis</i>	0.86	-.02	SOR 90		
224003	Low discrimination				224003
<i>Salmonella serovar enteritidis</i>	73.73	0.39	LYS 98		
<i>Citrobacter braakii</i>	9.08	0.35	SOR 95		
<i>Salmonella enterica subsp. houtenae</i>	6.42	0.18			
224013	Low discrimination				224013
<i>Citrobacter braakii</i>	63.42	0.42	SOR 99		
<i>Salmonella enterica subsp. houtenae</i>	22.08	0.18			
<i>Salmonella serovar enteritidis</i>	13.35	0.13			
224042	Very good identification				224042
<i>Salmonella enterica subsp. enterica</i>	96.02	0.64	LYS 95		
<i>Salmonella serovar enteritidis</i>	1.75	0.24			
<i>Citrobacter braakii</i>	1.12	0.35			
224043	Low discrimination				224043
<i>Salmonella serovar enteritidis</i>	43.53	0.65	LYS 98		
<i>Citrobacter braakii</i>	27.93	0.76			
<i>Salmonella enterica subsp. houtenae</i>	19.75	0.59			
224051	Low discrimination				224051
<i>Citrobacter braakii</i>	57.34	0.42	MAN 99		
<i>Salmonella enterica subsp. houtenae</i>	40.34	0.24			
<i>Salmonella serovar enteritidis</i>	2.32	-.02			
224052	Low discrimination				224052
<i>Citrobacter braakii</i>	55.14	0.42	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	23.44	0.23			
<i>Salmonella enterica subsp. houtenae</i>	19.20	0.18			
224053	Low discrimination				224053
<i>Citrobacter braakii</i>	71.19	0.83			
<i>Salmonella enterica subsp. houtenae</i>	24.79	0.59			
<i>Salmonella serovar enteritidis</i>	2.88	0.39			
224063	Low discrimination				224063
<i>Citrobacter braakii</i>	60.60	0.53	SUC 7		
<i>Citrobacter freundii</i>	12.79	0.41			
<i>Salmonella serovar enteritidis</i>	12.67	0.24			
224073	Low discrimination				224073

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	85.26	0.59	SUC 7		
<i>Citrobacter freundii</i>	6.96	0.39			
<i>Salmonella enterica subsp. houtenae</i>	3.98	0.18			
224143	Identification to the genus				224143
<i>Salmonella enterica subsp. salamae</i>	86.22	0.59	LYS 99		
<i>Salmonella enterica subsp. diarizonae</i>	9.36	0.37			
<i>Salmonella serovar enteritidis</i>	1.34	0.24			
224153	Low discrimination				224153
<i>Citrobacter braakii</i>	50.26	0.42	MAL 1		
<i>Salmonella enterica subsp. salamae</i>	25.01	0.18			
<i>Salmonella enterica subsp. houtenae</i>	17.50	0.18			
224243	Very good identification				224243
<i>Salmonella serovar enteritidis</i>	97.28	0.60	LYS 98		
<i>Citrobacter braakii</i>	1.17	0.35			
<i>Salmonella enterica subsp. houtenae</i>	0.83	0.18			
225001	Very good identification				225001
<i>Proteus mirabilis</i>	99.96	0.65	URE 98		
<i>Morganella morganii subsp. sibonii</i>	0.04	0.03			
225021	Good identification				225021
<i>Proteus mirabilis</i>	99.71	0.50	URE 98		
<i>Proteus vulgaris</i>	0.29	0.10			
225053	Low discrimination				225053
<i>Citrobacter braakii</i>	72.01	0.42	PHE 1		
<i>Salmonella enterica subsp. houtenae</i>	25.08	0.18			
<i>Salmonella serovar enteritidis</i>	2.91	-.02			
226043	Low discrimination				226043
<i>Salmonella serovar enteritidis</i>	73.16	0.39	LYS 98		
<i>Citrobacter braakii</i>	9.01	0.35	ESL 5		
<i>Salmonella enterica subsp. salamae</i>	8.37	0.17			
226053	Low discrimination				226053
<i>Citrobacter braakii</i>	61.67	0.42	ESL 1		
<i>Salmonella enterica subsp. houtenae</i>	21.47	0.18			
<i>Salmonella serovar enteritidis</i>	12.98	0.13			
226143	Good identification				226143
<i>Salmonella enterica subsp. salamae</i>	98.93	0.43	LYS 99		
<i>Salmonella enterica subsp. diarizonae</i>	0.61	-.04			
<i>Salmonella serovar enteritidis</i>	0.46	-.02			
230000	Very good identification				230000
<i>Edwardsiella tarda</i>	96.68	0.59	LYS 99		
<i>Morganella morganii subsp. morganii</i>	3.30	0.33			
<i>Shigella dysenteriae (group A)</i>	0.02	-.04			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
230043	Low discrimination				230043
<i>Citrobacter braakii</i>	51.55	0.60			
<i>Salmonella</i> serovar <i>paratyphi</i>	42.14	0.39			
<i>Escherichia coli</i>	4.48	0.37			
230053	Good identification				230053
<i>Citrobacter braakii</i>	90.60	0.66			
<i>Yersinia kristensenii</i>	6.96	0.33			
<i>Salmonella</i> serovar <i>paratyphi</i>	1.92	0.13			
230063	Low discrimination				230063
<i>Citrobacter braakii</i>	44.79	0.37	SUC 7		
<i>Escherichia coli</i>	34.46	0.33			
<i>Citrobacter freundii</i>	7.09	0.22			
230073	Low discrimination				230073
<i>Citrobacter braakii</i>	64.36	0.43	SUC 7		
<i>Citrobacter farmeri</i>	20.40	0.18			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	9.10	0.23			
231000	Very good identification				231000
<i>Morganella morganii</i> subsp. <i>morganii</i>	98.34	0.59	URE 96		
<i>Edwardsiella tarda</i>	1.53	0.18			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.06	0.03			
231001	Low discrimination				231001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	67.44	0.44	H2S 6		
<i>Proteus mirabilis</i>	20.91	0.25	URE 97		
<i>Morganella morganii</i> subsp. <i>morganii</i>	11.65	0.18			
234013	Good identification				234013
<i>Citrobacter braakii</i>	95.84	0.35	SOR 99		
<i>Citrobacter amalonaticus</i>	4.17	-.10			
234043	Good identification				234043
<i>Citrobacter braakii</i>	93.94	0.70			
<i>Salmonella</i> serovar <i>enteritidis</i>	3.00	0.24			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	1.36	0.18			
234051	Good identification				234051
<i>Citrobacter braakii</i>	95.84	0.35	MAN 99		
<i>Citrobacter amalonaticus</i>	4.17	-.10			
234052	Good identification				234052
<i>Citrobacter braakii</i>	95.84	0.35	TRE 99		
<i>Citrobacter amalonaticus</i>	4.17	-.10			
234053	Good identification				234053
<i>Citrobacter braakii</i>	94.71	0.76			
<i>Citrobacter amalonaticus</i>	4.12	0.31			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.68	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
234063	Identification to the genus				234063
<i>Citrobacter braakii</i>	80.59	0.47	SUC 7		
<i>Citrobacter freundii</i>	17.00	0.35			
<i>Citrobacter youngae</i>	2.40	0.15			
234073	Identification to the genus				234073
<i>Citrobacter braakii</i>	87.55	0.53	SUC 7		
<i>Citrobacter freundii</i>	7.15	0.33			
<i>Citrobacter amalonaticus</i>	3.23	0.07			
234153	Good identification				234153
<i>Citrobacter braakii</i>	95.84	0.35	MAL 1		
<i>Citrobacter amalonaticus</i>	4.17	-.10			
234253	Acceptable identification				234253
<i>Citrobacter braakii</i>	91.94	0.35	INO 1		
<i>Salmonella serovar enteritidis</i>	4.06	-.08			
<i>Citrobacter amalonaticus</i>	4.00	-.10			
234453	Acceptable identification				234453
<i>Citrobacter braakii</i>	92.54	0.35	ADO 1		
<i>Citrobacter amalonaticus</i>	4.02	-.10			
<i>Salmonella enterica subsp. houtenae</i>	3.44	-.09			
235053	Good identification				235053
<i>Citrobacter braakii</i>	95.84	0.35	PHE 1		
<i>Citrobacter amalonaticus</i>	4.17	-.10			
236053	Identification to the genus				236053
<i>Citrobacter braakii</i>	70.15	0.35	ESL 1		
<i>Citrobacter amalonaticus</i>	29.85	0.11			
240001	Low discrimination				240001
<i>Morganella morganii subsp. sibonii</i>	81.33	0.47	H2S 6		
<i>Proteus mirabilis</i>	9.12	0.19	PHE 93		
<i>Shigella dysenteriae (group A)</i>	3.99	0.18			
240020	Identification to the genus				240020
<i>Proteus vulgaris</i>	50.36	0.59	PHE 99		
<i>Proteus penneri</i>	49.65	0.50			
240021	Identification to the genus				240021
<i>Proteus penneri</i>	72.39	0.51	PHE 99		
<i>Proteus vulgaris</i>	25.75	0.51			
<i>Morganella morganii subsp. sibonii</i>	1.43	0.23			
240043	Low discrimination				240043
<i>Citrobacter youngae</i>	84.98	0.71	ONP 90		
<i>Citrobacter freundii</i>	5.45	0.49			
<i>Salmonella serovar typhi</i>	4.25	0.24			
240053	Identification to the genus				240053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	85.91	0.69	ONP 90		
<i>Citrobacter braakii</i>	5.50	0.45			
<i>Citrobacter freundii</i>	5.29	0.47			
240063	Low discrimination				240063
<i>Citrobacter freundii</i>	46.94	0.68	ONP 88		
<i>Yersinia rohdei</i>	28.78	0.56			
<i>Citrobacter youngae</i>	24.06	0.59			
240073	Low discrimination				240073
<i>Citrobacter freundii</i>	55.37	0.66	ONP 88		
<i>Citrobacter youngae</i>	29.56	0.57			
<i>Yersinia rohdei</i>	14.40	0.47			
240143	Identification to the genus				240143
<i>Citrobacter werkmanii</i>	71.72	0.37	ONP 99		
<i>Citrobacter youngae</i>	25.36	0.45	SCI 92		
<i>Citrobacter freundii</i>	2.69	0.27			
240153	Identification to the genus				240153
<i>Citrobacter youngae</i>	87.04	0.43	ONP 90		
<i>Citrobacter freundii</i>	8.85	0.25	MAL 5		
<i>Citrobacter werkmanii</i>	3.04	-.04			
240163	Low discrimination				240163
<i>Citrobacter freundii</i>	70.68	0.46	ONP 88		
<i>Citrobacter youngae</i>	21.93	0.33	MAL 8		
<i>Yersinia rohdei</i>	5.03	0.15			
240173	Identification to the genus				240173
<i>Citrobacter freundii</i>	73.89	0.44	ONP 88		
<i>Citrobacter youngae</i>	23.88	0.31	MAL 8		
<i>Yersinia rohdei</i>	2.23	0.06			
240243	Good identification				240243
<i>Citrobacter youngae</i>	97.86	0.45	ONP 90		
<i>Citrobacter freundii</i>	1.20	0.08	INO 5		
<i>Salmonella serovar typhi</i>	0.94	-.17			
240253	Low discrimination				240253
<i>Citrobacter youngae</i>	87.43	0.43	ONP 90		
<i>Yersinia kristensenii</i>	10.46	0.14	INO 5		
<i>Citrobacter braakii</i>	1.08	0.04			
241000	Low discrimination				241000
<i>Proteus vulgaris</i>	68.83	0.69	SUC 97		
<i>Proteus penneri</i>	22.16	0.50			
<i>Morganella morganii subsp. morganii</i>	6.94	0.35			
241001	Low discrimination				241001
<i>Morganella morganii subsp. sibonii</i>	51.99	0.70	H2S 6		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus mirabilis</i>	21.50	0.53			
<i>Proteus vulgaris</i>	13.80	0.61			
241020	Identification to the genus				241020
<i>Proteus vulgaris</i>	50.35	1.00			
<i>Proteus penneri</i>	49.64	0.91			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.00	0.05			
241021	Identification to the genus				241021
<i>Proteus penneri</i>	73.46	0.92			
<i>Proteus vulgaris</i>	26.13	0.92			
<i>Proteus mirabilis</i>	0.22	0.38			
241022	Identification to the genus				241022
<i>Proteus vulgaris</i>	50.36	0.59	MAN 1		
<i>Proteus penneri</i>	49.65	0.50			
241023	Identification to the genus				241023
<i>Proteus penneri</i>	73.46	0.51	MAN 1		
<i>Proteus vulgaris</i>	26.13	0.51			
<i>Proteus mirabilis</i>	0.22	-.03			
241030	Identification to the genus				241030
<i>Proteus vulgaris</i>	50.36	0.59	CEL 1		
<i>Proteus penneri</i>	49.65	0.50			
241031	Identification to the genus				241031
<i>Proteus penneri</i>	73.46	0.51	CEL 1		
<i>Proteus vulgaris</i>	26.13	0.51			
<i>Proteus mirabilis</i>	0.22	-.03			
241060	Identification to the genus				241060
<i>Proteus vulgaris</i>	50.36	0.59	SOR 1		
<i>Proteus penneri</i>	49.65	0.50			
241061	Identification to the genus				241061
<i>Proteus penneri</i>	73.46	0.51	SOR 1		
<i>Proteus vulgaris</i>	26.13	0.51			
<i>Proteus mirabilis</i>	0.22	-.03			
241120	Identification to the genus				241120
<i>Proteus vulgaris</i>	50.36	0.59	MAL 1		
<i>Proteus penneri</i>	49.65	0.50			
241121	Identification to the genus				241121
<i>Proteus penneri</i>	73.29	0.51	MAL 1		
<i>Proteus vulgaris</i>	26.07	0.51			
<i>Proteus mirabilis</i>	0.45	0.03			
241220	Identification to the genus				241220
<i>Proteus vulgaris</i>	50.36	0.59	INO 1		
<i>Proteus penneri</i>	49.65	0.50			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
241221	Identification to the genus				241221
<i>Proteus penneri</i>	73.46	0.51	INO 1		
<i>Proteus vulgaris</i>	26.13	0.51			
<i>Proteus mirabilis</i>	0.22	-.03			
241420	Identification to the genus				241420
<i>Proteus vulgaris</i>	50.36	0.59	ADO 1		
<i>Proteus penneri</i>	49.65	0.50			
241421	Identification to the genus				241421
<i>Proteus penneri</i>	73.46	0.51	ADO 1		
<i>Proteus vulgaris</i>	26.13	0.51			
<i>Proteus mirabilis</i>	0.22	-.03			
242003	Good identification				242003
<i>Yersinia pseudotuberculosis</i>	99.93	0.51	H2S 1		
<i>Citrobacter youngae</i>	0.08	0.04			
242020	Very good identification				242020
<i>Proteus vulgaris</i>	99.01	0.59	PHE 99		
<i>Proteus penneri</i>	0.99	0.09			
242021	Good identification				242021
<i>Proteus vulgaris</i>	97.24	0.51	PHE 99		
<i>Proteus penneri</i>	2.76	0.10			
242043	Low discrimination				242043
<i>Citrobacter youngae</i>	86.42	0.45	ONP 90		
<i>Yersinia pseudotuberculosis</i>	11.69	0.10	ESL 5		
<i>Citrobacter freundii</i>	1.06	0.08			
242053	Good identification				242053
<i>Citrobacter youngae</i>	97.65	0.43	ONP 90		
<i>Citrobacter braakii</i>	1.20	0.04	ESL 5		
<i>Citrobacter freundii</i>	1.15	0.06			
243000	Very good identification				243000
<i>Proteus vulgaris</i>	99.58	0.69	SUC 97		
<i>Proteus penneri</i>	0.32	0.09			
<i>Morganella morganii subsp. morganii</i>	0.10	-.06			
243001	Good identification				243001
<i>Proteus vulgaris</i>	94.07	0.61	SUC 97		
<i>Morganella morganii subsp. sibonii</i>	3.58	0.29			
<i>Proteus mirabilis</i>	1.48	0.12			
243020	Excellent identification				243020
<i>Proteus vulgaris</i>	99.01	1.00			
<i>Proteus penneri</i>	0.99	0.50			
243021	Very good identification				243021

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus vulgaris</i>	97.22	0.92			
<i>Proteus penneri</i>	2.76	0.51			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.01	0.05			
243022	Very good identification				243022
<i>Proteus vulgaris</i>	99.01	0.59	MAN 1		
<i>Proteus penneri</i>	0.99	0.09			
243023	Good identification				243023
<i>Proteus vulgaris</i>	97.24	0.51	MAN 1		
<i>Proteus penneri</i>	2.76	0.10			
243030	Very good identification				243030
<i>Proteus vulgaris</i>	99.01	0.59	CEL 1		
<i>Proteus penneri</i>	0.99	0.09			
243031	Good identification				243031
<i>Proteus vulgaris</i>	97.24	0.51	CEL 1		
<i>Proteus penneri</i>	2.76	0.10			
243060	Very good identification				243060
<i>Proteus vulgaris</i>	99.01	0.59	SOR 1		
<i>Proteus penneri</i>	0.99	0.09			
243061	Good identification				243061
<i>Proteus vulgaris</i>	97.24	0.51	SOR 1		
<i>Proteus penneri</i>	2.76	0.10			
243120	Very good identification				243120
<i>Proteus vulgaris</i>	99.01	0.59	MAL 1		
<i>Proteus penneri</i>	0.99	0.09			
243121	Good identification				243121
<i>Proteus vulgaris</i>	97.24	0.51	MAL 1		
<i>Proteus penneri</i>	2.76	0.10			
243220	Very good identification				243220
<i>Proteus vulgaris</i>	99.01	0.59	INO 1		
<i>Proteus penneri</i>	0.99	0.09			
243221	Good identification				243221
<i>Proteus vulgaris</i>	97.24	0.51	INO 1		
<i>Proteus penneri</i>	2.76	0.10			
243420	Very good identification				243420
<i>Proteus vulgaris</i>	99.01	0.59	ADO 1		
<i>Proteus penneri</i>	0.99	0.09			
243421	Good identification				243421
<i>Proteus vulgaris</i>	97.24	0.51	ADO 1		
<i>Proteus penneri</i>	2.76	0.10			
244003	Identification to the genus				244003

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	59.08	0.39	ONP 90		
<i>Citrobacter werkmanii</i>	33.99	0.17	SOR 99		
<i>Citrobacter freundii</i>	5.32	0.20			
244013	Identification to the genus				244013
<i>Citrobacter youngae</i>	86.65	0.38	ONP 90		
<i>Citrobacter freundii</i>	7.50	0.18	SOR 99		
<i>Citrobacter braakii</i>	5.85	0.14			
244020	Acceptable identification				244020
<i>Proteus vulgaris</i>	94.66	0.43	PHE 99		
<i>Proteus penneri</i>	5.34	0.09			
244021	Identification to the genus				244021
<i>Proteus vulgaris</i>	74.53	0.36	PHE 99		
<i>Proteus mirabilis</i>	13.47	0.09			
<i>Proteus penneri</i>	12.00	0.10			
244023	Identification to the genus				244023
<i>Citrobacter freundii</i>	73.27	0.39	ONP 88		
<i>Citrobacter youngae</i>	26.73	0.27	SOR 99		
244033	Identification to the genus				244033
<i>Citrobacter freundii</i>	72.47	0.37	ONP 88		
<i>Citrobacter youngae</i>	27.53	0.26	SOR 99		
244041	Identification to the genus				244041
<i>Citrobacter youngae</i>	85.50	0.39	ONP 90		
<i>Citrobacter freundii</i>	7.70	0.20	MAN 99		
<i>Citrobacter werkmanii</i>	4.47	-.04			
244042	Identification to the genus				244042
<i>Citrobacter youngae</i>	85.50	0.39	ONP 90		
<i>Citrobacter freundii</i>	7.70	0.20	TRE 99		
<i>Citrobacter werkmanii</i>	4.47	-.04			
244043	Identification to the genus				244043
<i>Citrobacter youngae</i>	85.47	0.80	ONP 90		
<i>Citrobacter freundii</i>	7.70	0.61			
<i>Citrobacter werkmanii</i>	4.47	0.37			
244051	Identification to the genus				244051
<i>Citrobacter youngae</i>	86.65	0.38	ONP 90		
<i>Citrobacter freundii</i>	7.50	0.18	MAN 99		
<i>Citrobacter braakii</i>	5.85	0.14			
244052	Identification to the genus				244052
<i>Citrobacter youngae</i>	86.65	0.38	ONP 90		
<i>Citrobacter freundii</i>	7.50	0.18	TRE 99		
<i>Citrobacter braakii</i>	5.85	0.14			
244053	Identification to the genus				244053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	86.53	0.79	ONP 90		
<i>Citrobacter freundii</i>	7.49	0.59			
<i>Citrobacter braakii</i>	5.84	0.55			
244061	Identification to the genus				244061
<i>Citrobacter freundii</i>	73.27	0.39	ONP 88		
<i>Citrobacter youngae</i>	26.73	0.27	MAN 99		
244062	Identification to the genus				244062
<i>Citrobacter freundii</i>	73.27	0.39	ONP 88		
<i>Citrobacter youngae</i>	26.73	0.27	TRE 99		
244063	Identification to the genus				244063
<i>Citrobacter freundii</i>	73.00	0.80	ONP 88		
<i>Citrobacter youngae</i>	26.63	0.69			
<i>Citrobacter braakii</i>	0.21	0.26			
244071	Identification to the genus				244071
<i>Citrobacter freundii</i>	72.47	0.37	ONP 88		
<i>Citrobacter youngae</i>	27.53	0.26	MAN 99		
244072	Identification to the genus				244072
<i>Citrobacter freundii</i>	72.47	0.37	ONP 88		
<i>Citrobacter youngae</i>	27.53	0.26	TRE 99		
244073	Identification to the genus				244073
<i>Citrobacter freundii</i>	72.06	0.78	ONP 88		
<i>Citrobacter youngae</i>	27.37	0.67			
<i>Citrobacter braakii</i>	0.52	0.32			
244103	Good identification				244103
<i>Citrobacter werkmanii</i>	99.21	0.39	ONP 99		
<i>Citrobacter youngae</i>	0.79	0.13	SOR 90		
244143	Good identification				244143
<i>Citrobacter werkmanii</i>	90.83	0.59	ONP 99		
<i>Citrobacter youngae</i>	7.95	0.54			
<i>Citrobacter freundii</i>	1.18	0.40			
244153	Identification to the genus				244153
<i>Citrobacter youngae</i>	77.10	0.52	ONP 90		
<i>Citrobacter freundii</i>	11.02	0.37	MAL 5		
<i>Citrobacter werkmanii</i>	10.88	0.18			
244163	Identification to the genus				244163
<i>Citrobacter freundii</i>	75.95	0.58	ONP 88		
<i>Citrobacter youngae</i>	16.77	0.42	MAL 8		
<i>Citrobacter werkmanii</i>	7.28	0.18			
244173	Identification to the genus				244173
<i>Citrobacter freundii</i>	81.31	0.56	ONP 88		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	18.69	0.40	MAL 8		
244243	Very good identification				244243
<i>Citrobacter youngae</i>	96.57	0.54	ONP 90		
<i>Citrobacter freundii</i>	1.67	0.20	INO 5		
<i>Citrobacter werkmanii</i>	0.97	-.04			
244253	Good identification				244253
<i>Citrobacter youngae</i>	97.13	0.52	ONP 90		
<i>Citrobacter freundii</i>	1.61	0.18	INO 5		
<i>Citrobacter braakii</i>	1.26	0.14			
244263	Identification to the genus				244263
<i>Citrobacter youngae</i>	65.53	0.42	ONP 90		
<i>Citrobacter freundii</i>	34.48	0.39	INO 5		
244273	Identification to the genus				244273
<i>Citrobacter youngae</i>	66.43	0.40	ONP 90		
<i>Citrobacter freundii</i>	33.57	0.37	INO 5		
244443	Identification to the genus				244443
<i>Citrobacter youngae</i>	85.50	0.39	ONP 90		
<i>Citrobacter freundii</i>	7.70	0.20	ADO 1		
<i>Citrobacter werkmanii</i>	4.47	-.04			
244453	Identification to the genus				244453
<i>Citrobacter youngae</i>	86.65	0.38	ONP 90		
<i>Citrobacter freundii</i>	7.50	0.18	ADO 1		
<i>Citrobacter braakii</i>	5.85	0.14			
244463	Identification to the genus				244463
<i>Citrobacter freundii</i>	73.27	0.39	ONP 88		
<i>Citrobacter youngae</i>	26.73	0.27	ADO 1		
244473	Identification to the genus				244473
<i>Citrobacter freundii</i>	72.47	0.37	ONP 88		
<i>Citrobacter youngae</i>	27.53	0.26	ADO 1		
245000	Identification to the genus				245000
<i>Proteus vulgaris</i>	85.65	0.53	SUC 97		
<i>Proteus mirabilis</i>	12.28	0.24			
<i>Proteus penneri</i>	1.58	0.09			
245001	Good identification				245001
<i>Proteus mirabilis</i>	92.82	0.59	ORN 99		
<i>Proteus vulgaris</i>	5.66	0.46			
<i>Morganella morganii subsp. sibonii</i>	1.22	0.29			
245020	Good identification				245020
<i>Proteus vulgaris</i>	94.59	0.85			
<i>Proteus penneri</i>	5.34	0.50			
<i>Proteus mirabilis</i>	0.07	0.09			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
245021	Identification to the genus				245021
<i>Proteus vulgaris</i>	79.95	0.77			
<i>Proteus penneri</i>	12.87	0.51			
<i>Proteus mirabilis</i>	7.15	0.43			
245022	Acceptable identification				245022
<i>Proteus vulgaris</i>	94.66	0.43	MAN 1		
<i>Proteus penneri</i>	5.34	0.09			
245023	Identification to the genus				245023
<i>Proteus vulgaris</i>	79.97	0.36	MAN 1		
<i>Proteus penneri</i>	12.87	0.10			
<i>Proteus mirabilis</i>	7.16	0.02			
245030	Acceptable identification				245030
<i>Proteus vulgaris</i>	94.66	0.43	CEL 1		
<i>Proteus penneri</i>	5.34	0.09			
245031	Identification to the genus				245031
<i>Proteus vulgaris</i>	79.97	0.36	CEL 1		
<i>Proteus penneri</i>	12.87	0.10			
<i>Proteus mirabilis</i>	7.16	0.02			
245043	Identification to the genus				245043
<i>Citrobacter youngae</i>	85.50	0.39	ONP 90		
<i>Citrobacter freundii</i>	7.70	0.20	PHE 1		
<i>Citrobacter werkmanii</i>	4.47	-0.04			
245053	Identification to the genus				245053
<i>Citrobacter youngae</i>	86.65	0.38	ONP 90		
<i>Citrobacter freundii</i>	7.50	0.18	PHE 1		
<i>Citrobacter braakii</i>	5.85	0.14			
245060	Acceptable identification				245060
<i>Proteus vulgaris</i>	94.66	0.43	SOR 1		
<i>Proteus penneri</i>	5.34	0.09			
245061	Identification to the genus				245061
<i>Proteus vulgaris</i>	79.97	0.36	SOR 1		
<i>Proteus penneri</i>	12.87	0.10			
<i>Proteus mirabilis</i>	7.16	0.02			
245063	Identification to the genus				245063
<i>Citrobacter freundii</i>	73.27	0.39	ONP 88		
<i>Citrobacter youngae</i>	26.73	0.27	PHE 1		
245073	Identification to the genus				245073
<i>Citrobacter freundii</i>	72.47	0.37	ONP 88		
<i>Citrobacter youngae</i>	27.53	0.26	PHE 1		
245120	Acceptable identification				245120

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus vulgaris</i>	94.66	0.43	MAL 1		
<i>Proteus penneri</i>	5.34	0.09			
245121	Identification to the genus				245121
<i>Proteus vulgaris</i>	74.53	0.36	MAL 1		
<i>Proteus mirabilis</i>	13.47	0.09			
<i>Proteus penneri</i>	12.00	0.10			
245220	Acceptable identification				245220
<i>Proteus vulgaris</i>	94.66	0.43	INO 1		
<i>Proteus penneri</i>	5.34	0.09			
245221	Low discrimination				245221
<i>Proteus vulgaris</i>	69.39	0.36	INO 1		
<i>Providencia stuartii</i>	13.23	0.17			
<i>Proteus penneri</i>	11.17	0.10			
245420	Acceptable identification				245420
<i>Proteus vulgaris</i>	94.66	0.43	ADO 1		
<i>Proteus penneri</i>	5.34	0.09			
245421	Identification to the genus				245421
<i>Proteus vulgaris</i>	79.97	0.36	ADO 1		
<i>Proteus penneri</i>	12.87	0.10			
<i>Proteus mirabilis</i>	7.16	0.02			
246020	Good identification				246020
<i>Proteus vulgaris</i>	100.0	0.43	PHE 99		
246021	Good identification				246021
<i>Proteus vulgaris</i>	100.0	0.36	PHE 99		
246043	Very good identification				246043
<i>Citrobacter youngae</i>	96.85	0.54	ONP 90		
<i>Citrobacter freundii</i>	1.67	0.20	ESL 5		
<i>Citrobacter werkmanii</i>	0.97	-.04			
246053	Good identification				246053
<i>Citrobacter youngae</i>	97.13	0.52	ONP 90		
<i>Citrobacter freundii</i>	1.61	0.18	ESL 5		
<i>Citrobacter braakii</i>	1.26	0.14			
246063	Identification to the genus				246063
<i>Citrobacter youngae</i>	65.53	0.42	ONP 90		
<i>Citrobacter freundii</i>	34.48	0.39	ESL 5		
246073	Identification to the genus				246073
<i>Citrobacter youngae</i>	66.43	0.40	ONP 90		
<i>Citrobacter freundii</i>	33.57	0.37	ESL 5		
247000	Very good identification				247000
<i>Proteus vulgaris</i>	100.0	0.53	SUC 97		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
247001	Identification to the genus				247001
<i>Proteus vulgaris</i>	85.79	0.46	SUC 97		
<i>Proteus mirabilis</i>	14.21	0.18			
247020	Very good identification				247020
<i>Proteus vulgaris</i>	99.94	0.85			
<i>Proteus penneri</i>	0.06	0.09			
247021	Very good identification				247021
<i>Proteus vulgaris</i>	99.75	0.77			
<i>Proteus penneri</i>	0.16	0.10			
<i>Proteus mirabilis</i>	0.09	0.02			
247022	Good identification				247022
<i>Proteus vulgaris</i>	100.0	0.43	MAN 1		
247023	Good identification				247023
<i>Proteus vulgaris</i>	100.0	0.36	MAN 1		
247030	Good identification				247030
<i>Proteus vulgaris</i>	100.0	0.43	CEL 1		
247031	Good identification				247031
<i>Proteus vulgaris</i>	100.0	0.36	CEL 1		
247060	Good identification				247060
<i>Proteus vulgaris</i>	100.0	0.43	SOR 1		
247061	Good identification				247061
<i>Proteus vulgaris</i>	100.0	0.36	SOR 1		
247120	Good identification				247120
<i>Proteus vulgaris</i>	100.0	0.43	MAL 1		
247121	Good identification				247121
<i>Proteus vulgaris</i>	100.0	0.36	MAL 1		
247220	Good identification				247220
<i>Proteus vulgaris</i>	100.0	0.43	INO 1		
247221	Good identification				247221
<i>Proteus vulgaris</i>	100.0	0.36	INO 1		
247420	Good identification				247420
<i>Proteus vulgaris</i>	100.0	0.43	ADO 1		
247421	Good identification				247421
<i>Proteus vulgaris</i>	100.0	0.36	ADO 1		
250000	Low discrimination				250000

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	89.47	0.35	ORN 95		
<i>Proteus vulgaris</i>	8.96	0.28	PHE 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.09	0.06			
250001	Acceptable identification				250001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	92.24	0.47	H2S 6		
<i>Shigella dysenteriae</i> (group A)	3.70	0.16	PHE 93		
<i>Proteus vulgaris</i>	3.29	0.20			
250020	Very good identification				250020
<i>Proteus vulgaris</i>	98.71	0.59	PHE 99		
<i>Proteus penneri</i>	0.98	0.09			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.31	-0.06			
250021	Acceptable identification				250021
<i>Proteus vulgaris</i>	92.27	0.51	PHE 99		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	5.11	0.23			
<i>Proteus penneri</i>	2.62	0.10			
250043	Identification to the genus				250043
<i>Citrobacter youngae</i>	78.14	0.56	ONP 90		
<i>Citrobacter freundii</i>	13.98	0.43			
<i>Citrobacter braakii</i>	5.63	0.33			
250053	Low discrimination				250053
<i>Citrobacter youngae</i>	69.58	0.54	ONP 90		
<i>Citrobacter braakii</i>	12.44	0.39			
<i>Citrobacter freundii</i>	11.95	0.41			
250063	Identification to the genus				250063
<i>Citrobacter freundii</i>	83.33	0.61	ONP 88		
<i>Citrobacter youngae</i>	15.31	0.44			
<i>Yersinia rohdei</i>	1.05	0.15			
250073	Identification to the genus				250073
<i>Citrobacter freundii</i>	82.58	0.59	ONP 88		
<i>Citrobacter youngae</i>	15.79	0.42			
<i>Citrobacter braakii</i>	0.80	0.16			
250163	Identification to the genus				250163
<i>Citrobacter freundii</i>	90.00	0.40	ONP 88		
<i>Citrobacter youngae</i>	10.01	0.17	MAL 8		
250173	Identification to the genus				250173
<i>Citrobacter freundii</i>	89.62	0.37	ONP 88		
<i>Citrobacter youngae</i>	10.38	0.16	MAL 8		
251000	Low discrimination				251000
<i>Morganella morganii</i> subsp. <i>morganii</i>	65.28	0.61	ORN 95		
<i>Proteus vulgaris</i>	34.06	0.69			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.56	0.29			
251001	Low discrimination				251001

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	77.59	0.70	H2S 6		
<i>Proteus vulgaris</i>	20.60	0.61			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.93	0.20			
251020	Very good identification				251020
<i>Proteus vulgaris</i>	98.95	1.00			
<i>Proteus penneri</i>	0.99	0.50			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.06	0.20			
251021	Very good identification				251021
<i>Proteus vulgaris</i>	96.52	0.92			
<i>Proteus penneri</i>	2.74	0.51			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.72	0.46			
251022	Very good identification				251022
<i>Proteus vulgaris</i>	99.01	0.59	MAN 1		
<i>Proteus penneri</i>	0.99	0.09			
251023	Good identification				251023
<i>Proteus vulgaris</i>	96.54	0.51	MAN 1		
<i>Proteus penneri</i>	2.74	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.72	0.05			
251030	Very good identification				251030
<i>Proteus vulgaris</i>	99.01	0.59	CEL 1		
<i>Proteus penneri</i>	0.99	0.09			
251031	Good identification				251031
<i>Proteus vulgaris</i>	96.54	0.51	CEL 1		
<i>Proteus penneri</i>	2.74	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.72	0.05			
251060	Very good identification				251060
<i>Proteus vulgaris</i>	99.01	0.59	SOR 1		
<i>Proteus penneri</i>	0.99	0.09			
251061	Good identification				251061
<i>Proteus vulgaris</i>	96.54	0.51	SOR 1		
<i>Proteus penneri</i>	2.74	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.72	0.05			
251120	Very good identification				251120
<i>Proteus vulgaris</i>	99.01	0.59	MAL 1		
<i>Proteus penneri</i>	0.99	0.09			
251121	Good identification				251121
<i>Proteus vulgaris</i>	96.54	0.51	MAL 1		
<i>Proteus penneri</i>	2.74	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.72	0.05			
251220	Very good identification				251220

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus vulgaris</i>	99.01	0.59	INO 1		
<i>Proteus penneri</i>	0.99	0.09			
251221	Low discrimination				251221
<i>Proteus vulgaris</i>	86.21	0.51	INO 1		
<i>Providencia stuartii</i>	10.70	0.28			
<i>Proteus penneri</i>	2.45	0.10			
251420	Very good identification				251420
<i>Proteus vulgaris</i>	99.01	0.59	ADO 1		
<i>Proteus penneri</i>	0.99	0.09			
251421	Good identification				251421
<i>Proteus vulgaris</i>	96.54	0.51	ADO 1		
<i>Proteus penneri</i>	2.74	0.10			
<i>Morganella morganii subsp. sibonii</i>	0.72	0.05			
252020	Very good identification				252020
<i>Proteus vulgaris</i>	100.0	0.59	PHE 99		
252021	Good identification				252021
<i>Proteus vulgaris</i>	100.0	0.51	PHE 99		
253000	Very good identification				253000
<i>Proteus vulgaris</i>	98.10	0.69	SUC 97		
<i>Morganella morganii subsp. morganii</i>	1.90	0.20			
253001	Very good identification				253001
<i>Proteus vulgaris</i>	96.33	0.61	SUC 97		
<i>Morganella morganii subsp. sibonii</i>	3.67	0.29			
253020	Excellent identification				253020
<i>Proteus vulgaris</i>	99.99	1.00			
<i>Proteus penneri</i>	0.01	0.09			
253021	Very good identification				253021
<i>Proteus vulgaris</i>	99.96	0.92			
<i>Proteus penneri</i>	0.03	0.10			
<i>Morganella morganii subsp. sibonii</i>	0.01	0.05			
253022	Very good identification				253022
<i>Proteus vulgaris</i>	100.0	0.59	MAN 1		
253023	Good identification				253023
<i>Proteus vulgaris</i>	100.0	0.51	MAN 1		
253030	Very good identification				253030
<i>Proteus vulgaris</i>	100.0	0.59	CEL 1		
253031	Good identification				253031
<i>Proteus vulgaris</i>	100.0	0.51	CEL 1		
253060	Very good identification				253060

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus vulgaris</i>	100.0	0.59	SOR 1		
253061	Good identification				253061
<i>Proteus vulgaris</i>	100.0	0.51	SOR 1		
253120	Very good identification				253120
<i>Proteus vulgaris</i>	100.0	0.59	MAL 1		
253121	Good identification				253121
<i>Proteus vulgaris</i>	100.0	0.51	MAL 1		
253220	Very good identification				253220
<i>Proteus vulgaris</i>	100.0	0.59	INO 1		
253221	Good identification				253221
<i>Proteus vulgaris</i>	100.0	0.51	INO 1		
253420	Very good identification				253420
<i>Proteus vulgaris</i>	100.0	0.59	ADO 1		
253421	Good identification				253421
<i>Proteus vulgaris</i>	100.0	0.51	ADO 1		
254020	Good identification				254020
<i>Proteus vulgaris</i>	100.0	0.43	PHE 99		
254021	Good identification				254021
<i>Proteus vulgaris</i>	97.48	0.36	PHE 99		
<i>Providencia stuartii</i>	2.52	-.01			
254043	Identification to the genus				254043
<i>Citrobacter youngae</i>	75.17	0.65	ONP 90		
<i>Citrobacter freundii</i>	18.90	0.55			
<i>Citrobacter braakii</i>	5.71	0.42			
254053	Low discrimination				254053
<i>Citrobacter youngae</i>	66.09	0.63	ONP 90		
<i>Citrobacter freundii</i>	15.96	0.53			
<i>Citrobacter braakii</i>	12.46	0.49			
254063	Identification to the genus				254063
<i>Citrobacter freundii</i>	88.22	0.74	ONP 88		
<i>Citrobacter youngae</i>	11.53	0.53			
<i>Citrobacter braakii</i>	0.25	0.19			
254073	Identification to the genus				254073
<i>Citrobacter freundii</i>	87.26	0.72	ONP 88		
<i>Citrobacter youngae</i>	11.88	0.51			
<i>Citrobacter braakii</i>	0.63	0.26			
254143	Identification to the genus				254143

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	48.32	0.39	ONP 90		
<i>Citrobacter werkmanii</i>	31.61	0.18	MAL 5		
<i>Citrobacter freundii</i>	20.07	0.33			
254153	Identification to the genus				254153
<i>Citrobacter youngae</i>	69.69	0.37	ONP 90		
<i>Citrobacter freundii</i>	27.79	0.31	MAL 5		
<i>Citrobacter braakii</i>	2.52	0.08			
254163	Acceptable identification				254163
<i>Citrobacter freundii</i>	92.67	0.52	ONP 88		
<i>Citrobacter youngae</i>	7.33	0.27	MAL 8		
254173	Acceptable identification				254173
<i>Citrobacter freundii</i>	92.39	0.50	ONP 88		
<i>Citrobacter youngae</i>	7.61	0.25	MAL 8		
254243	Good identification				254243
<i>Citrobacter youngae</i>	95.40	0.39	ONP 90		
<i>Citrobacter freundii</i>	4.60	0.14	INO 5		
254253	Acceptable identification				254253
<i>Citrobacter youngae</i>	92.38	0.37	ONP 90		
<i>Citrobacter freundii</i>	4.28	0.12	INO 5		
<i>Citrobacter braakii</i>	3.34	0.08			
255000	Low discrimination				255000
<i>Proteus vulgaris</i>	89.70	0.53	SUC 97		
<i>Morganella morganii subsp. morganii</i>	9.84	0.20			
<i>Proteus mirabilis</i>	0.26	-.11			
255001	Low discrimination				255001
<i>Proteus vulgaris</i>	58.45	0.46	SUC 97		
<i>Proteus mirabilis</i>	19.56	0.24			
<i>Morganella morganii subsp. sibonii</i>	12.60	0.29			
255020	Very good identification				255020
<i>Proteus vulgaris</i>	99.94	0.85			
<i>Proteus penneri</i>	0.06	0.09			
255021	Very good identification				255021
<i>Proteus vulgaris</i>	99.12	0.77			
<i>Providencia stuartii</i>	0.49	0.25			
<i>Proteus mirabilis</i>	0.18	0.09			
255022	Good identification				255022
<i>Proteus vulgaris</i>	100.0	0.43	MAN 1		
255023	Acceptable identification				255023
<i>Proteus vulgaris</i>	94.82	0.36	MAN 1		
<i>Providencia stuartii</i>	5.18	0.05			
255030	Good identification				255030

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
<i>Proteus vulgaris</i>		100.0	0.43	CEL 1		
255031	Good identification					255031
<i>Proteus vulgaris</i>		97.48	0.36	CEL 1		
<i>Providencia stuartii</i>		2.52	-.01			
255060	Good identification					255060
<i>Proteus vulgaris</i>		100.0	0.43	SOR 1		
255061	Good identification					255061
<i>Proteus vulgaris</i>		100.0	0.36	SOR 1		
255120	Good identification					255120
<i>Proteus vulgaris</i>		100.0	0.43	MAL 1		
255121	Good identification					255121
<i>Proteus vulgaris</i>		100.0	0.36	MAL 1		
255201	Good identification					255201
<i>Providencia stuartii</i>		99.67	0.51	H2S 1		
<i>Proteus vulgaris</i>		0.33	0.05			
255220	Acceptable identification					255220
<i>Proteus vulgaris</i>		92.45	0.43	INO 1		
<i>Providencia stuartii</i>		7.56	0.17			
255221	Acceptable identification					255221
<i>Providencia stuartii</i>		90.33	0.51	H2S 1		
<i>Proteus vulgaris</i>		9.67	0.36			
255402	Good identification					255402
<i>Providencia rettgeri</i>		99.67	0.39	H2S 1		
<i>Providencia alcalifaciens</i>		0.33	-.17	INO 90		
255420	Acceptable identification					255420
<i>Proteus vulgaris</i>		94.43	0.43	ADO 1		
<i>Providencia alcalifaciens</i>		5.57	0.02			
255421	Good identification					255421
<i>Proteus vulgaris</i>		97.48	0.36	ADO 1		
<i>Providencia stuartii</i>		2.52	-.01			
255602	Very good identification					255602
<i>Providencia rettgeri</i>		100.0	0.59	H2S 1		
255622	Good identification					255622
<i>Providencia rettgeri</i>		100.0	0.43	H2S 1		
256020	Good identification					256020
<i>Proteus vulgaris</i>		100.0	0.43	PHE 99		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
256021	Good identification					256021
<i>Proteus vulgaris</i>		100.0	0.36	PHE 99		
256043	Good identification					256043
<i>Citrobacter youngae</i>		95.40	0.39	ONP 90		
<i>Citrobacter freundii</i>		4.60	0.14	ESL 5		
256053	Identification to the genus					256053
<i>Citrobacter youngae</i>		80.73	0.37	ONP 90		
<i>Citrobacter amalonaticus</i>		12.61	0.04	ESL 5		
<i>Citrobacter freundii</i>		3.74	0.12			
257000	Very good identification					257000
<i>Proteus vulgaris</i>		100.0	0.53	SUC 97		
257001	Good identification					257001
<i>Proteus vulgaris</i>		100.0	0.46	SUC 97		
257020	Very good identification					257020
<i>Proteus vulgaris</i>		100.0	0.85			
257021	Very good identification					257021
<i>Proteus vulgaris</i>		100.0	0.77			
257022	Good identification					257022
<i>Proteus vulgaris</i>		100.0	0.43	MAN 1		
257023	Good identification					257023
<i>Proteus vulgaris</i>		100.0	0.36	MAN 1		
257030	Good identification					257030
<i>Proteus vulgaris</i>		100.0	0.43	CEL 1		
257031	Good identification					257031
<i>Proteus vulgaris</i>		100.0	0.36	CEL 1		
257060	Good identification					257060
<i>Proteus vulgaris</i>		100.0	0.43	SOR 1		
257061	Good identification					257061
<i>Proteus vulgaris</i>		100.0	0.36	SOR 1		
257120	Good identification					257120
<i>Proteus vulgaris</i>		100.0	0.43	MAL 1		
257121	Good identification					257121
<i>Proteus vulgaris</i>		100.0	0.36	MAL 1		
257220	Good identification					257220
<i>Proteus vulgaris</i>		100.0	0.43	INO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
257221	Acceptable identification				257221
<i>Proteus vulgaris</i>	91.38	0.36	INO 1		
<i>Providencia stuartii</i>	8.62	0.10			
257420	Good identification				257420
<i>Proteus vulgaris</i>	100.0	0.43	ADO 1		
257421	Good identification				257421
<i>Proteus vulgaris</i>	100.0	0.36	ADO 1		
257602	Very good identification				257602
<i>Providencia rettgeri</i>	100.0	0.53	H2S 1		
257622	Good identification				257622
<i>Providencia rettgeri</i>	100.0	0.38	H2S 1		
260000	Low discrimination				260000
<i>Morganella morganii</i> subsp. <i>morganii</i>	77.25	0.35	IND 95		
<i>Proteus mirabilis</i>	21.08	0.25	PHE 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.67	0.11			
260001	Low discrimination				260001
<i>Proteus mirabilis</i>	86.14	0.60	PHE 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	13.80	0.52			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.07	-0.6			
260021	Acceptable identification				260021
<i>Proteus mirabilis</i>	92.54	0.44	PHE 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	5.36	0.28			
<i>Proteus penneri</i>	1.55	0.10			
260043	Low discrimination				260043
<i>Citrobacter braakii</i>	56.49	0.62			
<i>Salmonella</i> serovar <i>paratyphi</i>	37.11	0.39			
<i>Citrobacter youngae</i>	5.09	0.40			
260053	Low discrimination				260053
<i>Citrobacter braakii</i>	65.01	0.68			
<i>Yersinia kristensenii</i>	31.34	0.51			
<i>Citrobacter youngae</i>	2.36	0.38			
260063	Low discrimination				260063
<i>Yersinia rohdei</i>	69.04	0.47	H2S 1		
<i>Citrobacter braakii</i>	16.82	0.39			
<i>Citrobacter youngae</i>	5.36	0.28			
260073	Low discrimination				260073
<i>Citrobacter braakii</i>	43.74	0.45	SUC 7		
<i>Yersinia rohdei</i>	29.47	0.37			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	14.91	0.33			
260253	Low discrimination				260253

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia kristensenii</i>	87.63	0.36	H2S 1		
<i>Citrobacter braakii</i>	10.40	0.27			
<i>Citrobacter youngae</i>	1.97	0.12			
261000	Low discrimination				261000
<i>Morganella morganii</i> subsp. <i>morganii</i>	57.94	0.61	IND 95		
<i>Proteus mirabilis</i>	40.78	0.60			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.88	0.34			
261001	Very good identification				261001
<i>Proteus mirabilis</i>	95.80	0.95			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.16	0.75			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.03	0.20			
261003	Very good identification				261003
<i>Proteus mirabilis</i>	95.84	0.53	MAN 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.16	0.34			
261011	Very good identification				261011
<i>Proteus mirabilis</i>	95.84	0.53	CEL 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.16	0.34			
261020	Identification to the genus				261020
<i>Proteus vulgaris</i>	35.98	0.59	ORN 1		
<i>Proteus penneri</i>	35.47	0.50			
<i>Proteus mirabilis</i>	26.22	0.44			
261021	Good identification				261021
<i>Proteus mirabilis</i>	94.21	0.79			
<i>Proteus penneri</i>	3.18	0.51			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.48	0.51			
261023	Acceptable identification				261023
<i>Proteus mirabilis</i>	94.21	0.38	MAN 1		
<i>Proteus penneri</i>	3.18	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.48	0.10			
261031	Acceptable identification				261031
<i>Proteus mirabilis</i>	94.21	0.38	CEL 1		
<i>Proteus penneri</i>	3.18	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.48	0.10			
261041	Very good identification				261041
<i>Proteus mirabilis</i>	95.84	0.53	SOR 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.16	0.34			
261061	Acceptable identification				261061
<i>Proteus mirabilis</i>	94.21	0.38	SOR 1		
<i>Proteus penneri</i>	3.18	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.48	0.10			
261101	Very good identification				261101

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus mirabilis</i>	97.90	0.60	MAL 2		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	2.10	0.34			
261121	Good identification				261121
<i>Proteus mirabilis</i>	97.05	0.44	MAL 2		
<i>Proteus penneri</i>	1.62	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.75	0.10			
261201	Very good identification				261201
<i>Proteus mirabilis</i>	95.84	0.53	INO 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.16	0.34			
261221	Acceptable identification				261221
<i>Proteus mirabilis</i>	94.21	0.38	INO 1		
<i>Proteus penneri</i>	3.18	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.48	0.10			
261401	Very good identification				261401
<i>Proteus mirabilis</i>	95.84	0.53	ADO 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.16	0.34			
261421	Acceptable identification				261421
<i>Proteus mirabilis</i>	94.21	0.38	ADO 1		
<i>Proteus penneri</i>	3.18	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.48	0.10			
263001	Very good identification				263001
<i>Proteus mirabilis</i>	95.25	0.53	ESL 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.14	0.34			
<i>Proteus vulgaris</i>	0.62	0.20			
263020	Very good identification				263020
<i>Proteus vulgaris</i>	98.30	0.59	ORN 1		
<i>Proteus penneri</i>	0.98	0.09			
<i>Proteus mirabilis</i>	0.72	0.03			
263021	Identification to the genus				263021
<i>Proteus vulgaris</i>	53.10	0.51	ORN 1		
<i>Proteus mirabilis</i>	44.69	0.38			
<i>Proteus penneri</i>	1.51	0.10			
264001	Very good identification				264001
<i>Proteus mirabilis</i>	99.91	0.65	PHE 98		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.09	0.11			
264013	Good identification				264013
<i>Citrobacter braakii</i>	96.67	0.37	SOR 99		
<i>Citrobacter youngae</i>	3.33	0.06			
264021	Good identification				264021
<i>Proteus mirabilis</i>	100.0	0.50	PHE 98		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
264043	Low discrimination				264043
<i>Citrobacter braakii</i>	87.47	0.72			
<i>Citrobacter youngae</i>	7.48	0.49			
<i>Salmonella serovar enteritidis</i>	2.25	0.24			
264051	Acceptable identification				264051
<i>Citrobacter braakii</i>	94.53	0.37	MAN 99		
<i>Citrobacter youngae</i>	3.26	0.06			
<i>Salmonella enterica subsp. houtenae</i>	2.21	-.11			
264052	Good identification				264052
<i>Citrobacter braakii</i>	96.67	0.37	TRE 99		
<i>Citrobacter youngae</i>	3.33	0.06			
264053	Good identification				264053
<i>Citrobacter braakii</i>	93.84	0.78			
<i>Citrobacter youngae</i>	3.24	0.48			
<i>Citrobacter amalonaticus</i>	1.53	0.25			
264063	Identification to the genus				264063
<i>Citrobacter braakii</i>	63.04	0.49	SUC 7		
<i>Citrobacter youngae</i>	19.04	0.37			
<i>Citrobacter freundii</i>	17.05	0.39			
264073	Identification to the genus				264073
<i>Citrobacter braakii</i>	79.90	0.55	SUC 7		
<i>Citrobacter youngae</i>	9.73	0.36			
<i>Citrobacter freundii</i>	8.36	0.37			
264153	Identification to the genus				264153
<i>Citrobacter braakii</i>	75.45	0.37	MAL 1		
<i>Citrobacter youngae</i>	13.55	0.21			
<i>Citrobacter sedlakii</i>	11.01	0.04			
264253	Low discrimination				264253
<i>Citrobacter braakii</i>	80.42	0.37	INO 1		
<i>Citrobacter youngae</i>	14.44	0.21			
<i>Salmonella serovar enteritidis</i>	2.85	-.08			
264453	Acceptable identification				264453
<i>Citrobacter braakii</i>	91.33	0.37	ADO 1		
<i>Salmonella enterica subsp. houtenae</i>	5.52	-.02			
<i>Citrobacter youngae</i>	3.15	0.06			
265000	Very good identification				265000
<i>Proteus mirabilis</i>	99.16	0.65	TRE 98		
<i>Morganella morganii subsp. morganii</i>	0.77	0.20			
<i>Proteus vulgaris</i>	0.07	0.12			
265001	Excellent identification				265001
<i>Proteus mirabilis</i>	99.98	1.00			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.02	0.34			
<i>Proteus vulgaris</i>	0.00	0.05			
265003	Very good identification				265003
<i>Proteus mirabilis</i>	100.0	0.59	MAN 1		
265011	Very good identification				265011
<i>Proteus mirabilis</i>	100.0	0.59	CEL 1		
265020	Identification to the genus				265020
<i>Proteus mirabilis</i>	87.89	0.50	TRE 98		
<i>Proteus vulgaris</i>	11.46	0.43			
<i>Proteus penneri</i>	0.65	0.09			
265021	Very good identification				265021
<i>Proteus mirabilis</i>	99.86	0.85			
<i>Proteus vulgaris</i>	0.11	0.36			
<i>Proteus penneri</i>	0.02	0.10			
265023	Good identification				265023
<i>Proteus mirabilis</i>	100.0	0.43	MAN 1		
265031	Good identification				265031
<i>Proteus mirabilis</i>	100.0	0.43	CEL 1		
265041	Very good identification				265041
<i>Proteus mirabilis</i>	100.0	0.59	SOR 1		
265053	Good identification				265053
<i>Citrobacter braakii</i>	96.67	0.37	PHE 1		
<i>Citrobacter youngae</i>	3.33	0.06			
265061	Good identification				265061
<i>Proteus mirabilis</i>	100.0	0.43	SOR 1		
265101	Very good identification				265101
<i>Proteus mirabilis</i>	100.0	0.65	MAL 2		
265121	Good identification				265121
<i>Proteus mirabilis</i>	100.0	0.50	MAL 2		
265201	Very good identification				265201
<i>Proteus mirabilis</i>	100.0	0.59	INO 1		
265221	Good identification				265221
<i>Proteus mirabilis</i>	100.0	0.43	INO 1		
265401	Very good identification				265401
<i>Proteus mirabilis</i>	100.0	0.59	ADO 1		
265421	Good identification				265421

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus mirabilis</i>	100.0	0.43	ADO 1		
266053	Identification to the genus				266053
<i>Citrobacter braakii</i>	74.64	0.37	ESL 1		
<i>Citrobacter youngae</i>	13.41	0.21			
<i>Citrobacter amalonaticus</i>	11.95	0.04			
267001	Very good identification				267001
<i>Proteus mirabilis</i>	99.94	0.59	ESL 1		
<i>Proteus vulgaris</i>	0.06	0.05			
267020	Acceptable identification				267020
<i>Proteus vulgaris</i>	92.81	0.43	ORN 1		
<i>Proteus mirabilis</i>	7.19	0.09			
267021	Identification to the genus				267021
<i>Proteus mirabilis</i>	89.86	0.43	ESL 1		
<i>Proteus vulgaris</i>	10.14	0.36			
270000	Very good identification				270000
<i>Morganella morganii</i> subsp. <i>morganii</i>	98.64	0.61	PHE 95		
<i>Edwardsiella tarda</i>	1.22	0.18			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.11	0.11			
270001	Low discrimination				270001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	82.17	0.52	H2S 6		
<i>Proteus mirabilis</i>	10.47	0.25	PHE 93		
<i>Morganella morganii</i> subsp. <i>morganii</i>	7.36	0.20			
270043	Good identification				270043
<i>Citrobacter braakii</i>	94.84	0.56			
<i>Citrobacter youngae</i>	3.06	0.24			
<i>Salmonella</i> serovar <i>paratyphi</i>	1.28	-0.02			
270053	Low discrimination				270053
<i>Citrobacter braakii</i>	68.92	0.62			
<i>Yersinia kristensenii</i>	28.91	0.44			
<i>Citrobacter amalonaticus</i>	1.09	0.08			
270073	Low discrimination				270073
<i>Citrobacter braakii</i>	44.19	0.39	SUC 7		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	30.58	0.33			
<i>Citrobacter farmeri</i>	17.24	0.15			
271000	Very good identification				271000
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.82	0.88			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.08	0.34			
<i>Proteus mirabilis</i>	0.08	0.25			
271001	Low discrimination				271001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	62.51	0.75	H2S 6		
<i>Proteus mirabilis</i>	29.38	0.60			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	8.01	0.47			
271002	Good identification				271002
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.47	MAN 1		
271010	Good identification				271010
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.47	CEL 1		
271020	Low discrimination				271020
<i>Morganella morganii</i> subsp. <i>morganii</i>	52.22	0.47	SUC 1		
<i>Proteus vulgaris</i>	46.36	0.59			
<i>Proteus mirabilis</i>	0.69	0.09			
271021	Low discrimination				271021
<i>Proteus mirabilis</i>	41.84	0.44	IND 2		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	32.20	0.51			
<i>Proteus vulgaris</i>	24.60	0.51			
271040	Good identification				271040
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.47	SOR 1		
271100	Good identification				271100
<i>Morganella morganii</i> subsp. <i>morganii</i>	99.85	0.47	MAL 1		
<i>Proteus mirabilis</i>	0.15	-.10			
271200	Good identification				271200
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.47	INO 1		
271400	Good identification				271400
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.47	ADO 1		
273000	Good identification				273000
<i>Morganella morganii</i> subsp. <i>morganii</i>	97.33	0.47	ESL 1		
<i>Proteus vulgaris</i>	2.67	0.28			
273020	Very good identification				273020
<i>Proteus vulgaris</i>	98.88	0.59	ORN 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	1.13	0.05			
273021	Good identification				273021
<i>Proteus vulgaris</i>	97.05	0.51	ORN 1		
<i>Proteus mirabilis</i>	1.67	0.03			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.28	0.10			
274043	Very good identification				274043
<i>Citrobacter braakii</i>	95.80	0.66			
<i>Citrobacter youngae</i>	2.94	0.34			
<i>Citrobacter amalonaticus</i>	1.02	0.08			
274053	Identification to the genus				274053
<i>Citrobacter braakii</i>	65.16	0.72			
<i>Citrobacter amalonaticus</i>	33.88	0.49			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	0.81	0.32			
274063	Identification to the genus				274063
<i>Citrobacter braakii</i>	72.53	0.42	SUC 7		
<i>Citrobacter freundii</i>	19.62	0.33			
<i>Citrobacter youngae</i>	7.85	0.22			
274073	Identification to the genus				274073
<i>Citrobacter braakii</i>	62.35	0.49	SUC 7		
<i>Citrobacter amalonaticus</i>	27.50	0.25			
<i>Citrobacter freundii</i>	6.53	0.31			
275000	Low discrimination				275000
<i>Morganella morganii subsp. morganii</i>	87.43	0.47	SCI 1		
<i>Proteus mirabilis</i>	12.15	0.30			
<i>Proteus vulgaris</i>	0.42	0.12			
275001	Very good identification				275001
<i>Proteus mirabilis</i>	98.68	0.65	IND 2		
<i>Morganella morganii subsp. sibonii</i>	1.14	0.34			
<i>Morganella morganii subsp. morganii</i>	0.15	0.05			
275020	Low discrimination				275020
<i>Proteus vulgaris</i>	81.90	0.43	ORN 1		
<i>Proteus mirabilis</i>	12.82	0.15			
<i>Morganella morganii subsp. morganii</i>	5.28	0.05			
275021	Acceptable identification				275021
<i>Proteus mirabilis</i>	94.33	0.50	IND 2		
<i>Proteus vulgaris</i>	5.27	0.36			
<i>Morganella morganii subsp. sibonii</i>	0.40	0.10			
277020	Good identification				277020
<i>Proteus vulgaris</i>	100.0	0.43	ORN 1		
277021	Identification to the genus				277021
<i>Proteus vulgaris</i>	84.69	0.36	ORN 1		
<i>Proteus mirabilis</i>	15.31	0.09			
300001	Good identification				300001
<i>Shigella dysenteriae (group A)</i>	98.65	0.51	H2S 1		
<i>Shigella boydii (group C)</i>	1.05	0.08			
<i>Shigella sonnei</i>	0.16	-.17			
300003	Low discrimination				300003
<i>Shigella boydii (group C)</i>	43.60	0.39	ONP 10		
<i>Shigella sonnei</i>	20.52	0.24	H2S 1		
<i>Citrobacter youngae</i>	19.03	0.42			
300023	Low discrimination				300023
<i>Citrobacter freundii</i>	74.17	0.47	SOR 99		
<i>Citrobacter youngae</i>	16.47	0.31			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia rohdei</i>	6.46	0.18			
300033	Low discrimination				300033
<i>Citrobacter freundii</i>	73.17	0.44	SOR 99		
<i>Citrobacter youngae</i>	16.92	0.29			
<i>Escherichia vulneris</i>	7.21	0.06			
300041	Low discrimination				300041
<i>Shigella dysenteriae</i> (group A)	68.93	0.44	H2S 1		
<i>Citrobacter youngae</i>	24.04	0.42			
<i>Citrobacter freundii</i>	3.56	0.28			
300042	Low discrimination				300042
<i>Citrobacter youngae</i>	63.12	0.42	TRE 99		
<i>Shigella boydii</i> (group C)	19.26	0.21			
<i>Citrobacter freundii</i>	9.34	0.28			
300043	Low discrimination				300043
<i>Citrobacter youngae</i>	79.17	0.84			
<i>Citrobacter freundii</i>	11.71	0.69			
<i>Citrobacter braakii</i>	4.03	0.58			
300051	Identification to the genus				300051
<i>Citrobacter youngae</i>	76.71	0.41	MAN 99		
<i>Citrobacter freundii</i>	10.90	0.26			
<i>Citrobacter braakii</i>	9.68	0.23			
300052	Identification to the genus				300052
<i>Citrobacter youngae</i>	78.85	0.41	TRE 99		
<i>Citrobacter freundii</i>	11.20	0.26			
<i>Citrobacter braakii</i>	9.95	0.23			
300053	Identification to the genus				300053
<i>Citrobacter youngae</i>	78.36	0.82			
<i>Citrobacter freundii</i>	11.13	0.67			
<i>Citrobacter braakii</i>	9.89	0.64			
300061	Low discrimination				300061
<i>Citrobacter freundii</i>	75.00	0.47	MAN 99		
<i>Citrobacter youngae</i>	16.66	0.31			
<i>Yersinia rohdei</i>	6.53	0.18			
300062	Low discrimination				300062
<i>Citrobacter freundii</i>	76.39	0.47	TRE 99		
<i>Citrobacter youngae</i>	16.96	0.31			
<i>Yersinia rohdei</i>	6.65	0.18			
300063	Low discrimination				300063
<i>Citrobacter freundii</i>	76.10	0.88			
<i>Citrobacter youngae</i>	16.90	0.72			
<i>Yersinia rohdei</i>	6.63	0.59			
300071	Identification to the genus				300071

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	78.85	0.44	MAN 99		
<i>Citrobacter youngae</i>	18.24	0.29			
<i>Yersinia rohdei</i>	2.91	0.08			
300072	Identification to the genus				300072
<i>Citrobacter freundii</i>	78.85	0.44	TRE 99		
<i>Citrobacter youngae</i>	18.24	0.29			
<i>Yersinia rohdei</i>	2.91	0.08			
300073	Identification to the genus				300073
<i>Citrobacter freundii</i>	78.25	0.86			
<i>Citrobacter youngae</i>	18.10	0.70			
<i>Yersinia rohdei</i>	2.89	0.49			
300103	Good identification				300103
<i>Citrobacter werkmanii</i>	95.60	0.37	URE 92		
<i>Escherichia vulneris</i>	1.67	0.02	SCI 92		
<i>Citrobacter youngae</i>	1.44	0.16	SOR 90		
300113	Good identification				300113
<i>Escherichia vulneris</i>	98.56	0.43	H2S 1		
<i>Citrobacter youngae</i>	0.70	0.14			
<i>Citrobacter werkmanii</i>	0.58	-.04			
300143	Identification to the genus				300143
<i>Citrobacter werkmanii</i>	82.67	0.56	URE 92		
<i>Citrobacter youngae</i>	13.73	0.57	SCI 92		
<i>Citrobacter freundii</i>	3.36	0.47			
300153	Identification to the genus				300153
<i>Citrobacter youngae</i>	74.21	0.55	MAL 5		
<i>Citrobacter freundii</i>	17.42	0.45			
<i>Citrobacter werkmanii</i>	5.52	0.15			
300163	Identification to the genus				300163
<i>Citrobacter freundii</i>	85.09	0.66	MAL 8		
<i>Citrobacter youngae</i>	11.44	0.45			
<i>Citrobacter werkmanii</i>	2.62	0.15			
300173	Identification to the genus				300173
<i>Citrobacter freundii</i>	87.39	0.64	MAL 8		
<i>Citrobacter youngae</i>	12.23	0.44			
<i>Yersinia rohdei</i>	0.38	0.08			
300243	Very good identification				300243
<i>Citrobacter youngae</i>	95.31	0.57	INO 5		
<i>Citrobacter freundii</i>	2.71	0.28			
<i>Citrobacter braakii</i>	0.93	0.16			
300253	Good identification				300253
<i>Citrobacter youngae</i>	92.34	0.55	INO 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	2.52	0.26			
<i>Citrobacter braakii</i>	2.24	0.23			
300263	Identification to the genus				300263
<i>Citrobacter youngae</i>	51.17	0.45	INO 5		
<i>Citrobacter freundii</i>	44.22	0.47			
<i>Yersinia rohdei</i>	3.85	0.18			
300273	Identification to the genus				300273
<i>Citrobacter youngae</i>	52.20	0.44	INO 5		
<i>Citrobacter freundii</i>	43.32	0.44			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.88	0.15			
300413	Good identification				300413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.62	0.39	H2S 1		
<i>Escherichia vulneris</i>	2.38	-.13			
300443	Low discrimination				300443
<i>Citrobacter youngae</i>	75.33	0.42	ADO 1		
<i>Citrobacter freundii</i>	11.14	0.28			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.37	0.23			
300453	Low discrimination				300453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	44.15	0.45	H2S 1		
<i>Citrobacter youngae</i>	44.03	0.41			
<i>Citrobacter freundii</i>	6.26	0.26			
300463	Low discrimination				300463
<i>Citrobacter freundii</i>	75.53	0.47	ADO 1		
<i>Citrobacter youngae</i>	16.77	0.31			
<i>Yersinia rohdei</i>	6.58	0.18			
300473	Low discrimination				300473
<i>Citrobacter freundii</i>	67.28	0.44	ADO 1		
<i>Citrobacter youngae</i>	15.56	0.29			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	14.67	0.32			
300613	Good identification				300613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	H2S 1		
300653	Acceptable identification				300653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.18	0.47	H2S 1	1	
<i>Citrobacter youngae</i>	4.04	0.14		1	
<i>Serratia odorifera</i> biovar 2	1.78	0.03		99	
301043	Identification to the genus				301043
<i>Citrobacter youngae</i>	79.61	0.42	PHE 1		
<i>Citrobacter freundii</i>	11.78	0.28			
<i>Citrobacter braakii</i>	4.05	0.16			
301053	Identification to the genus				301053
<i>Citrobacter youngae</i>	78.85	0.41	PHE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	11.20	0.26			
<i>Citrobacter braakii</i>	9.95	0.23			
301063	Low discrimination				301063
<i>Citrobacter freundii</i>	76.39	0.47	PHE 1		
<i>Citrobacter youngae</i>	16.96	0.31			
<i>Yersinia rohdei</i>	6.65	0.18			
301073	Identification to the genus				301073
<i>Citrobacter freundii</i>	78.85	0.44	PHE 1		
<i>Citrobacter youngae</i>	18.24	0.29			
<i>Yersinia rohdei</i>	2.91	0.08			
302043	Good identification				302043
<i>Citrobacter youngae</i>	94.34	0.57	ESL 5		
<i>Citrobacter freundii</i>	2.68	0.28			
<i>Citrobacter braakii</i>	0.92	0.16			
302053	Good identification				302053
<i>Citrobacter youngae</i>	93.00	0.55	ESL 5		
<i>Citrobacter freundii</i>	2.54	0.26			
<i>Citrobacter braakii</i>	2.25	0.23			
302063	Low discrimination				302063
<i>Citrobacter youngae</i>	50.81	0.45	ESL 5		
<i>Citrobacter freundii</i>	43.91	0.47			
<i>Yersinia rohdei</i>	3.82	0.18			
302073	Low discrimination				302073
<i>Citrobacter youngae</i>	45.95	0.44	ESL 5		
<i>Citrobacter freundii</i>	38.13	0.44			
<i>Serratia ficaria</i>	11.51	0.16			
302123	Good identification				302123
<i>Pantoea agglomerans</i>	100.0	0.47	H2S 1		
302133	Good identification				302133
<i>Pantoea agglomerans</i>	97.23	0.44	H2S 1		
<i>Escherichia vulneris</i>	2.50	0.09			
<i>Leclercia adecarboxylata</i>	0.27	-.05			
302413	Good identification				302413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.52	H2S 1		
302433	Low discrimination				302433
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	85.32	0.39	H2S 1	1	
<i>Serratia rubidaea</i>	11.98	0.06		99	
<i>Leclercia adecarboxylata</i>	2.70	-.05		1	
302443	Low discrimination				302443
<i>Klebsiella pneumoniae subsp. ozaenae</i>	84.43	0.35	H2S 1		
<i>Citrobacter youngae</i>	15.57	0.16	CEL 92		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
302453	Very good identification				302453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.71	0.57	H2S 1		
<i>Citrobacter youngae</i>	1.30	0.14			
302473	Good identification				302473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.62	0.45	H2S 1		
<i>Citrobacter youngae</i>	1.38	0.03			
302613	Very good identification				302613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.53	H2S 1		
302633	Good identification				302633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.21	0.41	H2S 1	1	
<i>Serratia rubidaea</i>	2.79	-.06		99	
302643	Good identification				302643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	H2S 1		
302653	Very good identification				302653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.69	0.59	H2S 1	1	
<i>Serratia odorifera</i> biovar 2	0.31	0.00		99	
302673	Good identification				302673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.47	H2S 1		
304003	Identification to the genus				304003
<i>Citrobacter werkmanii</i>	49.03	0.37	URE 92		
<i>Citrobacter youngae</i>	40.03	0.52	MAL 92		
<i>Citrobacter freundii</i>	8.32	0.40	SOR 90		
304013	Identification to the genus				304013
<i>Citrobacter youngae</i>	73.94	0.50	SOR 99		
<i>Citrobacter freundii</i>	14.76	0.38			
<i>Citrobacter braakii</i>	9.84	0.33			
304023	Identification to the genus				304023
<i>Citrobacter freundii</i>	85.63	0.59	SOR 99		
<i>Citrobacter youngae</i>	13.53	0.40			
<i>Citrobacter werkmanii</i>	0.63	-.04			
304033	Identification to the genus				304033
<i>Citrobacter freundii</i>	85.42	0.57	SOR 99		
<i>Citrobacter youngae</i>	14.06	0.38			
<i>Citrobacter braakii</i>	0.53	0.09			
304041	Identification to the genus				304041
<i>Citrobacter youngae</i>	72.30	0.52	MAN 99		
<i>Citrobacter freundii</i>	15.03	0.40			
<i>Citrobacter werkmanii</i>	8.05	0.15			
304042	Identification to the genus				304042

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	72.84	0.52	TRE 99		
<i>Citrobacter freundii</i>	15.14	0.40			
<i>Citrobacter werkmanii</i>	8.11	0.15			
304043	Identification to the genus				304043
<i>Citrobacter youngae</i>	72.71	0.93			
<i>Citrobacter freundii</i>	15.12	0.81			
<i>Citrobacter werkmanii</i>	8.10	0.56			
304051	Identification to the genus				304051
<i>Citrobacter youngae</i>	75.04	0.50	MAN 99		
<i>Citrobacter freundii</i>	14.98	0.38			
<i>Citrobacter braakii</i>	9.98	0.33			
304052	Identification to the genus				304052
<i>Citrobacter youngae</i>	75.04	0.50	TRE 99		
<i>Citrobacter freundii</i>	14.98	0.38			
<i>Citrobacter braakii</i>	9.98	0.33			
304053	Identification to the genus				304053
<i>Citrobacter youngae</i>	74.93	0.91			
<i>Citrobacter freundii</i>	14.96	0.79			
<i>Citrobacter braakii</i>	9.97	0.74			
304061	Identification to the genus				304061
<i>Citrobacter freundii</i>	86.18	0.59	MAN 99		
<i>Citrobacter youngae</i>	13.62	0.40			
<i>Citrobacter braakii</i>	0.21	0.03			
304062	Identification to the genus				304062
<i>Citrobacter freundii</i>	86.18	0.59	TRE 99		
<i>Citrobacter youngae</i>	13.62	0.40			
<i>Citrobacter braakii</i>	0.21	0.03			
304063	Identification to the genus				304063
<i>Citrobacter freundii</i>	86.11	1.00			
<i>Citrobacter youngae</i>	13.61	0.81			
<i>Citrobacter braakii</i>	0.21	0.44			
304071	Identification to the genus				304071
<i>Citrobacter freundii</i>	85.42	0.57	MAN 99		
<i>Citrobacter youngae</i>	14.06	0.38			
<i>Citrobacter braakii</i>	0.53	0.09			
304072	Identification to the genus				304072
<i>Citrobacter freundii</i>	85.42	0.57	TRE 99		
<i>Citrobacter youngae</i>	14.06	0.38			
<i>Citrobacter braakii</i>	0.53	0.09			
304073	Identification to the genus				304073
<i>Citrobacter freundii</i>	85.33	0.98			
<i>Citrobacter youngae</i>	14.04	0.79			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	0.53	0.51			
304103	Very good identification				304103
<i>Citrobacter werkmanii</i>	99.50	0.59	URE 92		
<i>Citrobacter youngae</i>	0.37	0.25	SOR 90		
<i>Citrobacter freundii</i>	0.13	0.18			
304123	Low discrimination				304123
<i>Citrobacter freundii</i>	37.06	0.37	MAL 8		
<i>Citrobacter werkmanii</i>	36.05	0.17	SOR 99		
<i>Pantoea agglomerans</i>	23.35	0.18			
304141	Acceptable identification				304141
<i>Citrobacter werkmanii</i>	94.77	0.37	URE 92		
<i>Citrobacter youngae</i>	3.90	0.25	MAN 99		
<i>Citrobacter freundii</i>	1.34	0.18			
304142	Acceptable identification				304142
<i>Citrobacter werkmanii</i>	94.77	0.37	URE 92		
<i>Citrobacter youngae</i>	3.90	0.25	TRE 99		
<i>Citrobacter freundii</i>	1.34	0.18			
304143	Good identification				304143
<i>Citrobacter werkmanii</i>	94.43	0.78	URE 92		
<i>Citrobacter youngae</i>	3.88	0.67			
<i>Citrobacter freundii</i>	1.33	0.60			
304153	Identification to the genus				304153
<i>Citrobacter youngae</i>	60.40	0.65	MAL 5		
<i>Citrobacter freundii</i>	19.92	0.57			
<i>Citrobacter werkmanii</i>	18.14	0.37			
304161	Identification to the genus				304161
<i>Citrobacter freundii</i>	84.45	0.37	MAL 8		
<i>Citrobacter youngae</i>	8.08	0.14	MAN 99		
<i>Citrobacter werkmanii</i>	7.47	-.04			
304162	Identification to the genus				304162
<i>Citrobacter freundii</i>	84.45	0.37	MAL 8		
<i>Citrobacter youngae</i>	8.08	0.14	TRE 99		
<i>Citrobacter werkmanii</i>	7.47	-.04			
304163	Identification to the genus				304163
<i>Citrobacter freundii</i>	84.39	0.78	MAL 8		
<i>Citrobacter youngae</i>	8.07	0.55			
<i>Citrobacter werkmanii</i>	7.46	0.37			
304173	Good identification				304173
				VPT	
<i>Citrobacter freundii</i>	90.06	0.76	MAL 8	1	
<i>Citrobacter youngae</i>	8.97	0.53		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.81	0.25		99	
304243	Good identification				304243

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	93.19	0.67	INO 5		
<i>Citrobacter freundii</i>	3.72	0.40			
<i>Citrobacter werkmanii</i>	1.99	0.15			
304253	Good identification				304253
				VPT	
<i>Citrobacter youngae</i>	90.40	0.65	INO 5	1	
<i>Serratia odorifera biovar 2</i>	3.73	0.33		99	
<i>Citrobacter freundii</i>	3.46	0.38		1	
304263	Identification to the genus				304263
<i>Citrobacter freundii</i>	54.77	0.59	INO 1		
<i>Citrobacter youngae</i>	45.10	0.55			
<i>Citrobacter braakii</i>	0.13	0.03			
304273	Low discrimination				304273
<i>Citrobacter freundii</i>	51.01	0.57	INO 1		
<i>Citrobacter youngae</i>	43.74	0.53			
<i>Serratia ficaria</i>	4.71	0.18			
304343	Identification to the genus				304343
<i>Citrobacter werkmanii</i>	81.42	0.37	URE 92		
<i>Citrobacter youngae</i>	17.44	0.40	INO 1		
<i>Citrobacter freundii</i>	1.15	0.18			
304353	Identification to the genus				304353
<i>Citrobacter youngae</i>	89.21	0.38	MAL 5		
<i>Citrobacter freundii</i>	5.65	0.16	INO 5		
<i>Citrobacter werkmanii</i>	5.14	-.04			
304363	Identification to the genus				304363
<i>Citrobacter freundii</i>	63.02	0.37	MAL 8		
<i>Citrobacter youngae</i>	31.41	0.28	INO 1		
<i>Citrobacter werkmanii</i>	5.57	-.04			
304443	Identification to the genus				304443
<i>Citrobacter youngae</i>	72.27	0.52	ADO 1		
<i>Citrobacter freundii</i>	15.03	0.40			
<i>Citrobacter werkmanii</i>	8.05	0.15			
304453	Low discrimination				304453
<i>Citrobacter youngae</i>	67.40	0.50	ADO 1		
<i>Citrobacter freundii</i>	13.46	0.38			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	10.18	0.37			
304463	Identification to the genus				304463
<i>Citrobacter freundii</i>	86.18	0.59	ADO 1		
<i>Citrobacter youngae</i>	13.62	0.40			
<i>Citrobacter braakii</i>	0.21	0.03			
304473	Identification to the genus				304473
<i>Citrobacter freundii</i>	83.15	0.57	ADO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	13.68	0.38			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.94	0.25			
304543	Acceptable identification				304543
<i>Citrobacter werkmanii</i>	94.77	0.37	URE 92		
<i>Citrobacter youngae</i>	3.90	0.25	ADO 1		
<i>Citrobacter freundii</i>	1.34	0.18			
304563	Identification to the genus				304563
<i>Citrobacter freundii</i>	84.45	0.37	MAL 8		
<i>Citrobacter youngae</i>	8.08	0.14	ADO 1		
<i>Citrobacter werkmanii</i>	7.47	-.04			
305043	Identification to the genus				305043
<i>Citrobacter youngae</i>	72.84	0.52	PHE 1		
<i>Citrobacter freundii</i>	15.14	0.40			
<i>Citrobacter werkmanii</i>	8.11	0.15			
305053	Identification to the genus				305053
<i>Citrobacter youngae</i>	75.04	0.50	PHE 1		
<i>Citrobacter freundii</i>	14.98	0.38			
<i>Citrobacter braakii</i>	9.98	0.33			
305063	Identification to the genus				305063
<i>Citrobacter freundii</i>	86.18	0.59	PHE 1		
<i>Citrobacter youngae</i>	13.62	0.40			
<i>Citrobacter braakii</i>	0.21	0.03			
305073	Identification to the genus				305073
<i>Citrobacter freundii</i>	85.42	0.57	PHE 1		
<i>Citrobacter youngae</i>	14.06	0.38			
<i>Citrobacter braakii</i>	0.53	0.09			
305143	Acceptable identification				305143
<i>Citrobacter werkmanii</i>	94.77	0.37	URE 92		
<i>Citrobacter youngae</i>	3.90	0.25	PHE 1		
<i>Citrobacter freundii</i>	1.34	0.18			
305163	Identification to the genus				305163
<i>Citrobacter freundii</i>	84.45	0.37	PHE 1		
<i>Citrobacter youngae</i>	8.08	0.14	MAL 8		
<i>Citrobacter werkmanii</i>	7.47	-.04			
306043	Good identification				306043
<i>Citrobacter youngae</i>	93.32	0.67	ESL 5		
<i>Citrobacter freundii</i>	3.72	0.40			
<i>Citrobacter werkmanii</i>	1.99	0.15			
306053	Good identification				306053
<i>Citrobacter youngae</i>	91.60	0.65	ESL 5		
<i>Citrobacter freundii</i>	3.51	0.38			
<i>Citrobacter braakii</i>	2.34	0.33			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
306063	Identification to the genus				306063
<i>Citrobacter freundii</i>	53.05	0.59	ESL 1		
<i>Citrobacter youngae</i>	43.68	0.55			
<i>Serratia ficaria</i>	3.15	0.16			
306073	Low discrimination				306073
<i>Serratia ficaria</i>	79.92	0.57	H2S 1		
<i>Citrobacter freundii</i>	10.70	0.57			
<i>Citrobacter youngae</i>	9.17	0.53			
306123	Very good identification				306123
<i>Pantoea agglomerans</i>	99.95	0.59	H2S 1		
<i>Serratia rubidaea</i>	0.05	-.09			
306133	Very good identification				306133
<i>Pantoea agglomerans</i>	98.53	0.57	H2S 1		
<i>Serratia rubidaea</i>	0.90	0.16			
<i>Cronobacter sakazakii</i>	0.57	0.15			
306143	Identification to the genus				306143
<i>Citrobacter werkmanii</i>	81.18	0.37	URE 92		
<i>Citrobacter youngae</i>	17.38	0.40	ESL 1		
<i>Citrobacter freundii</i>	1.15	0.18			
306153	Identification to the genus				306153
<i>Citrobacter youngae</i>	89.21	0.38	ESL 5		
<i>Citrobacter freundii</i>	5.65	0.16	MAL 5		
<i>Citrobacter werkmanii</i>	5.14	-.04			
306163	Low discrimination				306163
<i>Citrobacter freundii</i>	45.11	0.37	ESL 1		
<i>Pantoea agglomerans</i>	28.43	0.18	MAL 8		
<i>Citrobacter youngae</i>	22.48	0.28			
306233	Low discrimination				306233
<i>Cronobacter sakazakii</i>	82.19	0.38	H2S 1		
<i>Serratia ficaria</i>	17.81	0.18	ORN 91		
306243	Good identification				306243
<i>Citrobacter youngae</i>	100.0	0.40	ESL 5		
306253	Low discrimination				306253
				VPT	
<i>Citrobacter youngae</i>	46.54	0.38	ESL 5	1	
<i>Serratia ficaria</i>	25.28	0.18	INO 5	75	
<i>Serratia odorifera</i> biovar 2	24.31	0.29		99	
306273	Very good identification				306273
<i>Serratia ficaria</i>	99.31	0.59	H2S 1		
<i>Citrobacter youngae</i>	0.49	0.27			
<i>Citrobacter freundii</i>	0.11	0.16			
306413	Good identification				306413

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.45	0.44	H2S 1	1	
<i>Serratia rubidaea</i>	1.55	-.09		99	
306453	Acceptable identification				306453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.98	0.50	H2S 1		
<i>Citrobacter youngae</i>	8.02	0.24			
306473	Low discrimination				306473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	48.05	0.37	H2S 1		
<i>Serratia ficaria</i>	38.79	0.16			
<i>Citrobacter freundii</i>	5.19	0.16			
306533	Very good identification				306533
<i>Serratia rubidaea</i>	98.90	0.57	H2S 1		
<i>Pantoea agglomerans</i>	1.10	0.16			
306613	Good identification				306613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.46	H2S 1		
306653	Low discrimination				306653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	80.83	0.51	H2S 1	1	
<i>Serratia odorifera</i> biovar 2	19.17	0.31		99	
306673	Low discrimination				306673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	55.33	0.39	H2S 1		
<i>Serratia ficaria</i>	44.67	0.18			
306733	Good identification				306733
<i>Serratia rubidaea</i>	100.0	0.45	H2S 1		
307123	Good identification				307123
<i>Pantoea agglomerans</i>	100.0	0.38	H2S 1		
307133	Acceptable identification				307133
<i>Pantoea agglomerans</i>	94.51	0.36	H2S 1		
<i>Cronobacter sakazakii</i>	5.49	0.15	PHE 9		
307233	Good identification				307233
<i>Cronobacter sakazakii</i>	100.0	0.38	H2S 1		
310001	Good identification				310001
<i>Shigella dysenteriae</i> (group A)	99.36	0.50	H2S 1		
<i>Shigella boydii</i> (group C)	0.43	-.02			
<i>Escherichia coli</i>	0.21	0.02			
310023	Low discrimination				310023
<i>Citrobacter freundii</i>	75.19	0.40	SOR 99		
<i>Escherichia coli</i>	18.82	0.24			
<i>Citrobacter youngae</i>	5.98	0.15			
310033	Low discrimination				310033

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	70.18	0.38	SOR 99		
<i>Escherichia hermannii</i>	24.00	0.16			
<i>Citrobacter youngae</i>	5.82	0.13			
310041	Low discrimination				310041
<i>Shigella dysenteriae</i> (group A)	86.13	0.42	H2S 1		
<i>Citrobacter youngae</i>	6.48	0.27			
<i>Escherichia coli</i>	3.14	0.20			
310043	Low discrimination				310043
<i>Citrobacter youngae</i>	59.25	0.68			
<i>Citrobacter freundii</i>	24.46	0.63			
<i>Citrobacter braakii</i>	8.41	0.51			
310053	Identification to the genus				310053
<i>Citrobacter youngae</i>	56.58	0.66			
<i>Citrobacter freundii</i>	22.44	0.60			
<i>Citrobacter braakii</i>	19.93	0.58			
310061	Low discrimination				310061
<i>Citrobacter freundii</i>	82.21	0.40	MAN 99		
<i>Escherichia coli</i>	7.94	0.16			
<i>Citrobacter youngae</i>	6.54	0.15			
310062	Low discrimination				310062
<i>Citrobacter freundii</i>	85.02	0.40	TRE 99		
<i>Escherichia coli</i>	8.21	0.16			
<i>Citrobacter youngae</i>	6.77	0.15			
310063	Good identification				310063
<i>Citrobacter freundii</i>	90.59	0.81			
<i>Citrobacter youngae</i>	7.21	0.56			
<i>Escherichia coli</i>	1.68	0.42			
310071	Acceptable identification				310071
<i>Citrobacter freundii</i>	92.35	0.38	MAN 99		
<i>Citrobacter youngae</i>	7.65	0.13			
310072	Acceptable identification				310072
<i>Citrobacter freundii</i>	92.35	0.38	TRE 99		
<i>Citrobacter youngae</i>	7.65	0.13			
310073	Good identification				310073
<i>Citrobacter freundii</i>	90.69	0.79			
<i>Citrobacter youngae</i>	7.52	0.54			
<i>Citrobacter braakii</i>	0.75	0.34			
310143	Identification to the genus				310143
<i>Citrobacter youngae</i>	48.27	0.42	MAL 5		
<i>Citrobacter freundii</i>	32.92	0.41			
<i>Citrobacter werkmanii</i>	16.64	0.15			
310153	Identification to the genus				310153

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	58.05	0.40	MAL 5		
<i>Citrobacter freundii</i>	38.03	0.39			
<i>Citrobacter braakii</i>	3.93	0.16			
310163	Very good identification				310163
<i>Citrobacter freundii</i>	95.21	0.59	MAL 8		
<i>Citrobacter youngae</i>	4.59	0.30			
<i>Escherichia coli</i>	0.21	0.01			
310173	Very good identification				310173
<i>Citrobacter freundii</i>	95.22	0.57	MAL 8		
<i>Citrobacter youngae</i>	4.78	0.28			
310243	Identification to the genus				310243
<i>Citrobacter youngae</i>	88.94	0.42	INO 5		
<i>Citrobacter freundii</i>	7.05	0.22			
<i>Citrobacter braakii</i>	2.42	0.10			
310253	Low discrimination				310253
<i>Citrobacter youngae</i>	82.35	0.40	INO 5		
<i>Citrobacter freundii</i>	6.27	0.19			
<i>Citrobacter braakii</i>	5.57	0.16			
310263	Identification to the genus				310263
<i>Citrobacter freundii</i>	68.10	0.40	INO 1		
<i>Citrobacter youngae</i>	28.23	0.30			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.41	0.05			
310273	Low discrimination				310273
<i>Citrobacter freundii</i>	63.83	0.38	INO 1		
<i>Citrobacter youngae</i>	27.56	0.28			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	8.61	0.15			
310463	Low discrimination				310463
<i>Citrobacter freundii</i>	85.02	0.40	ADO 1		
<i>Escherichia coli</i>	8.21	0.16			
<i>Citrobacter youngae</i>	6.77	0.15			
310473	Acceptable identification				310473
<i>Citrobacter freundii</i>	92.35	0.38	ADO 1		
<i>Citrobacter youngae</i>	7.65	0.13			
311063	Acceptable identification				311063
<i>Citrobacter freundii</i>	91.07	0.40	PHE 1		
<i>Citrobacter youngae</i>	7.25	0.15			
<i>Escherichia coli</i>	1.69	0.01			
311073	Acceptable identification				311073
<i>Citrobacter freundii</i>	92.35	0.38	PHE 1		
<i>Citrobacter youngae</i>	7.65	0.13			
312043	Low discrimination				312043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	64.61	0.42	ESL 5		
<i>Escherichia coli</i>	28.51	0.33			
<i>Citrobacter freundii</i>	5.12	0.22			
312053	Identification to the genus				312053
<i>Citrobacter youngae</i>	87.44	0.40	ESL 5		
<i>Citrobacter freundii</i>	6.65	0.19			
<i>Citrobacter braakii</i>	5.91	0.16			
312063	Low discrimination				312063
<i>Citrobacter freundii</i>	52.60	0.40	ESL 1		
<i>Escherichia coli</i>	24.14	0.30			
<i>Citrobacter youngae</i>	21.81	0.30			
312073	Low discrimination				312073
<i>Citrobacter freundii</i>	65.08	0.38	ESL 1		
<i>Citrobacter youngae</i>	28.10	0.28			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	6.83	0.13			
312133	Good identification				312133
<i>Leclercia adecarboxylata</i>	96.41	0.36	H2S 1		
<i>Pantoea agglomerans</i>	3.59	0.03	ADO 93		
312433	Good identification				312433
<i>Leclercia adecarboxylata</i>	100.0	0.36	H2S 1		
312513	Very good identification				312513
<i>Leclercia adecarboxylata</i>	100.0	0.53	H2S 1		
312533	Very good identification				312533
<i>Leclercia adecarboxylata</i>	100.0	0.59	H2S 1		
314003	Identification to the genus				314003
<i>Citrobacter youngae</i>	55.56	0.36	SOR 99		
<i>Citrobacter freundii</i>	32.24	0.34			
<i>Citrobacter braakii</i>	8.31	0.20			
314023	Acceptable identification				314023
<i>Citrobacter freundii</i>	94.64	0.53	SOR 99		
<i>Citrobacter youngae</i>	5.36	0.24			
314033	Acceptable identification				314033
<i>Citrobacter freundii</i>	93.88	0.50	SOR 99		
<i>Citrobacter youngae</i>	5.54	0.23			
<i>Citrobacter braakii</i>	0.58	0.03			
314041	Identification to the genus				314041
<i>Citrobacter youngae</i>	56.27	0.36	MAN 99		
<i>Citrobacter freundii</i>	32.65	0.34			
<i>Citrobacter braakii</i>	8.42	0.20			
314042	Identification to the genus				314042

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	57.81	0.36	TRE 99		
<i>Citrobacter freundii</i>	33.54	0.34			
<i>Citrobacter braakii</i>	8.65	0.20			
314043	Identification to the genus				314043
<i>Citrobacter youngae</i>	57.57	0.77			
<i>Citrobacter freundii</i>	33.41	0.75			
<i>Citrobacter braakii</i>	8.62	0.61			
314053	Identification to the genus				314053
<i>Citrobacter youngae</i>	50.70	0.76			
<i>Citrobacter freundii</i>	28.25	0.73			
<i>Citrobacter braakii</i>	18.83	0.67			
314061	Acceptable identification				314061
<i>Citrobacter freundii</i>	94.64	0.53	MAN 99		
<i>Citrobacter youngae</i>	5.36	0.24			
314062	Acceptable identification				314062
<i>Citrobacter freundii</i>	94.64	0.53	TRE 99		
<i>Citrobacter youngae</i>	5.36	0.24			
314063	Good identification				314063
<i>Citrobacter freundii</i>	94.42	0.94			
<i>Citrobacter youngae</i>	5.35	0.66			
<i>Citrobacter braakii</i>	0.23	0.38			
314071	Acceptable identification				314071
<i>Citrobacter freundii</i>	93.88	0.50	MAN 99		
<i>Citrobacter youngae</i>	5.54	0.23			
<i>Citrobacter braakii</i>	0.58	0.03			
314072	Acceptable identification				314072
<i>Citrobacter freundii</i>	93.88	0.50	TRE 99		
<i>Citrobacter youngae</i>	5.54	0.23			
<i>Citrobacter braakii</i>	0.58	0.03			
314073	Good identification				314073
<i>Citrobacter freundii</i>	93.81	0.92			
<i>Citrobacter youngae</i>	5.53	0.64			
<i>Citrobacter braakii</i>	0.58	0.44			
314143	Identification to the genus				314143
<i>Citrobacter werkmanii</i>	41.15	0.37	IND 1		
<i>Citrobacter youngae</i>	29.55	0.51	URE 92		
<i>Citrobacter freundii</i>	28.33	0.53			
314153	Identification to the genus				314153
<i>Citrobacter youngae</i>	49.57	0.49	MAL 5		
<i>Citrobacter freundii</i>	45.63	0.51			
<i>Citrobacter braakii</i>	3.53	0.26			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
314163	Very good identification				314163
<i>Citrobacter freundii</i>	96.52	0.72	MAL 8		
<i>Citrobacter youngae</i>	3.31	0.39			
<i>Citrobacter werkmanii</i>	0.18	-.04			
314173	Very good identification				314173
<i>Citrobacter freundii</i>	96.49	0.70	MAL 8		
<i>Citrobacter youngae</i>	3.44	0.37			
<i>Citrobacter braakii</i>	0.07	0.03			
314243	Identification to the genus				314243
<i>Citrobacter youngae</i>	87.71	0.51	INO 5		
<i>Citrobacter freundii</i>	9.77	0.34			
<i>Citrobacter braakii</i>	2.52	0.20			
314253	Low discrimination				314253
				VPT	
<i>Citrobacter youngae</i>	70.41	0.49	INO 5	1	
<i>Serratia odorifera</i> biovar 2	16.46	0.33		99	
<i>Citrobacter freundii</i>	7.53	0.32		1	
314263	Identification to the genus				314263
<i>Citrobacter freundii</i>	77.22	0.53	INO 1		
<i>Citrobacter youngae</i>	22.78	0.39			
314273	Identification to the genus				314273
<i>Citrobacter freundii</i>	76.14	0.50	INO 1		
<i>Citrobacter youngae</i>	23.39	0.37			
<i>Citrobacter braakii</i>	0.47	0.03			
314443	Identification to the genus				314443
<i>Citrobacter youngae</i>	57.81	0.36	ADO 1		
<i>Citrobacter freundii</i>	33.54	0.34			
<i>Citrobacter braakii</i>	8.65	0.20			
314463	Acceptable identification				314463
<i>Citrobacter freundii</i>	94.64	0.53	ADO 1		
<i>Citrobacter youngae</i>	5.36	0.24			
314473	Acceptable identification				314473
<i>Citrobacter freundii</i>	93.88	0.50	ADO 1		
<i>Citrobacter youngae</i>	5.54	0.23			
<i>Citrobacter braakii</i>	0.58	0.03			
315043	Identification to the genus				315043
<i>Citrobacter youngae</i>	57.81	0.36	PHE 1		
<i>Citrobacter freundii</i>	33.54	0.34			
<i>Citrobacter braakii</i>	8.65	0.20			
315063	Acceptable identification				315063
<i>Citrobacter freundii</i>	94.64	0.53	PHE 1		
<i>Citrobacter youngae</i>	5.36	0.24			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
315073	Acceptable identification				315073
<i>Citrobacter freundii</i>	93.88	0.50	PHE 1		
<i>Citrobacter youngae</i>	5.54	0.23			
<i>Citrobacter braakii</i>	0.58	0.03			
315201	Good identification				315201
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
315221	Good identification				315221
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
316043	Identification to the genus				316043
<i>Citrobacter youngae</i>	87.71	0.51	ESL 5		
<i>Citrobacter freundii</i>	9.77	0.34			
<i>Citrobacter braakii</i>	2.52	0.20			
316053	Low discrimination				316053
<i>Citrobacter youngae</i>	79.32	0.49	ESL 5		
<i>Citrobacter freundii</i>	8.48	0.32			
<i>Citrobacter amalonaticus</i>	6.55	0.11			
316063	Identification to the genus				316063
<i>Citrobacter freundii</i>	77.22	0.53	ESL 1		
<i>Citrobacter youngae</i>	22.78	0.39			
316073	Low discrimination				316073
<i>Citrobacter freundii</i>	67.90	0.50	ESL 1		
<i>Citrobacter youngae</i>	20.86	0.37			
<i>Serratia ficaria</i>	10.40	0.16			
320003	Very good identification				320003
<i>Shigella sonnei</i>	97.96	0.59	H2S 1		
<i>Citrobacter braakii</i>	1.25	0.40			
<i>Salmonella serovar paratyphi</i>	0.54	0.13			
320041	Low discrimination				320041
<i>Citrobacter braakii</i>	80.62	0.40	MAN 99		
<i>Salmonella serovar paratyphi</i>	6.65	-.02			
<i>Salmonella bongori</i>	4.29	-.07			
320043	Low discrimination				320043
<i>Citrobacter braakii</i>	82.82	0.81			
<i>Salmonella serovar paratyphi</i>	6.83	0.39			
<i>Salmonella bongori</i>	4.40	0.34			
320051	Acceptable identification				320051
<i>Citrobacter braakii</i>	94.28	0.46	MAN 99		
<i>Yersinia kristensenii</i>	3.98	0.07			
<i>Citrobacter youngae</i>	1.74	0.10			
320052	Acceptable identification				320052

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	93.59	0.46	TRE	99	
<i>Yersinia kristensenii</i>	3.95	0.07			
<i>Citrobacter youngae</i>	1.73	0.10			
320053	Good identification				320053
<i>Citrobacter braakii</i>	93.85	0.87			
<i>Yersinia kristensenii</i>	3.96	0.48			
<i>Citrobacter youngae</i>	1.73	0.51			
320063	Low discrimination				320063
<i>Citrobacter braakii</i>	43.36	0.58	SUC	7	
<i>Yersinia rohdei</i>	29.61	0.49			
<i>Citrobacter freundii</i>	10.31	0.47			
320073	Low discrimination				320073
<i>Citrobacter braakii</i>	63.29	0.64	SUC	7	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	17.15	0.49			
<i>Yersinia rohdei</i>	7.10	0.39			
320153	Low discrimination				320153
<i>Citrobacter braakii</i>	85.86	0.46	MAL	1	
<i>Citrobacter youngae</i>	8.25	0.24			
<i>Yersinia kristensenii</i>	3.62	0.07			
320243	Low discrimination				320243
<i>Citrobacter braakii</i>	67.07	0.40	INO	1	
<i>Citrobacter youngae</i>	15.99	0.26			
<i>Salmonella</i> serovar <i>paratyphi</i>	5.53	-.02			
320253	Low discrimination				320253
<i>Citrobacter braakii</i>	53.23	0.46	INO	1	
<i>Yersinia kristensenii</i>	39.23	0.33			
<i>Citrobacter youngae</i>	5.12	0.24			
320273	Low discrimination				320273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	88.12	0.42	H2S	1	
<i>Citrobacter braakii</i>	7.66	0.23			
<i>Citrobacter youngae</i>	2.60	0.13			
320443	Low discrimination				320443
<i>Citrobacter braakii</i>	83.51	0.40	ADO	1	
<i>Salmonella</i> serovar <i>paratyphi</i>	6.89	-.02			
<i>Salmonella bongori</i>	4.44	-.07			
320453	Acceptable identification				320453
<i>Citrobacter braakii</i>	92.67	0.46	ADO	1	
<i>Yersinia kristensenii</i>	3.91	0.07			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.71	0.14			
321043	Low discrimination				321043
<i>Citrobacter braakii</i>	83.51	0.40	PHE	1	
<i>Salmonella</i> serovar <i>paratyphi</i>	6.89	-.02			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella bongori</i>	4.44	-.07			
321053	Acceptable identification				321053
<i>Citrobacter braakii</i>	94.28	0.46	PHE 1		
<i>Yersinia kristensenii</i>	3.98	0.07			
<i>Citrobacter youngae</i>	1.74	0.10			
322043	Low discrimination				322043
<i>Citrobacter braakii</i>	67.99	0.40	ESL 1		
<i>Citrobacter youngae</i>	16.21	0.26			
<i>Salmonella serovar paratyphi</i>	5.61	-.02			
322053	Low discrimination				322053
<i>Citrobacter braakii</i>	85.20	0.46	ESL 1		
<i>Citrobacter youngae</i>	8.19	0.24			
<i>Yersinia kristensenii</i>	3.59	0.07			
322073	Low discrimination				322073
<i>Yersinia enterocolitica ssp. enterocolitica</i>	86.04	0.39	H2S 1		
<i>Citrobacter braakii</i>	9.62	0.23			
<i>Citrobacter youngae</i>	3.27	0.13			
324003	Low discrimination				324003
<i>Citrobacter braakii</i>	59.61	0.49	SOR 99		
<i>Salmonella bongori</i>	16.55	0.18			
<i>Shigella sonnei</i>	15.70	0.18			
324013	Good identification				324013
<i>Citrobacter braakii</i>	92.96	0.56	SOR 99		
<i>Yokenella regensburgei</i>	4.37	0.12			
<i>Citrobacter youngae</i>	1.63	0.19			
324041	Low discrimination				324041
<i>Citrobacter braakii</i>	73.70	0.49	MAN 99		
<i>Salmonella bongori</i>	20.47	0.18			
<i>Citrobacter youngae</i>	3.20	0.21			
324042	Low discrimination				324042
<i>Citrobacter braakii</i>	65.21	0.49	TRE 99		
<i>Salmonella bongori</i>	18.11	0.18			
<i>Salmonella enterica subsp. enterica</i>	11.53	0.23			
324043	Low discrimination				324043
<i>Citrobacter braakii</i>	73.25	0.90			
<i>Salmonella bongori</i>	20.34	0.59			
<i>Citrobacter youngae</i>	3.18	0.62			
324051	Very good identification				324051
<i>Citrobacter braakii</i>	97.86	0.56	MAN 99		
<i>Citrobacter youngae</i>	1.71	0.19			
<i>Citrobacter amalonaticus</i>	0.43	-.10			
324052	Very good identification				324052

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	97.86	0.56	TRE 99		
<i>Citrobacter youngae</i>	1.71	0.19			
<i>Citrobacter amalonaticus</i>	0.43	-.10			
324053	Very good identification				324053
<i>Citrobacter braakii</i>	97.49	0.97			
<i>Citrobacter youngae</i>	1.71	0.60			
<i>Citrobacter amalonaticus</i>	0.43	0.31			
324063	Identification to the genus				324063
<i>Citrobacter braakii</i>	65.62	0.67	SUC 7		
<i>Citrobacter freundii</i>	20.80	0.59			
<i>Citrobacter youngae</i>	10.06	0.50			
324073	Low discrimination				324073
				VPT	
<i>Citrobacter braakii</i>	78.98	0.74	SUC 7	1	
<i>Citrobacter freundii</i>	9.69	0.57		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.96	0.44		99	
324143	Low discrimination				324143
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	47.36	0.59	LYS 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	41.39	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	5.85	0.43			
324153	Low discrimination				324153
<i>Citrobacter braakii</i>	67.77	0.56	MAL 1		
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	9.87	0.18			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	8.62	0.18			
324173	Good identification				324173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	90.08	0.53	H2S 1	99	
<i>Citrobacter freundii</i>	4.24	0.35		1	
<i>Citrobacter braakii</i>	4.02	0.33		1	
324243	Low discrimination				324243
<i>Citrobacter braakii</i>	52.90	0.49	INO 1		
<i>Salmonella serovar enteritidis</i>	18.37	0.25			
<i>Salmonella bongori</i>	14.69	0.18			
324253	Good identification				324253
<i>Citrobacter braakii</i>	90.08	0.56	INO 1		
<i>Citrobacter youngae</i>	8.21	0.34			
<i>Salmonella serovar enteritidis</i>	0.81	-.01			
324373	Good identification				324373
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	100.0	0.38	H2S 1		
324443	Low discrimination				324443
<i>Citrobacter braakii</i>	73.29	0.49	ADO 1		
<i>Salmonella bongori</i>	20.35	0.18			
<i>Citrobacter youngae</i>	3.18	0.21			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
324453	Very good identification				324453
				VPT	
<i>Citrobacter braakii</i>	96.71	0.56	ADO 1	1	
<i>Citrobacter youngae</i>	1.69	0.19		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.56	0.03		99	
324573	Good identification				324573
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	95.87	0.44	H2S 1	99	
<i>Citrobacter koseri</i>	4.13	0.14		1	
325043	Low discrimination				325043
<i>Citrobacter braakii</i>	73.70	0.49	PHE 1		
<i>Salmonella bongori</i>	20.47	0.18			
<i>Citrobacter youngae</i>	3.20	0.21			
325053	Very good identification				325053
<i>Citrobacter braakii</i>	97.86	0.56	PHE 1		
<i>Citrobacter youngae</i>	1.71	0.19			
<i>Citrobacter amalonaticus</i>	0.43	-10			
326033	Good identification				326033
<i>Cronobacter sakazakii</i>	99.04	0.49	H2S 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.96	0.10			
326043	Low discrimination				326043
<i>Citrobacter braakii</i>	62.48	0.49	ESL 1		
<i>Salmonella bongori</i>	17.35	0.18			
<i>Citrobacter youngae</i>	14.13	0.35			
326053	Identification to the genus				326053
<i>Citrobacter braakii</i>	87.60	0.56	ESL 1		
<i>Citrobacter youngae</i>	7.99	0.34			
<i>Citrobacter amalonaticus</i>	3.76	0.11			
326073	Low discrimination				326073
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	55.44	0.36	H2S 1	99	
<i>Citrobacter braakii</i>	17.32	0.33		1	
<i>Serratia ficaria</i>	15.87	0.16		75	
326133	Low discrimination				326133
<i>Cronobacter sakazakii</i>	72.55	0.36	H2S 1		
<i>Pantoea agglomerans</i>	12.63	0.16			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	9.59	0.20			
326173	Good identification				326173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	97.74	0.46	H2S 1	99	
<i>Kluyvera ascorbata</i>	1.87	0.02		1	
<i>Cronobacter sakazakii</i>	0.39	-06		99	
326233	Very good identification				326233
<i>Cronobacter sakazakii</i>	100.0	0.59	H2S 1		
326333	Good identification				326333

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Cronobacter sakazakii</i>	99.23	0.45	H2S 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.77	0.04			
326573	Acceptable identification				326573
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	94.68	0.36	H2S 1		
<i>Enterobacter aerogenes</i>	5.32	-.02			
327033	Good identification				327033
<i>Cronobacter sakazakii</i>	100.0	0.49	H2S 1		
327133	Good identification				327133
<i>Cronobacter sakazakii</i>	98.31	0.36	H2S 1		
<i>Pantoea agglomerans</i>	1.69	-.05			
327233	Very good identification				327233
<i>Cronobacter sakazakii</i>	100.0	0.59	H2S 1		
327333	Good identification				327333
<i>Cronobacter sakazakii</i>	100.0	0.45	H2S 1		
330013	Very good identification				330013
<i>Escherichia hermannii</i>	96.09	0.59	H2S 1		
<i>Citrobacter braakii</i>	3.39	0.40			
<i>Escherichia fergusonii</i>	0.26	0.10			
330033	Very good identification				330033
<i>Escherichia hermannii</i>	97.48	0.57	H2S 1		
<i>Citrobacter farmeri</i>	2.03	0.18			
<i>Citrobacter braakii</i>	0.32	0.16			
330043	Good identification				330043
<i>Citrobacter braakii</i>	92.82	0.74			
<i>Escherichia coli</i>	4.95	0.47			
<i>Citrobacter youngae</i>	1.52	0.37			
330051	Good identification				330051
<i>Citrobacter braakii</i>	96.46	0.40	MAN 99		
<i>Yersinia kristensenii</i>	3.54	-.01			
330052	Good identification				330052
<i>Citrobacter braakii</i>	96.46	0.40	TRE 99		
<i>Yersinia kristensenii</i>	3.54	-.01			
330053	Good identification				330053
<i>Citrobacter braakii</i>	94.44	0.81			
<i>Yersinia kristensenii</i>	3.47	0.41			
<i>Citrobacter youngae</i>	0.62	0.35			
330063	Low discrimination				330063
<i>Citrobacter braakii</i>	43.74	0.51	SUC 7		
<i>Escherichia coli</i>	20.67	0.43			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	16.29	0.39			
330073	Low discrimination				330073
<i>Citrobacter farmeri</i>	78.96	0.59	H2S 1		
<i>Citrobacter braakii</i>	12.29	0.58			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	6.76	0.49			
330153	Low discrimination				330153
<i>Citrobacter braakii</i>	84.56	0.40	MAL 1		
<i>Citrobacter sedlakii</i>	9.43	0.04			
<i>Yersinia kristensenii</i>	3.10	-0.01			
330253	Low discrimination				330253
<i>Citrobacter braakii</i>	56.56	0.40	INO 1		
<i>Yersinia kristensenii</i>	36.26	0.25			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.23	0.15			
330273	Low discrimination				330273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	75.87	0.42	H2S 1		
<i>Citrobacter farmeri</i>	20.89	0.18			
<i>Citrobacter braakii</i>	3.25	0.16			
330453	Good identification				330453
<i>Citrobacter braakii</i>	96.46	0.40	ADO 1		
<i>Yersinia kristensenii</i>	3.54	-0.01			
331000	Good identification				331000
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.40	ONP 10		
331053	Good identification				331053
<i>Citrobacter braakii</i>	96.46	0.40	PHE 1		
<i>Yersinia kristensenii</i>	3.54	-0.01			
332013	Very good identification				332013
<i>Escherichia hermannii</i>	99.65	0.55	H2S 1		
<i>Escherichia fergusonii</i>	0.35	0.08			
332033	Very good identification				332033
<i>Escherichia hermannii</i>	100.0	0.54	H2S 1		
332053	Low discrimination				332053
<i>Citrobacter braakii</i>	72.70	0.40	ESL 1		
<i>Escherichia hermannii</i>	13.89	0.14			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.23	0.13			
332073	Low discrimination				332073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	65.64	0.39	H2S 1		
<i>Citrobacter farmeri</i>	23.23	0.18			
<i>Escherichia hermannii</i>	7.51	0.12			
334003	Good identification				334003
<i>Citrobacter braakii</i>	98.47	0.43	SOR 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	1.53	0.05			
334013	Low discrimination				334013
<i>Citrobacter braakii</i>	80.22	0.49	SOR 99		
<i>Citrobacter amalonaticus</i>	11.19	0.15			
<i>Escherichia hermannii</i>	7.66	0.18			
334041	Good identification				334041
<i>Citrobacter braakii</i>	98.47	0.43	MAN 99		
<i>Citrobacter youngae</i>	1.53	0.05			
334042	Good identification				334042
<i>Citrobacter braakii</i>	98.47	0.43	TRE 99		
<i>Citrobacter youngae</i>	1.53	0.05			
334043	Very good identification				334043
<i>Citrobacter braakii</i>	97.25	0.84			
<i>Citrobacter youngae</i>	1.51	0.46			
<i>Salmonella bongori</i>	0.55	0.18			
334051	Identification to the genus				334051
<i>Citrobacter braakii</i>	87.28	0.49	MAN 99		
<i>Citrobacter amalonaticus</i>	12.17	0.15			
<i>Citrobacter youngae</i>	0.55	0.03			
334052	Identification to the genus				334052
<i>Citrobacter braakii</i>	87.28	0.49	TRE 99		
<i>Citrobacter amalonaticus</i>	12.17	0.15			
<i>Citrobacter youngae</i>	0.55	0.03			
334053	Identification to the genus				334053
<i>Citrobacter braakii</i>	87.15	0.90			
<i>Citrobacter amalonaticus</i>	12.16	0.56			
<i>Citrobacter youngae</i>	0.55	0.45			
334063	Identification to the genus				334063
<i>Citrobacter braakii</i>	72.43	0.61	SUC 7		
<i>Citrobacter freundii</i>	22.95	0.53			
<i>Citrobacter youngae</i>	3.98	0.34			
334073	Low discrimination				334073
<i>Citrobacter braakii</i>	66.35	0.67	SUC 7		
<i>Citrobacter farmeri</i>	15.79	0.39			
<i>Citrobacter freundii</i>	8.14	0.50			
334153	Low discrimination				334153
<i>Citrobacter braakii</i>	58.16	0.49	MAL 1		
<i>Citrobacter koseri</i>	20.40	0.31			
<i>Citrobacter sedlakii</i>	10.56	0.18			
334243	Acceptable identification				334243
<i>Citrobacter braakii</i>	92.50	0.43	INO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	7.50	0.20			
334253	Identification to the genus				334253
<i>Citrobacter braakii</i>	85.32	0.49	INO 1		
<i>Citrobacter amalonaticus</i>	11.90	0.15			
<i>Citrobacter youngae</i>	2.79	0.18			
334443	Acceptable identification				334443
<i>Citrobacter braakii</i>	94.25	0.43	ADO 1		
<i>Citrobacter koseri</i>	4.28	0.07			
<i>Citrobacter youngae</i>	1.47	0.05			
334453	Identification to the genus				334453
<i>Citrobacter braakii</i>	66.82	0.49	ADO 1		
<i>Citrobacter koseri</i>	23.44	0.31			
<i>Citrobacter amalonaticus</i>	9.32	0.15			
334553	Very good identification				334553
<i>Citrobacter koseri</i>	99.82	0.56	H2S 1		
<i>Citrobacter braakii</i>	0.18	0.08			
334573	Very good identification				334573
				VPT	
<i>Citrobacter koseri</i>	99.76	0.55	H2S 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.24	0.03		99	
335043	Good identification				335043
<i>Citrobacter braakii</i>	98.47	0.43	PHE 1		
<i>Citrobacter youngae</i>	1.53	0.05			
335053	Identification to the genus				335053
<i>Citrobacter braakii</i>	87.28	0.49	PHE 1		
<i>Citrobacter amalonaticus</i>	12.17	0.15			
<i>Citrobacter youngae</i>	0.55	0.03			
336043	Acceptable identification				336043
<i>Citrobacter braakii</i>	90.17	0.43	ESL 1		
<i>Citrobacter youngae</i>	7.31	0.20			
<i>Citrobacter amalonaticus</i>	2.53	-0.06			
336053	Identification to the genus				336053
<i>Citrobacter amalonaticus</i>	56.94	0.35	H2S 5		
<i>Citrobacter braakii</i>	41.70	0.49	URE 88		
<i>Citrobacter youngae</i>	1.36	0.18	ESL 9		
336233	Good identification				336233
<i>Cronobacter sakazakii</i>	100.0	0.40	H2S 1		
337233	Good identification				337233
<i>Cronobacter sakazakii</i>	100.0	0.40	H2S 1		
340003	Low discrimination				340003
<i>Citrobacter werkmanii</i>	43.51	0.37	SCI 92		

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Citrobacter youngae</i>	27.78	0.50	MAL 92		
<i>Yersinia pseudotuberculosis</i>	26.44	0.33	SOR 90		
340013	Identification to the genus				340013
<i>Citrobacter youngae</i>	88.41	0.48	SOR 99		
<i>Citrobacter freundii</i>	4.43	0.24			
<i>Citrobacter braakii</i>	3.07	0.18			
340023	Low discrimination				340023
<i>Citrobacter freundii</i>	56.40	0.44	SOR 99		
<i>Citrobacter youngae</i>	35.49	0.38			
<i>Yersinia rohdei</i>	4.72	0.15			
340033	Identification to the genus				340033
<i>Citrobacter freundii</i>	59.15	0.42	SOR 99		
<i>Citrobacter youngae</i>	38.75	0.36			
<i>Yersinia rohdei</i>	2.10	0.06			
340041	Identification to the genus				340041
<i>Citrobacter youngae</i>	81.86	0.50	MAN 99		
<i>Citrobacter werkmanii</i>	11.66	0.15			
<i>Citrobacter freundii</i>	4.28	0.26			
340042	Identification to the genus				340042
<i>Citrobacter youngae</i>	82.74	0.50	TRE 99		
<i>Citrobacter werkmanii</i>	11.78	0.15			
<i>Citrobacter freundii</i>	4.32	0.26			
340043	Identification to the genus				340043
<i>Citrobacter youngae</i>	82.69	0.91			
<i>Citrobacter werkmanii</i>	11.78	0.56			
<i>Citrobacter freundii</i>	4.32	0.67			
340051	Acceptable identification				340051
<i>Citrobacter youngae</i>	91.40	0.48	MAN 99		
<i>Citrobacter freundii</i>	4.58	0.24			
<i>Citrobacter braakii</i>	3.18	0.18			
340052	Acceptable identification				340052
<i>Citrobacter youngae</i>	91.40	0.48	TRE 99		
<i>Citrobacter freundii</i>	4.58	0.24			
<i>Citrobacter braakii</i>	3.18	0.18			
340053	Good identification				340053
<i>Citrobacter youngae</i>	91.23	0.89			
<i>Citrobacter freundii</i>	4.58	0.65			
<i>Citrobacter braakii</i>	3.17	0.59			
340061	Identification to the genus				340061
<i>Citrobacter freundii</i>	58.39	0.44	MAN 99		
<i>Citrobacter youngae</i>	36.73	0.38			
<i>Yersinia rohdei</i>	4.88	0.15			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
340062	Identification to the genus				340062
<i>Citrobacter freundii</i>	58.39	0.44	TRE 99		
<i>Citrobacter youngae</i>	36.73	0.38			
<i>Yersinia rohdei</i>	4.88	0.15			
340063	Low discrimination				340063
<i>Citrobacter freundii</i>	58.13	0.86			
<i>Citrobacter youngae</i>	36.57	0.79			
<i>Yersinia rohdei</i>	4.86	0.56			
340071	Identification to the genus				340071
<i>Citrobacter freundii</i>	59.15	0.42	MAN 99		
<i>Citrobacter youngae</i>	38.75	0.36			
<i>Yersinia rohdei</i>	2.10	0.06			
340072	Identification to the genus				340072
<i>Citrobacter freundii</i>	59.15	0.42	TRE 99		
<i>Citrobacter youngae</i>	38.75	0.36			
<i>Yersinia rohdei</i>	2.10	0.06			
340073	Identification to the genus				340073
<i>Citrobacter freundii</i>	58.71	0.83			
<i>Citrobacter youngae</i>	38.46	0.77			
<i>Yersinia rohdei</i>	2.08	0.47			
340103	Very good identification				340103
<i>Citrobacter werkmanii</i>	99.63	0.59	SCI 92		
<i>Citrobacter youngae</i>	0.29	0.23	SOR 90		
<i>Yersinia pseudotuberculosis</i>	0.05	-.09			
340141	Good identification				340141
<i>Citrobacter werkmanii</i>	96.63	0.37	SCI 92		
<i>Citrobacter youngae</i>	3.11	0.23	MAN 99		
<i>Citrobacter freundii</i>	0.27	0.04			
340142	Good identification				340142
<i>Citrobacter werkmanii</i>	96.63	0.37	SCI 92		
<i>Citrobacter youngae</i>	3.11	0.23	TRE 99		
<i>Citrobacter freundii</i>	0.27	0.04			
340143	Very good identification				340143
<i>Citrobacter werkmanii</i>	96.62	0.78	SCI 92		
<i>Citrobacter youngae</i>	3.11	0.64			
<i>Citrobacter freundii</i>	0.27	0.45			
340153	Identification to the genus				340153
<i>Citrobacter youngae</i>	67.70	0.63	MAL 5		
<i>Citrobacter werkmanii</i>	26.01	0.37			
<i>Citrobacter freundii</i>	5.61	0.43			
340163	Identification to the genus				340163

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Citrobacter freundii</i>	54.33	0.64	MAL 8		
<i>Citrobacter werkmanii</i>	24.46	0.37			
<i>Citrobacter youngae</i>	20.69	0.53			
340173	Identification to the genus				340173
<i>Citrobacter freundii</i>	71.10	0.62	MAL 8		
<i>Citrobacter youngae</i>	28.19	0.51			
<i>Citrobacter werkmanii</i>	0.41	-0.04			
340243	Very good identification				340243
<i>Citrobacter youngae</i>	96.15	0.64	INO 5		
<i>Citrobacter werkmanii</i>	2.63	0.15			
<i>Citrobacter freundii</i>	0.96	0.26			
340253	Very good identification				340253
<i>Citrobacter youngae</i>	95.48	0.63	INO 5		
<i>Yersinia kristensenii</i>	2.96	0.22			
<i>Citrobacter freundii</i>	0.92	0.24			
340263	Identification to the genus				340263
<i>Citrobacter youngae</i>	74.03	0.53	INO 5		
<i>Citrobacter freundii</i>	22.58	0.44			
<i>Yersinia rohdei</i>	1.89	0.15			
340273	Low discrimination				340273
<i>Citrobacter youngae</i>	72.59	0.51	INO 5		
<i>Citrobacter freundii</i>	21.26	0.42			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.40	0.25			
340343	Identification to the genus				340343
<i>Citrobacter werkmanii</i>	85.45	0.37	SCI 92		
<i>Citrobacter youngae</i>	14.31	0.38	INO 1		
<i>Citrobacter freundii</i>	0.24	0.04			
340353	Acceptable identification				340353
<i>Citrobacter youngae</i>	93.13	0.36	MAL 5		
<i>Citrobacter werkmanii</i>	6.87	-0.04	INO 5		
340443	Identification to the genus				340443
<i>Citrobacter youngae</i>	82.74	0.50	ADO 1		
<i>Citrobacter werkmanii</i>	11.78	0.15			
<i>Citrobacter freundii</i>	4.32	0.26			
340453	Low discrimination				340453
<i>Citrobacter youngae</i>	87.40	0.48	ADO 1		
<i>Citrobacter freundii</i>	4.38	0.24			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.38	0.25			
340463	Identification to the genus				340463
<i>Citrobacter freundii</i>	58.39	0.44	ADO 1		
<i>Citrobacter youngae</i>	36.73	0.38			
<i>Yersinia rohdei</i>	4.88	0.15			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
340473	Identification to the genus				340473
<i>Citrobacter freundii</i>	58.09	0.42	ADO 1		
<i>Citrobacter youngae</i>	38.06	0.36			
<i>Yersinia rohdei</i>	2.06	0.06			
340543	Good identification				340543
<i>Citrobacter werkmanii</i>	96.63	0.37	SCI 92		
<i>Citrobacter youngae</i>	3.11	0.23	ADO 1		
<i>Citrobacter freundii</i>	0.27	0.04			
341020	Identification to the genus				341020
<i>Proteus vulgaris</i>	50.36	0.59	ONP 1		
<i>Proteus penneri</i>	49.65	0.50			
341021	Identification to the genus				341021
<i>Proteus penneri</i>	73.46	0.51	ONP 1		
<i>Proteus vulgaris</i>	26.13	0.51			
<i>Proteus mirabilis</i>	0.22	-.03			
341043	Identification to the genus				341043
<i>Citrobacter youngae</i>	82.74	0.50	PHE 1		
<i>Citrobacter werkmanii</i>	11.78	0.15			
<i>Citrobacter freundii</i>	4.32	0.26			
341053	Acceptable identification				341053
<i>Citrobacter youngae</i>	91.40	0.48	PHE 1		
<i>Citrobacter freundii</i>	4.58	0.24			
<i>Citrobacter braakii</i>	3.18	0.18			
341063	Identification to the genus				341063
<i>Citrobacter freundii</i>	58.39	0.44	PHE 1		
<i>Citrobacter youngae</i>	36.73	0.38			
<i>Yersinia rohdei</i>	4.88	0.15			
341073	Identification to the genus				341073
<i>Citrobacter freundii</i>	59.15	0.42	PHE 1		
<i>Citrobacter youngae</i>	38.75	0.36			
<i>Yersinia rohdei</i>	2.10	0.06			
341143	Good identification				341143
<i>Citrobacter werkmanii</i>	96.63	0.37	PHE 1		
<i>Citrobacter youngae</i>	3.11	0.23	SCI 92		
<i>Citrobacter freundii</i>	0.27	0.04			
342003	Very good identification				342003
<i>Yersinia pseudotuberculosis</i>	99.62	0.59	H2S 1		
<i>Citrobacter youngae</i>	0.29	0.23			
<i>Citrobacter werkmanii</i>	0.09	-.04			
342043	Good identification				342043
<i>Citrobacter youngae</i>	93.02	0.64	ESL 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia pseudotuberculosis</i>	3.26	0.18			
<i>Citrobacter werkmanii</i>	2.54	0.15			
342053	Very good identification				342053
<i>Citrobacter youngae</i>	98.11	0.63	ESL 5		
<i>Citrobacter freundii</i>	0.94	0.24			
<i>Citrobacter braakii</i>	0.65	0.18			
342063	Identification to the genus				342063
<i>Citrobacter youngae</i>	74.28	0.53	ESL 5		
<i>Citrobacter freundii</i>	22.66	0.44			
<i>Yersinia rohdei</i>	1.89	0.15			
342073	Low discrimination				342073
<i>Citrobacter youngae</i>	73.47	0.51	ESL 5		
<i>Citrobacter freundii</i>	21.52	0.42			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.25	0.23			
342143	Identification to the genus				342143
<i>Citrobacter werkmanii</i>	85.45	0.37	ESL 1		
<i>Citrobacter youngae</i>	14.31	0.38	SCI 92		
<i>Citrobacter freundii</i>	0.24	0.04			
342153	Acceptable identification				342153
<i>Citrobacter youngae</i>	93.13	0.36	ESL 5		
<i>Citrobacter werkmanii</i>	6.87	-.04	MAL 5		
342243	Good identification				342243
<i>Citrobacter youngae</i>	100.0	0.38	ESL 5		
342253	Good identification				342253
<i>Citrobacter youngae</i>	97.31	0.36	ESL 5		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.69	0.08	INO 5		
342453	Low discrimination				342453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.19	0.38	H2S 1		
<i>Citrobacter youngae</i>	20.81	0.22	URE 10		
342653	Good identification				342653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.39	H2S 1		
343020	Very good identification				343020
<i>Proteus vulgaris</i>	99.01	0.59	ONP 1		
<i>Proteus penneri</i>	0.99	0.09			
343021	Good identification				343021
<i>Proteus vulgaris</i>	97.24	0.51	ONP 1		
<i>Proteus penneri</i>	2.76	0.10			
344003	Identification to the genus				344003
<i>Citrobacter werkmanii</i>	85.29	0.59	MAL 92		
<i>Citrobacter youngae</i>	13.48	0.59	SOR 90		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	0.99	0.38			
344013	Identification to the genus				344013
<i>Citrobacter youngae</i>	84.37	0.57	SOR 99		
<i>Citrobacter werkmanii</i>	6.59	0.17			
<i>Citrobacter freundii</i>	5.95	0.36			
344023	Identification to the genus				344023
<i>Citrobacter freundii</i>	64.30	0.57	SOR 99		
<i>Citrobacter youngae</i>	28.78	0.47			
<i>Citrobacter werkmanii</i>	6.92	0.17			
344033	Identification to the genus				344033
<i>Citrobacter freundii</i>	67.98	0.55	SOR 99		
<i>Citrobacter youngae</i>	31.69	0.45			
<i>Citrobacter braakii</i>	0.33	0.05			
344041	Identification to the genus				344041
<i>Citrobacter youngae</i>	60.12	0.59	MAN 99		
<i>Citrobacter werkmanii</i>	34.59	0.37			
<i>Citrobacter freundii</i>	4.41	0.38			
344042	Identification to the genus				344042
<i>Citrobacter youngae</i>	60.12	0.59	TRE 99		
<i>Citrobacter werkmanii</i>	34.59	0.37			
<i>Citrobacter freundii</i>	4.41	0.38			
344043	Identification to the genus				344043
<i>Citrobacter youngae</i>	60.12	1.00			
<i>Citrobacter werkmanii</i>	34.59	0.78			
<i>Citrobacter freundii</i>	4.41	0.79			
344051	Identification to the genus				344051
<i>Citrobacter youngae</i>	89.75	0.57	MAN 99		
<i>Citrobacter freundii</i>	6.33	0.36			
<i>Citrobacter braakii</i>	3.29	0.28			
344052	Identification to the genus				344052
<i>Citrobacter youngae</i>	89.75	0.57	TRE 99		
<i>Citrobacter freundii</i>	6.33	0.36			
<i>Citrobacter braakii</i>	3.29	0.28			
344053	Identification to the genus				344053
<i>Citrobacter youngae</i>	89.62	0.98			
<i>Citrobacter freundii</i>	6.32	0.77			
<i>Citrobacter braakii</i>	3.28	0.69			
344061	Identification to the genus				344061
<i>Citrobacter freundii</i>	68.61	0.57	MAN 99		
<i>Citrobacter youngae</i>	30.72	0.47			
<i>Citrobacter werkmanii</i>	0.67	-.04			
344062	Identification to the genus				344062

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	68.61	0.57	TRE 99		
<i>Citrobacter youngae</i>	30.72	0.47			
<i>Citrobacter werkmanii</i>	0.67	-0.04			
344063	Identification to the genus				344063
<i>Citrobacter freundii</i>	68.52	0.98			
<i>Citrobacter youngae</i>	30.67	0.88			
<i>Citrobacter werkmanii</i>	0.67	0.37			
344071	Identification to the genus				344071
<i>Citrobacter freundii</i>	67.98	0.55	MAN 99		
<i>Citrobacter youngae</i>	31.69	0.45			
<i>Citrobacter braakii</i>	0.33	0.05			
344072	Identification to the genus				344072
<i>Citrobacter freundii</i>	67.98	0.55	TRE 99		
<i>Citrobacter youngae</i>	31.69	0.45			
<i>Citrobacter braakii</i>	0.33	0.05			
344073	Identification to the genus				344073
<i>Citrobacter freundii</i>	67.93	0.96			
<i>Citrobacter youngae</i>	31.67	0.86			
<i>Citrobacter braakii</i>	0.33	0.46			
344101	Good identification				344101
<i>Citrobacter werkmanii</i>	100.0	0.39	SOR 90		
344102	Good identification				344102
<i>Citrobacter werkmanii</i>	100.0	0.39	SOR 90		
344103	Very good identification				344103
<i>Citrobacter werkmanii</i>	99.92	0.80	SOR 90		
<i>Citrobacter youngae</i>	0.07	0.33			
<i>Citrobacter freundii</i>	0.01	0.16			
344113	Acceptable identification				344113
<i>Citrobacter werkmanii</i>	93.86	0.39	CEL 1		
<i>Citrobacter youngae</i>	5.50	0.31	SOR 90		
<i>Citrobacter freundii</i>	0.64	0.14			
344123	Acceptable identification				344123
<i>Citrobacter werkmanii</i>	91.81	0.39	SUC 1		
<i>Citrobacter freundii</i>	6.45	0.35	SOR 90		
<i>Citrobacter youngae</i>	1.75	0.21			
344141	Very good identification				344141
<i>Citrobacter werkmanii</i>	99.12	0.59	MAN 99		
<i>Citrobacter youngae</i>	0.79	0.33			
<i>Citrobacter freundii</i>	0.10	0.16			
344142	Very good identification				344142

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter werkmanii</i>	99.12	0.59	TRE 99		
<i>Citrobacter youngae</i>	0.79	0.33			
<i>Citrobacter freundii</i>	0.10	0.16			
344143	Excellent identification				344143
<i>Citrobacter werkmanii</i>	99.11	1.00			
<i>Citrobacter youngae</i>	0.79	0.74			
<i>Citrobacter freundii</i>	0.10	0.57			
344153	Identification to the genus				344153
<i>Citrobacter werkmanii</i>	57.93	0.59	CEL 1		
<i>Citrobacter youngae</i>	37.33	0.72			
<i>Citrobacter freundii</i>	4.35	0.55			
344163	Identification to the genus				344163
<i>Citrobacter werkmanii</i>	50.46	0.59	SUC 1		
<i>Citrobacter freundii</i>	38.98	0.76			
<i>Citrobacter youngae</i>	10.56	0.62			
344173	Identification to the genus				344173
				VPT	
<i>Citrobacter freundii</i>	75.73	0.74	MAL 8	1	
<i>Citrobacter youngae</i>	21.37	0.60		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.60	0.31		99	
344243	Identification to the genus				344243
<i>Citrobacter youngae</i>	88.71	0.74	INO 5		
<i>Citrobacter werkmanii</i>	9.80	0.37			
<i>Citrobacter freundii</i>	1.25	0.38			
344253	Very good identification				344253
<i>Citrobacter youngae</i>	97.86	0.72	INO 5		
<i>Citrobacter freundii</i>	1.32	0.36			
<i>Citrobacter braakii</i>	0.69	0.28			
344263	Identification to the genus				344263
<i>Citrobacter youngae</i>	69.79	0.62	INO 5		
<i>Citrobacter freundii</i>	29.92	0.57			
<i>Citrobacter werkmanii</i>	0.29	-0.04			
344273	Identification to the genus				344273
				VPT	
<i>Citrobacter youngae</i>	70.52	0.60	INO 5	1	
<i>Citrobacter freundii</i>	29.03	0.55		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.31	0.05		99	
344303	Good identification				344303
<i>Citrobacter werkmanii</i>	99.63	0.39	INO 1		
<i>Citrobacter youngae</i>	0.38	0.06	SOR 90		
344343	Very good identification				344343
<i>Citrobacter werkmanii</i>	95.93	0.59	INO 1		
<i>Citrobacter youngae</i>	3.98	0.47			
<i>Citrobacter freundii</i>	0.09	0.16			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
344353	Identification to the genus				344353
<i>Citrobacter youngae</i>	75.75	0.46	MAL 5		
<i>Citrobacter werkmanii</i>	22.56	0.18	INO 5		
<i>Citrobacter freundii</i>	1.69	0.14			
344363	Identification to the genus				344363
<i>Citrobacter youngae</i>	38.09	0.36	MAL 5		
<i>Citrobacter werkmanii</i>	34.92	0.18	INO 5		
<i>Citrobacter freundii</i>	26.98	0.35			
344443	Identification to the genus				344443
<i>Citrobacter youngae</i>	60.12	0.59	ADO 1		
<i>Citrobacter werkmanii</i>	34.59	0.37			
<i>Citrobacter freundii</i>	4.41	0.38			
344453	Identification to the genus				344453
<i>Citrobacter youngae</i>	89.15	0.57	ADO 1		
<i>Citrobacter freundii</i>	6.28	0.36			
<i>Citrobacter braakii</i>	3.27	0.28			
344463	Identification to the genus				344463
<i>Citrobacter freundii</i>	68.61	0.57	ADO 1		
<i>Citrobacter youngae</i>	30.72	0.47			
<i>Citrobacter werkmanii</i>	0.67	-.04			
344473	Identification to the genus				344473
				VPT	
<i>Citrobacter freundii</i>	67.06	0.55	ADO 1	1	
<i>Citrobacter youngae</i>	31.26	0.45		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.35	0.11		99	
344503	Good identification				344503
<i>Citrobacter werkmanii</i>	100.0	0.39	ADO 1		
344543	Very good identification				344543
<i>Citrobacter werkmanii</i>	99.12	0.59	ADO 1		
<i>Citrobacter youngae</i>	0.79	0.33			
<i>Citrobacter freundii</i>	0.10	0.16			
345020	Acceptable identification				345020
<i>Proteus vulgaris</i>	94.66	0.43	ONP 1		
<i>Proteus penneri</i>	5.34	0.09			
345021	Identification to the genus				345021
<i>Proteus vulgaris</i>	79.97	0.36	ONP 1		
<i>Proteus penneri</i>	12.87	0.10			
<i>Proteus mirabilis</i>	7.16	0.02			
345043	Identification to the genus				345043
<i>Citrobacter youngae</i>	60.12	0.59	PHE 1		
<i>Citrobacter werkmanii</i>	34.59	0.37			
<i>Citrobacter freundii</i>	4.41	0.38			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
345053	Identification to the genus				345053
<i>Citrobacter youngae</i>	89.75	0.57	PHE 1		
<i>Citrobacter freundii</i>	6.33	0.36			
<i>Citrobacter braakii</i>	3.29	0.28			
345063	Identification to the genus				345063
<i>Citrobacter freundii</i>	68.61	0.57	PHE 1		
<i>Citrobacter youngae</i>	30.72	0.47			
<i>Citrobacter werkmanii</i>	0.67	-.04			
345073	Identification to the genus				345073
<i>Citrobacter freundii</i>	67.98	0.55	PHE 1		
<i>Citrobacter youngae</i>	31.69	0.45			
<i>Citrobacter braakii</i>	0.33	0.05			
345103	Good identification				345103
<i>Citrobacter werkmanii</i>	100.0	0.39	PHE 1		
345143	Very good identification				345143
<i>Citrobacter werkmanii</i>	99.12	0.59	PHE 1		
<i>Citrobacter youngae</i>	0.79	0.33			
<i>Citrobacter freundii</i>	0.10	0.16			
346043	Identification to the genus				346043
<i>Citrobacter youngae</i>	88.71	0.74	ESL 5		
<i>Citrobacter werkmanii</i>	9.80	0.37			
<i>Citrobacter freundii</i>	1.25	0.38			
346053	Very good identification				346053
<i>Citrobacter youngae</i>	97.56	0.72	ESL 5		
<i>Citrobacter freundii</i>	1.32	0.36			
<i>Citrobacter braakii</i>	0.69	0.28			
346063	Identification to the genus				346063
<i>Citrobacter youngae</i>	69.79	0.62	ESL 5		
<i>Citrobacter freundii</i>	29.92	0.57			
<i>Citrobacter werkmanii</i>	0.29	-.04			
346073	Identification to the genus				346073
<i>Citrobacter youngae</i>	68.31	0.60	ESL 5		
<i>Citrobacter freundii</i>	28.12	0.55			
<i>Serratia ficaria</i>	2.70	0.16			
346103	Good identification				346103
<i>Citrobacter werkmanii</i>	99.63	0.39	ESL 1		
<i>Citrobacter youngae</i>	0.38	0.06	SOR 90		
346143	Very good identification				346143
<i>Citrobacter werkmanii</i>	95.93	0.59	ESL 1		
<i>Citrobacter youngae</i>	3.98	0.47			
<i>Citrobacter freundii</i>	0.09	0.16			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
346153	Identification to the genus				346153
<i>Citrobacter youngae</i>	75.13	0.46	ESL 5		
<i>Citrobacter werkmanii</i>	22.38	0.18	MAL 5		
<i>Citrobacter freundii</i>	1.68	0.14			
346163	Identification to the genus				346163
<i>Citrobacter youngae</i>	38.09	0.36	ESL 5		
<i>Citrobacter werkmanii</i>	34.92	0.18	MAL 5		
<i>Citrobacter freundii</i>	26.98	0.35			
346243	Good identification				346243
<i>Citrobacter youngae</i>	97.93	0.47	ESL 5		
<i>Citrobacter werkmanii</i>	2.08	-.04	INO 5		
346253	Good identification				346253
<i>Citrobacter youngae</i>	100.0	0.46	ESL 5		
346263	Acceptable identification				346263
<i>Citrobacter youngae</i>	92.40	0.36	ESL 5		
<i>Citrobacter freundii</i>	7.60	0.16	INO 5		
347020	Good identification				347020
<i>Proteus vulgaris</i>	100.0	0.43	ONP 1		
347021	Good identification				347021
<i>Proteus vulgaris</i>	100.0	0.36	ONP 1		
350023	Identification to the genus				350023
<i>Citrobacter freundii</i>	81.61	0.38	SOR 99		
<i>Citrobacter youngae</i>	18.40	0.22			
350033	Identification to the genus				350033
<i>Citrobacter freundii</i>	80.99	0.36	SOR 99		
<i>Citrobacter youngae</i>	19.01	0.20			
350043	Identification to the genus				350043
<i>Citrobacter youngae</i>	83.79	0.75			
<i>Citrobacter freundii</i>	12.21	0.60			
<i>Citrobacter braakii</i>	3.28	0.47			
350053	Identification to the genus				350053
<i>Citrobacter youngae</i>	79.09	0.73			
<i>Citrobacter freundii</i>	11.07	0.58			
<i>Citrobacter braakii</i>	7.67	0.53			
350061	Identification to the genus				350061
<i>Citrobacter freundii</i>	81.61	0.38	MAN 99		
<i>Citrobacter youngae</i>	18.40	0.22			
350062	Identification to the genus				350062
<i>Citrobacter freundii</i>	81.61	0.38	TRE 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	18.40	0.22			
350063	Identification to the genus				350063
<i>Citrobacter freundii</i>	81.10	0.79			
<i>Citrobacter youngae</i>	18.28	0.63			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.26	0.23			
350071	Identification to the genus				350071
<i>Citrobacter freundii</i>	80.99	0.36	MAN 99		
<i>Citrobacter youngae</i>	19.01	0.20			
350072	Identification to the genus				350072
<i>Citrobacter freundii</i>	80.99	0.36	TRE 99		
<i>Citrobacter youngae</i>	19.01	0.20			
350073	Identification to the genus				350073
<i>Citrobacter freundii</i>	79.31	0.77			
<i>Citrobacter youngae</i>	18.62	0.62			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.96	0.33			
350143	Identification to the genus				350143
<i>Citrobacter werkmanii</i>	58.79	0.37	IND 1		
<i>Citrobacter youngae</i>	33.01	0.49	SCI 92		
<i>Citrobacter freundii</i>	7.95	0.39			
350153	Identification to the genus				350153
<i>Citrobacter youngae</i>	75.94	0.47	MAL 5		
<i>Citrobacter freundii</i>	17.56	0.36			
<i>Citrobacter sedlakii</i>	3.42	0.04			
350163	Identification to the genus				350163
<i>Citrobacter freundii</i>	87.29	0.57	MAL 8		
<i>Citrobacter youngae</i>	11.91	0.37			
<i>Citrobacter werkmanii</i>	0.81	-0.04			
350173	Identification to the genus				350173
<i>Citrobacter freundii</i>	87.56	0.55	MAL 8		
<i>Citrobacter youngae</i>	12.44	0.35			
350243	Good identification				350243
<i>Citrobacter youngae</i>	96.57	0.49	INO 5		
<i>Citrobacter freundii</i>	2.70	0.19			
<i>Citrobacter braakii</i>	0.73	0.06			
350253	Low discrimination				350253
<i>Citrobacter youngae</i>	89.22	0.47	INO 5		
<i>Yersinia kristensenii</i>	6.72	0.14			
<i>Citrobacter freundii</i>	2.40	0.17			
350263	Low discrimination				350263
<i>Citrobacter youngae</i>	50.86	0.37	INO 5		
<i>Citrobacter freundii</i>	43.30	0.38			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.84	0.15			
350273	Low discrimination				350273
<i>Citrobacter youngae</i>	44.67	0.35	INO 5		
<i>Citrobacter freundii</i>	36.52	0.36			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	18.81	0.25			
350463	Identification to the genus				350463
<i>Citrobacter freundii</i>	81.61	0.38	ADO 1		
<i>Citrobacter youngae</i>	18.40	0.22			
350473	Identification to the genus				350473
<i>Citrobacter freundii</i>	80.99	0.36	ADO 1		
<i>Citrobacter youngae</i>	19.01	0.20			
351000	Good identification				351000
<i>Morganella morganii</i> subsp. <i>morganii</i>	95.47	0.42	ONP 10		
<i>Proteus vulgaris</i>	4.53	0.28	ORN 95		
351020	Very good identification				351020
<i>Proteus vulgaris</i>	98.37	0.59	ONP 1		
<i>Proteus penneri</i>	0.98	0.09			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.65	0.01			
351021	Good identification				351021
<i>Proteus vulgaris</i>	96.54	0.51	ONP 1		
<i>Proteus penneri</i>	2.74	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.72	0.05			
351063	Identification to the genus				351063
<i>Citrobacter freundii</i>	81.61	0.38	PHE 1		
<i>Citrobacter youngae</i>	18.40	0.22			
351073	Identification to the genus				351073
<i>Citrobacter freundii</i>	80.99	0.36	PHE 1		
<i>Citrobacter youngae</i>	19.01	0.20			
352043	Good identification				352043
<i>Citrobacter youngae</i>	96.57	0.49	ESL 5		
<i>Citrobacter freundii</i>	2.70	0.19			
<i>Citrobacter braakii</i>	0.73	0.06			
352053	Acceptable identification				352053
<i>Citrobacter youngae</i>	94.94	0.47	ESL 5		
<i>Citrobacter freundii</i>	2.55	0.17			
<i>Citrobacter braakii</i>	1.77	0.12			
352063	Identification to the genus				352063
<i>Citrobacter youngae</i>	51.53	0.37	ESL 5		
<i>Citrobacter freundii</i>	43.87	0.38			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.60	0.13			
352073	Low discrimination				352073

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	46.62	0.35	ESL 5		
<i>Citrobacter freundii</i>	38.11	0.36			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	15.27	0.23			
352133	Good identification				352133
<i>Leclercia adecarboxylata</i>	100.0	0.36	H2S 1		
352433	Good identification				352433
<i>Leclercia adecarboxylata</i>	100.0	0.36	H2S 1		
352513	Very good identification				352513
<i>Leclercia adecarboxylata</i>	100.0	0.53	H2S 1		
352533	Very good identification				352533
<i>Leclercia adecarboxylata</i>	100.0	0.59	H2S 1		
353020	Very good identification				353020
<i>Proteus vulgaris</i>	100.0	0.59	ONP 1		
353021	Good identification				353021
<i>Proteus vulgaris</i>	100.0	0.51	ONP 1		
354003	Identification to the genus				354003
<i>Citrobacter youngae</i>	62.18	0.43	SOR 99		
<i>Citrobacter werkmanii</i>	22.52	0.17			
<i>Citrobacter freundii</i>	12.74	0.32			
354013	Low discrimination				354013
<i>Citrobacter youngae</i>	69.27	0.42	SOR 99		
<i>Citrobacter freundii</i>	13.63	0.30			
<i>Citrobacter amalonaticus</i>	10.02	0.08			
354023	Identification to the genus				354023
<i>Citrobacter freundii</i>	86.18	0.50	SOR 99		
<i>Citrobacter youngae</i>	13.82	0.32			
354033	Identification to the genus				354033
<i>Citrobacter freundii</i>	85.69	0.48	SOR 99		
<i>Citrobacter youngae</i>	14.31	0.30			
354041	Identification to the genus				354041
<i>Citrobacter youngae</i>	78.19	0.43	MAN 99		
<i>Citrobacter freundii</i>	16.02	0.32			
<i>Citrobacter braakii</i>	3.22	0.16			
354042	Identification to the genus				354042
<i>Citrobacter youngae</i>	78.19	0.43	TRE 99		
<i>Citrobacter freundii</i>	16.02	0.32			
<i>Citrobacter braakii</i>	3.22	0.16			
354043	Identification to the genus				354043

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Citrobacter youngae</i>	78.12	0.85			
<i>Citrobacter freundii</i>	16.00	0.73			
<i>Citrobacter braakii</i>	3.22	0.57			
354051	Low discrimination				354051
<i>Citrobacter youngae</i>	69.27	0.42	MAN 99		
<i>Citrobacter freundii</i>	13.63	0.30			
<i>Citrobacter amalonaticus</i>	10.02	0.08			
354052	Low discrimination				354052
<i>Citrobacter youngae</i>	69.27	0.42	TRE 99		
<i>Citrobacter freundii</i>	13.63	0.30			
<i>Citrobacter amalonaticus</i>	10.02	0.08			
354053	Low discrimination				354053
<i>Citrobacter youngae</i>	69.25	0.83			
<i>Citrobacter freundii</i>	13.62	0.71			
<i>Citrobacter amalonaticus</i>	10.02	0.49			
354061	Identification to the genus				354061
<i>Citrobacter freundii</i>	86.18	0.50	MAN 99		
<i>Citrobacter youngae</i>	13.82	0.32			
354062	Identification to the genus				354062
<i>Citrobacter freundii</i>	86.18	0.50	TRE 99		
<i>Citrobacter youngae</i>	13.82	0.32			
354063	Identification to the genus				354063
<i>Citrobacter freundii</i>	86.02	0.92			
<i>Citrobacter youngae</i>	13.80	0.73			
<i>Citrobacter braakii</i>	0.16	0.34			
354071	Identification to the genus				354071
<i>Citrobacter freundii</i>	85.69	0.48	MAN 99		
<i>Citrobacter youngae</i>	14.31	0.30			
354072	Identification to the genus				354072
<i>Citrobacter freundii</i>	85.69	0.48	TRE 99		
<i>Citrobacter youngae</i>	14.31	0.30			
354073	Identification to the genus				354073
<i>Citrobacter freundii</i>	84.90	0.89			
<i>Citrobacter youngae</i>	14.18	0.71			
<i>Citrobacter amalonaticus</i>	0.49	0.25			
354103	Good identification				354103
<i>Citrobacter werkmanii</i>	98.34	0.39	IND 1		
<i>Citrobacter youngae</i>	1.24	0.17	SOR 90		
<i>Citrobacter freundii</i>	0.42	0.10			
354143	Identification to the genus				354143
<i>Citrobacter werkmanii</i>	84.24	0.59	IND 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	11.71	0.58			
<i>Citrobacter freundii</i>	3.96	0.51			
354153	Low discrimination				354153
<i>Citrobacter youngae</i>	64.91	0.56	MAL 5		
<i>Citrobacter freundii</i>	21.10	0.49			
<i>Citrobacter werkmanii</i>	5.77	0.18			
354163	Identification to the genus				354163
<i>Citrobacter freundii</i>	89.00	0.70	MAL 8		
<i>Citrobacter youngae</i>	8.64	0.46			
<i>Citrobacter werkmanii</i>	2.36	0.18			
354173	Good identification				354173
<i>Citrobacter freundii</i>	90.82	0.68	MAL 8		
<i>Citrobacter youngae</i>	9.18	0.45			
354243	Good identification				354243
<i>Citrobacter youngae</i>	94.92	0.58	INO 5		
<i>Citrobacter freundii</i>	3.73	0.32			
<i>Citrobacter braakii</i>	0.75	0.16			
354253	Good identification				354253
<i>Citrobacter youngae</i>	92.15	0.56	INO 5		
<i>Citrobacter freundii</i>	3.48	0.30			
<i>Citrobacter amalonaticus</i>	2.56	0.08			
354263	Identification to the genus				354263
<i>Citrobacter freundii</i>	54.47	0.50	INO 1		
<i>Citrobacter youngae</i>	45.53	0.46			
354273	Identification to the genus				354273
<i>Citrobacter freundii</i>	53.47	0.48	INO 1		
<i>Citrobacter youngae</i>	46.53	0.45			
354443	Identification to the genus				354443
<i>Citrobacter youngae</i>	78.19	0.43	ADO 1		
<i>Citrobacter freundii</i>	16.02	0.32			
<i>Citrobacter braakii</i>	3.22	0.16			
354453	Low discrimination				354453
<i>Citrobacter youngae</i>	68.73	0.42	ADO 1		
<i>Citrobacter freundii</i>	13.52	0.30			
<i>Citrobacter amalonaticus</i>	9.95	0.08			
354463	Identification to the genus				354463
<i>Citrobacter freundii</i>	86.18	0.50	ADO 1		
<i>Citrobacter youngae</i>	13.82	0.32			
354473	Identification to the genus				354473
<i>Citrobacter freundii</i>	85.69	0.48	ADO 1		
<i>Citrobacter youngae</i>	14.31	0.30			

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
355020	Good identification					355020
<i>Proteus vulgaris</i>		100.0	0.43	ONP 1		
355021	Acceptable identification					355021
<i>Proteus vulgaris</i>		94.82	0.36	ONP 1		
<i>Providencia stuartii</i>		5.18	0.05			
355043	Identification to the genus					355043
<i>Citrobacter youngae</i>		78.19	0.43	PHE 1		
<i>Citrobacter freundii</i>		16.02	0.32			
<i>Citrobacter braakii</i>		3.22	0.16			
355053	Low discrimination					355053
<i>Citrobacter youngae</i>		69.27	0.42	PHE 1		
<i>Citrobacter freundii</i>		13.63	0.30			
<i>Citrobacter amalonaticus</i>		10.02	0.08			
355063	Identification to the genus					355063
<i>Citrobacter freundii</i>		86.18	0.50	PHE 1		
<i>Citrobacter youngae</i>		13.82	0.32			
355073	Identification to the genus					355073
<i>Citrobacter freundii</i>		85.69	0.48	PHE 1		
<i>Citrobacter youngae</i>		14.31	0.30			
356043	Good identification					356043
<i>Citrobacter youngae</i>		94.72	0.58	ESL 5		
<i>Citrobacter freundii</i>		3.72	0.32			
<i>Citrobacter braakii</i>		0.75	0.16			
356053	Identification to the genus					356053
<i>Citrobacter youngae</i>		75.23	0.56	ESL 5		
<i>Citrobacter amalonaticus</i>		20.46	0.28			
<i>Citrobacter freundii</i>		2.84	0.30			
356063	Identification to the genus					356063
<i>Citrobacter freundii</i>		54.47	0.50	ESL 1		
<i>Citrobacter youngae</i>		45.53	0.46			
356073	Identification to the genus					356073
<i>Citrobacter freundii</i>		51.89	0.48	ESL 1		
<i>Citrobacter youngae</i>		45.16	0.45			
<i>Citrobacter amalonaticus</i>		2.95	0.04			
357020	Good identification					357020
<i>Proteus vulgaris</i>		100.0	0.43	ONP 1		
357021	Good identification					357021
<i>Proteus vulgaris</i>		100.0	0.36	ONP 1		
360013	Low discrimination					360013

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	75.14	0.42	SOR 99		
<i>Yersinia kristensenii</i>	17.31	0.18			
<i>Citrobacter youngae</i>	5.03	0.17			
360041	Identification to the genus				360041
<i>Citrobacter braakii</i>	85.75	0.35	MAN 99		
<i>Citrobacter youngae</i>	14.25	0.19			
360042	Identification to the genus				360042
<i>Citrobacter braakii</i>	83.86	0.35	TRE 99		
<i>Citrobacter youngae</i>	13.94	0.19			
<i>Salmonella enterica subsp. enterica</i>	2.20	-.09			
360043	Identification to the genus				360043
<i>Citrobacter braakii</i>	84.16	0.76			
<i>Citrobacter youngae</i>	13.99	0.60			
<i>Citrobacter werkmanii</i>	0.65	0.15			
360051	Low discrimination				360051
<i>Citrobacter braakii</i>	77.08	0.42	MAN 99		
<i>Yersinia kristensenii</i>	17.76	0.18			
<i>Citrobacter youngae</i>	5.16	0.17			
360052	Low discrimination				360052
<i>Citrobacter braakii</i>	77.08	0.42	TRE 99		
<i>Yersinia kristensenii</i>	17.76	0.18			
<i>Citrobacter youngae</i>	5.16	0.17			
360053	Low discrimination				360053
<i>Citrobacter braakii</i>	76.60	0.83			
<i>Yersinia kristensenii</i>	17.65	0.59			
<i>Citrobacter youngae</i>	5.13	0.58			
360063	Low discrimination				360063
<i>Citrobacter braakii</i>	27.55	0.53	SUC 7		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	24.73	0.49			
<i>Yersinia rohdei</i>	23.16	0.47			
360073	Low discrimination				360073
<i>Yersinia enterocolitica ssp. enterocolitica</i>	45.80	0.59	H2S 1		
<i>Citrobacter braakii</i>	34.53	0.59			
<i>Citrobacter youngae</i>	8.17	0.46			
360143	Identification to the genus				360143
<i>Citrobacter werkmanii</i>	81.83	0.37	ORN 1		
<i>Citrobacter braakii</i>	9.30	0.35	SCI 92		
<i>Citrobacter youngae</i>	8.05	0.33			
360243	Low discrimination				360243
<i>Citrobacter braakii</i>	47.63	0.35	INO 1		
<i>Citrobacter youngae</i>	41.25	0.33			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	7.19	0.15			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
360253	Low discrimination				360253
<i>Yersinia kristensenii</i>	71.92	0.43	H2S 1		
<i>Citrobacter braakii</i>	17.87	0.42			
<i>Citrobacter youngae</i>	6.24	0.32			
360263	Low discrimination				360263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	88.60	0.42	H2S 1		
<i>Citrobacter youngae</i>	7.12	0.21			
<i>Citrobacter braakii</i>	2.33	0.12			
360273	Good identification				360273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	95.30	0.51	H2S 1		
<i>Citrobacter youngae</i>	2.09	0.20			
<i>Citrobacter braakii</i>	1.69	0.18			
360443	Identification to the genus				360443
<i>Citrobacter braakii</i>	85.75	0.35	ADO 1		
<i>Citrobacter youngae</i>	14.25	0.19			
360453	Low discrimination				360453
<i>Citrobacter braakii</i>	77.08	0.42	ADO 1		
<i>Yersinia kristensenii</i>	17.76	0.18			
<i>Citrobacter youngae</i>	5.16	0.17			
361000	Acceptable identification				361000
<i>Morganella morganii</i> subsp. <i>morganii</i>	93.99	0.42	ONP 10		
<i>Proteus mirabilis</i>	6.01	0.19	IND 95		
361001	Very good identification				361001
<i>Proteus mirabilis</i>	95.54	0.53	ONP 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.15	0.34			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.31	0.01			
361021	Acceptable identification				361021
<i>Proteus mirabilis</i>	94.21	0.38	ONP 1		
<i>Proteus penneri</i>	3.18	0.10			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.48	0.10			
361043	Identification to the genus				361043
<i>Citrobacter braakii</i>	85.75	0.35	PHE 1		
<i>Citrobacter youngae</i>	14.25	0.19			
361053	Low discrimination				361053
<i>Citrobacter braakii</i>	77.08	0.42	PHE 1		
<i>Yersinia kristensenii</i>	17.76	0.18			
<i>Citrobacter youngae</i>	5.16	0.17			
362043	Low discrimination				362043
<i>Citrobacter braakii</i>	50.42	0.35	ESL 1		
<i>Citrobacter youngae</i>	43.66	0.33			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.92	0.13			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
362053	Low discrimination				362053
<i>Citrobacter braakii</i>	56.55	0.42	ESL 1		
<i>Citrobacter youngae</i>	19.74	0.32			
<i>Yersinia kristensenii</i>	13.03	0.18			
362063	Low discrimination				362063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	85.81	0.39	H2S 1		
<i>Citrobacter youngae</i>	8.86	0.21			
<i>Citrobacter braakii</i>	2.90	0.12			
362073	Acceptable identification				362073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	94.54	0.49	H2S 1		
<i>Citrobacter youngae</i>	2.66	0.20			
<i>Citrobacter braakii</i>	2.16	0.18			
362273	Good identification				362273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.42	H2S 1		
364003	Identification to the genus				364003
<i>Citrobacter braakii</i>	66.48	0.45	SOR 99		
<i>Citrobacter werkmanii</i>	21.67	0.17			
<i>Citrobacter youngae</i>	10.48	0.28			
364013	Identification to the genus				364013
<i>Citrobacter braakii</i>	89.61	0.51	SOR 99		
<i>Citrobacter youngae</i>	5.69	0.26			
<i>Citrobacter amalonaticus</i>	4.70	0.08			
364041	Identification to the genus				364041
<i>Citrobacter braakii</i>	84.22	0.45	MAN 99		
<i>Citrobacter youngae</i>	13.28	0.28			
<i>Citrobacter werkmanii</i>	2.50	-.04			
364042	Identification to the genus				364042
<i>Citrobacter braakii</i>	84.22	0.45	TRE 99		
<i>Citrobacter youngae</i>	13.28	0.28			
<i>Citrobacter werkmanii</i>	2.50	-.04			
364043	Identification to the genus				364043
<i>Citrobacter braakii</i>	83.52	0.86			
<i>Citrobacter youngae</i>	13.17	0.69			
<i>Citrobacter werkmanii</i>	2.48	0.37			
364051	Identification to the genus				364051
<i>Citrobacter braakii</i>	89.61	0.51	MAN 99		
<i>Citrobacter youngae</i>	5.69	0.26			
<i>Citrobacter amalonaticus</i>	4.70	0.08			
364052	Identification to the genus				364052
<i>Citrobacter braakii</i>	89.61	0.51	TRE 99		
<i>Citrobacter youngae</i>	5.69	0.26			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter amalonaticus</i>	4.70	0.08			
364053	Identification to the genus				364053
<i>Citrobacter braakii</i>	89.35	0.92			
<i>Citrobacter youngae</i>	5.68	0.67			
<i>Citrobacter amalonaticus</i>	4.69	0.49			
364063	Identification to the genus				364063
<i>Citrobacter braakii</i>	50.57	0.63	SUC 7		
<i>Citrobacter youngae</i>	28.16	0.57			
<i>Citrobacter freundii</i>	20.54	0.57			
364073	Low discrimination				364073
				VPT	
<i>Citrobacter braakii</i>	60.22	0.69	SUC 7	1	
<i>Enterobacter cloacae subsp. cloacae</i>	13.77	0.49		99	
<i>Citrobacter youngae</i>	13.51	0.55		1	
364103	Good identification				364103
<i>Citrobacter werkmanii</i>	98.97	0.39	ORN 1		
<i>Hafnia alvei</i>	0.55	0.16	SOR 90		
<i>Citrobacter braakii</i>	0.27	0.04			
364143	Good identification				364143
<i>Citrobacter werkmanii</i>	92.14	0.59	ORN 1		
<i>Citrobacter braakii</i>	2.73	0.45			
<i>Citrobacter youngae</i>	2.24	0.43			
364153	Low discrimination				364153
<i>Citrobacter sedlakii</i>	63.15	0.45	H2S 1		
<i>Citrobacter braakii</i>	21.35	0.51			
<i>Citrobacter youngae</i>	7.07	0.41			
364173	Good identification				364173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	94.54	0.59	H2S 1	99	
<i>Citrobacter freundii</i>	1.88	0.33		1	
<i>Citrobacter youngae</i>	1.63	0.29		1	
364243	Identification to the genus				364243
<i>Citrobacter braakii</i>	54.02	0.45	INO 1		
<i>Citrobacter youngae</i>	44.38	0.43			
<i>Citrobacter werkmanii</i>	1.60	-0.04			
364253	Identification to the genus				364253
<i>Citrobacter braakii</i>	71.10	0.51	INO 1		
<i>Citrobacter youngae</i>	23.54	0.41			
<i>Citrobacter amalonaticus</i>	3.73	0.08			
364373	Good identification				364373
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	99.49	0.43	H2S 1	99	
<i>Citrobacter youngae</i>	0.51	0.03		1	
364443	Identification to the genus				364443

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	84.22	0.45	ADO 1		
<i>Citrobacter youngae</i>	13.28	0.28			
<i>Citrobacter werkmanii</i>	2.50	-.04			
364453	Identification to the genus				364453
<i>Citrobacter braakii</i>	87.90	0.51	ADO 1		
<i>Citrobacter youngae</i>	5.59	0.26			
<i>Citrobacter amalonaticus</i>	4.61	0.08			
364473	Low discrimination				364473
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	84.52	0.39	H2S 1	99	
<i>Citrobacter braakii</i>	11.20	0.28		1	
<i>Citrobacter youngae</i>	2.51	0.14		1	
364573	Good identification				364573
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	96.77	0.49	H2S 1	99	
<i>Citrobacter koseri</i>	3.23	0.17		1	
365001	Very good identification				365001
<i>Proteus mirabilis</i>	100.0	0.59	ONP 1		
365021	Good identification				365021
<i>Proteus mirabilis</i>	100.0	0.43	ONP 1		
365043	Identification to the genus				365043
<i>Citrobacter braakii</i>	84.22	0.45	PHE 1		
<i>Citrobacter youngae</i>	13.28	0.28			
<i>Citrobacter werkmanii</i>	2.50	-.04			
365053	Identification to the genus				365053
<i>Citrobacter braakii</i>	89.61	0.51	PHE 1		
<i>Citrobacter youngae</i>	5.69	0.26			
<i>Citrobacter amalonaticus</i>	4.70	0.08			
366043	Identification to the genus				366043
<i>Citrobacter braakii</i>	53.71	0.45	ESL 1		
<i>Citrobacter youngae</i>	44.13	0.43			
<i>Citrobacter werkmanii</i>	1.59	-.04			
366053	Identification to the genus				366053
<i>Citrobacter braakii</i>	53.38	0.51	ESL 1		
<i>Citrobacter amalonaticus</i>	27.42	0.28			
<i>Citrobacter youngae</i>	17.67	0.41			
366073	Low discrimination				366073
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	76.93	0.42	H2S 1	99	
<i>Citrobacter youngae</i>	9.27	0.29		1	
<i>Citrobacter braakii</i>	7.93	0.28		1	
366173	Good identification				366173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	99.51	0.51	H2S 1	99	
<i>Citrobacter sedlakii</i>	0.28	-.11		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	0.21	0.03		1	
366373	Good identification				366373
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.36	H2S 1		
366573	Good identification				366573
<i>Enterobacter cloacae subsp. cloacae</i>	100.0	0.42	H2S 1		
370000	Good identification				370000
<i>Morganella morganii subsp. morganii</i>	100.0	0.42	ONP 10		
370013	Low discrimination				370013
<i>Citrobacter braakii</i>	58.19	0.35	SOR 99		
<i>Escherichia hermannii</i>	27.20	0.18			
<i>Yersinia kristensenii</i>	11.67	0.10			
370043	Good identification				370043
<i>Citrobacter braakii</i>	92.97	0.70			
<i>Citrobacter youngae</i>	5.54	0.44			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.67	0.23			
370051	Low discrimination				370051
<i>Citrobacter braakii</i>	79.93	0.35	MAN 99		
<i>Yersinia kristensenii</i>	16.02	0.10			
<i>Citrobacter amalonaticus</i>	4.04	-.09			
370052	Low discrimination				370052
<i>Citrobacter braakii</i>	79.93	0.35	TRE 99		
<i>Yersinia kristensenii</i>	16.02	0.10			
<i>Citrobacter amalonaticus</i>	4.04	-.09			
370053	Low discrimination				370053
<i>Citrobacter braakii</i>	77.24	0.76			
<i>Yersinia kristensenii</i>	15.48	0.51			
<i>Citrobacter amalonaticus</i>	3.91	0.33			
370063	Low discrimination				370063
<i>Yersinia enterocolitica ssp. enterocolitica</i>	51.71	0.49	H2S 1		
<i>Citrobacter braakii</i>	28.37	0.47			
<i>Citrobacter freundii</i>	8.65	0.38			
370073	Low discrimination				370073
<i>Citrobacter farmeri</i>	66.61	0.56	H2S 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	22.68	0.59			
<i>Citrobacter braakii</i>	8.42	0.53			
370153	Acceptable identification				370153
<i>Citrobacter sedlakii</i>	92.78	0.45	H2S 1		
<i>Citrobacter braakii</i>	5.15	0.35			
<i>Yersinia kristensenii</i>	1.03	0.10			
370253	Low discrimination				370253

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yersinia kristensenii</i>	68.26	0.36	H2S 1		
<i>Citrobacter braakii</i>	19.49	0.35			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.82	0.25			
370263	Good identification				370263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.36	0.42	H2S 1		
<i>Citrobacter youngae</i>	1.38	0.06			
<i>Citrobacter braakii</i>	1.26	0.06			
370273	Acceptable identification				370273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	92.09	0.51	H2S 1		
<i>Citrobacter farmeri</i>	6.38	0.15			
<i>Citrobacter braakii</i>	0.81	0.12			
370453	Low discrimination				370453
<i>Citrobacter braakii</i>	78.37	0.35	ADO 1		
<i>Yersinia kristensenii</i>	15.71	0.10			
<i>Citrobacter amalonaticus</i>	3.96	-0.09			
371000	Very good identification				371000
<i>Morganella morganii</i> subsp. <i>morganii</i>	100.0	0.68	ONP 10		
371053	Low discrimination				371053
<i>Citrobacter braakii</i>	79.93	0.35	PHE 1		
<i>Yersinia kristensenii</i>	16.02	0.10			
<i>Citrobacter amalonaticus</i>	4.04	-0.09			
372053	Low discrimination				372053
<i>Citrobacter braakii</i>	45.25	0.35	ESL 1		
<i>Citrobacter amalonaticus</i>	22.40	0.12			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	15.93	0.23			
372063	Good identification				372063
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.63	0.39	H2S 1		
<i>Citrobacter youngae</i>	1.76	0.06			
<i>Citrobacter braakii</i>	1.61	0.06			
372073	Acceptable identification				372073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	90.09	0.49	H2S 1		
<i>Citrobacter farmeri</i>	8.02	0.15			
<i>Citrobacter braakii</i>	1.01	0.12			
372273	Good identification				372273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	100.0	0.42	H2S 1		
374003	Acceptable identification				374003
<i>Citrobacter braakii</i>	91.68	0.39	SOR 99		
<i>Citrobacter youngae</i>	5.18	0.12			
<i>Citrobacter amalonaticus</i>	3.14	-0.09			
374041	Acceptable identification				374041
<i>Citrobacter braakii</i>	91.68	0.39	MAN 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	5.18	0.12			
<i>Citrobacter amalonaticus</i>	3.14	-.09			
374042	Acceptable identification				374042
<i>Citrobacter braakii</i>	91.68	0.39	TRE 99		
<i>Citrobacter youngae</i>	5.18	0.12			
<i>Citrobacter amalonaticus</i>	3.14	-.09			
374043	Good identification				374043
<i>Citrobacter braakii</i>	91.32	0.80			
<i>Citrobacter youngae</i>	5.16	0.53			
<i>Citrobacter amalonaticus</i>	3.13	0.33			
374053	Identification to the genus				374053
<i>Citrobacter amalonaticus</i>	61.86	0.74	H2S 5		
<i>Citrobacter braakii</i>	37.07	0.86			
<i>Citrobacter youngae</i>	0.84	0.52			
374063	Identification to the genus				374063
<i>Citrobacter braakii</i>	60.72	0.57	SUC 7		
<i>Citrobacter freundii</i>	24.67	0.50			
<i>Citrobacter youngae</i>	12.11	0.42			
374073	Low discrimination				374073
<i>Citrobacter amalonaticus</i>	47.72	0.49	H2S 5		
<i>Citrobacter braakii</i>	33.72	0.63	SUC 6		
<i>Citrobacter farmeri</i>	9.88	0.37			
374143	Low discrimination				374143
<i>Citrobacter braakii</i>	35.99	0.39	MAL 1		
<i>Citrobacter werkmanii</i>	24.90	0.18			
<i>Citrobacter sedlakii</i>	21.64	0.18			
374153	Identification to the genus				374153
<i>Citrobacter sedlakii</i>	89.00	0.59	H2S 1		
<i>Citrobacter amalonaticus</i>	5.07	0.33			
<i>Citrobacter braakii</i>	3.04	0.45			
374243	Identification to the genus				374243
<i>Citrobacter braakii</i>	75.27	0.39	INO 1		
<i>Citrobacter youngae</i>	22.16	0.27			
<i>Citrobacter amalonaticus</i>	2.58	-.09			
374443	Identification to the genus				374443
<i>Citrobacter braakii</i>	83.51	0.39	ADO 1		
<i>Citrobacter koseri</i>	8.91	0.10			
<i>Citrobacter youngae</i>	4.72	0.12			
374553	Very good identification				374553
<i>Citrobacter koseri</i>	97.56	0.59	H2S 1		
<i>Citrobacter sedlakii</i>	2.24	0.18			
<i>Citrobacter amalonaticus</i>	0.13	-.09			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
374573	Very good identification				374573
				VPT	
<i>Citrobacter koseri</i>	99.70	0.58	H2S 1	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.30	0.08		99	
375043	Acceptable identification				375043
<i>Citrobacter braakii</i>	91.68	0.39	PHE 1		
<i>Citrobacter youngae</i>	5.18	0.12			
<i>Citrobacter amalonaticus</i>	3.14	-.09			
376043	Identification to the genus				376043
<i>Citrobacter braakii</i>	61.37	0.39	ESL 1		
<i>Citrobacter amalonaticus</i>	20.56	0.12			
<i>Citrobacter youngae</i>	18.07	0.27			
376053	Good identification				376053
<i>Citrobacter amalonaticus</i>	93.27	0.53	H2S 5		
<i>Citrobacter braakii</i>	5.71	0.45	ESL 9		
<i>Citrobacter youngae</i>	0.68	0.25			
376153	Good identification				376153
<i>Citrobacter sedlakii</i>	97.04	0.45	H2S 1		
<i>Citrobacter amalonaticus</i>	2.67	0.12			
<i>Citrobacter braakii</i>	0.16	0.04			
400000	Identification to the genus				400000
<i>Shigella dysenteriae</i> (group A)	76.40	0.39	LYS 1		
<i>Shigella flexneri</i> (group B)	16.61	0.26	TRE 90		
<i>Shigella boydii</i> (group C)	4.96	0.12			
400001	Identification to the genus				400001
<i>Shigella dysenteriae</i> (group A)	87.38	0.59	LYS 1		
<i>Shigella flexneri</i> (group B)	4.28	0.33			
<i>Shigella boydii</i> (group C)	3.57	0.28			
400002	Low discrimination				400002
<i>Shigella flexneri</i> (group B)	53.83	0.53	LYS 1		
<i>Shigella boydii</i> (group C)	27.35	0.43			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	17.06	0.39			
400003	Low discrimination				400003
<i>Shigella boydii</i> (group C)	44.43	0.59	LYS 1		
<i>Shigella flexneri</i> (group B)	31.33	0.59			
<i>Hafnia alvei</i>	13.53	0.65			
400013	Low discrimination				400013
<i>Escherichia vulneris</i>	77.27	0.43	ONP 99		
<i>Hafnia alvei</i>	14.18	0.50			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.89	0.33			
400023	Low discrimination				400023
<i>Escherichia coli</i>	59.03	0.46	IND 92		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	24.31	0.46	SOR 88		
<i>Shigella boydii</i> (group C)	7.26	0.18			
400041	Low discrimination				400041
<i>Shigella dysenteriae</i> (group A)	64.67	0.51	LYS 1		
<i>Salmonella</i> serovar typhi	17.93	0.28			
<i>Escherichia coli</i>	9.48	0.41			
400042	Low discrimination				400042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	70.54	0.59	ORN 99		
<i>Shigella flexneri</i> (group B)	10.10	0.45			
<i>Shigella boydii</i> (group C)	9.48	0.41			
400043	Low discrimination				400043
<i>Salmonella</i> serovar typhi	80.82	0.69	H2S 97		
<i>Escherichia coli</i>	8.20	0.68			
<i>Shigella boydii</i> (group C)	6.85	0.56			
400061	Low discrimination				400061
<i>Escherichia coli</i>	77.43	0.38	IND 92		
<i>Yersinia rohdei</i>	12.34	0.18	MAN 95		
<i>Shigella dysenteriae</i> (group A)	8.00	0.10			
400062	Low discrimination				400062
<i>Escherichia coli</i>	62.84	0.38	IND 92		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	19.83	0.18	TRE 95		
<i>Yersinia rohdei</i>	10.02	0.18			
400063	Low discrimination				400063
<i>Escherichia coli</i>	49.75	0.64	IND 92		
<i>Yersinia rohdei</i>	41.33	0.59			
<i>Salmonella</i> serovar typhi	7.43	0.28			
400073	Low discrimination				400073
<i>Yersinia rohdei</i>	87.77	0.49	LYS 1		
<i>Escherichia coli</i>	6.47	0.29			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.67	0.26			
400103	Low discrimination				400103
<i>Hafnia alvei</i>	89.39	0.65	ORN 98		
<i>Escherichia vulneris</i>	4.92	0.18			
<i>Shigella boydii</i> (group C)	2.97	0.18			
400113	Very good identification				400113
<i>Escherichia vulneris</i>	96.86	0.59	ONP 99		
<i>Hafnia alvei</i>	3.14	0.50			
400123	Acceptable identification				400123
<i>Hafnia alvei</i>	93.67	0.46	ORN 98		
<i>Escherichia vulneris</i>	4.04	-.04	SUC 10		
<i>Escherichia coli</i>	2.30	0.05			
400133	Good identification				400133

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia vulneris</i>	96.03	0.37	ONP 99		
<i>Hafnia alvei</i>	3.97	0.30	SUC 8		
400213	Low discrimination				400213
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.24	0.35	ADO 97		
<i>Escherichia vulneris</i>	17.54	0.02			
<i>Hafnia alvei</i>	3.22	0.09			
400253	Low discrimination				400253
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	63.13	0.41	ADO 97	1	
<i>Serratia odorifera biovar 2</i>	29.91	0.26		99	
<i>Yersinia kristensenii</i>	4.65	0.03		1	
400403	Low discrimination				400403
<i>Klebsiella pneumoniae subsp. ozaenae</i>	52.61	0.42	CEL 92		
<i>Shigella boydii (group C)</i>	17.29	0.18			
<i>Shigella flexneri (group B)</i>	12.19	0.18			
400413	Very good identification				400413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.28	0.64			
<i>Escherichia vulneris</i>	0.82	0.02			
<i>Escherichia fergusonii</i>	0.74	0.10			
400433	Good identification				400433
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.52			
400452	Good identification				400452
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.35	TRE 98		
400453	Very good identification				400453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.51	0.70			
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	0.21	-.04			
<i>Escherichia coli</i>	0.15	0.07			
400463	Low discrimination				400463
<i>Escherichia coli</i>	61.04	0.38	IND 92		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	27.48	0.36	ADO 5		
<i>Yersinia rohdei</i>	9.73	0.18			
400473	Very good identification				400473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.23	0.57			
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	2.40	0.06			
<i>Yersinia rohdei</i>	0.99	0.08			
400603	Good identification				400603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.44	CEL 92		
400613	Very good identification				400613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.66			
400633	Very good identification				400633

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.28	0.54			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.72	-.09			
400643	Good identification				400643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.72	0.50	CEL 92		
<i>Salmonella</i> serovar <i>typhi</i>	1.29	-.13			
400652	Good identification				400652
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	TRE 98		
400653	Very good identification				400653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.22	0.72		1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.08	0.23		1	
<i>Serratia odorifera</i> biovar 2	1.71	0.28		99	
400663	Good identification				400663
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.69	0.37	CEL 92		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	4.31	-.09			
400673	Identification to the genus				400673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	72.05	0.59			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	27.95	0.33			
400713	Identification to the genus				400713
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	72.85	0.35	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	27.15	0.08			
400753	Good identification				400753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	95.21	0.49	LYS 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.79	0.41			
400773	Very good identification				400773
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	99.58	0.59	LYS 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.42	0.28			
401001	Very good identification				401001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	98.17	0.56	URE 97		
<i>Shigella dysenteriae</i> (group A)	1.83	0.18			
402043	Low discrimination				402043
<i>Escherichia coli</i>	67.35	0.55	IND 92		
<i>Salmonella</i> serovar <i>typhi</i>	26.81	0.28			
<i>Shigella boydii</i> (group C)	2.27	0.15			
402053	Acceptable identification				402053
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.85	0.51	ADO 97		
<i>Escherichia coli</i>	5.27	0.20			
<i>Salmonella</i> serovar <i>typhi</i>	1.04	-.13			
402063	Good identification				402063
<i>Escherichia coli</i>	95.12	0.52	IND 92		
<i>Yersinia rohdei</i>	3.19	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.12	0.17			
402073	Low discrimination				402073
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.02	0.39	ADO 97		
<i>Escherichia coli</i>	12.26	0.17			
<i>Yersinia rohdei</i>	6.72	0.08			
402103	Low discrimination				402103
<i>Hafnia alvei</i>	88.98	0.46	ORN 98		
<i>Escherichia vulneris</i>	11.02	0.05	ESL 10		
402113	Good identification				402113
<i>Escherichia vulneris</i>	98.27	0.47	ONP 99		
<i>Hafnia alvei</i>	1.41	0.30			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.32	0.15			
402213	Good identification				402213
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.64	0.47	ADO 97		
<i>Escherichia vulneris</i>	1.37	-.10			
402233	Good identification				402233
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.35	ADO 97		
402253	Good identification				402253
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.68	0.53	ADO 97	1	
<i>Serratia odorifera</i> biovar 2	7.32	0.22		99	
402273	Good identification				402273
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	ADO 97		
402403	Very good identification				402403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.70	0.55	CEL 92		
<i>Escherichia coli</i>	1.30	0.11			
402411	Good identification				402411
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.36	MAN 99		
402412	Good identification				402412
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.42	TRE 98		
402413	Very good identification				402413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.79	0.77			
<i>Escherichia fergusonii</i>	0.16	0.09			
<i>Escherichia vulneris</i>	0.05	-.10			
402423	Good identification				402423
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.60	0.42	CEL 92		
<i>Escherichia coli</i>	3.40	0.08			
402433	Very good identification				402433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.97	0.64		1	
<i>Serratia rubidaea</i>	1.03	0.08		99	

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
402443	Good identification					402443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		94.69	0.60	CEL 92		
<i>Escherichia coli</i>		4.93	0.29			
<i>Salmonella</i> serovar <i>typhi</i>		0.38	-.13			
402451	Good identification					402451
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.41	MAN 99		
402452	Good identification					402452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.47	TRE 98		
402453	Very good identification					402453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		99.98	0.82			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>		0.02	-.11			
402463	Low discrimination					402463
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		87.81	0.48	CEL 92		
<i>Escherichia coli</i>		12.19	0.25			
402472	Good identification					402472
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.35	TRE 98		
402473	Very good identification					402473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		99.73	0.70			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>		0.27	-.01			
402513	Low discrimination					402513
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		87.94	0.46	MAL 3		
<i>Escherichia vulneris</i>		8.43	0.05			
<i>Escherichia fergusonii</i>		2.47	0.03			
402553	Identification to the genus					402553
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		87.96	0.51	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>		12.04	0.15			
402603	Very good identification					402603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.57	CEL 92		
402611	Good identification					402611
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.37	MAN 99		
402612	Good identification					402612
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.44	TRE 98		
402613	Very good identification					402613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.78			
402623	Good identification					402623
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.44	CEL 92		
402633	Very good identification					402633

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.79	0.66		1	
<i>Serratia rubidaea</i>	0.21	-.04		99	
402643	Very good identification				402643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.62	CEL 92		
402651	Good identification				402651
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	MAN 99		
402652	Good identification				402652
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.49	TRE 98		
402653	Very good identification				402653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.36	0.84		1	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	0.34	0.15		1	
<i>Serratia odorifera</i> biovar 2	0.30	0.24		99	
402663	Good identification				402663
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.97	0.50	CEL 92	1	
<i>Serratia marcescens</i>	1.03	-.06		98	
402672	Good identification				402672
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	TRE 98		
402673	Very good identification				402673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.01	0.72			
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.99	0.25			
402713	Good identification				402713
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.16	0.47	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	3.84	0.00			
402753	Identification to the genus				402753
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	68.03	0.42	LYS 1		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	31.97	0.53			
402773	Good identification				402773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	95.48	0.51	LYS 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.74	0.41		1	
<i>Enterobacter aerogenes</i>	0.41	-.02		98	
403413	Good identification				403413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.36	PHE 1		
403453	Good identification				403453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	PHE 1		
403613	Good identification				403613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.37	PHE 1		
403653	Good identification				403653

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	PHE 1		
404003	Good identification				404003
<i>Hafnia alvei</i>	90.38	0.65	ORN 98		
<i>Salmonella</i> serovar <i>enteritidis</i>	3.87	0.16			
<i>Shigella boydii</i> (group C)	3.00	0.18			
404013	Low discrimination				404013
<i>Hafnia alvei</i>	75.21	0.50	ORN 98		
<i>Yokenella regensburgei</i>	13.13	0.12			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.56	0.26			
404023	Good identification				404023
<i>Hafnia alvei</i>	97.61	0.46	ORN 98		
<i>Escherichia coli</i>	2.39	0.05	SUC 10		
404042	Good identification				404042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	98.16	0.49	ORN 99		
<i>Salmonella</i> serovar <i>enteritidis</i>	0.74	0.02			
<i>Shigella flexneri</i> (group B)	0.43	0.04			
404043	Low discrimination				404043
<i>Salmonella</i> serovar <i>enteritidis</i>	62.57	0.43	H2S 95		
<i>Salmonella</i> serovar <i>typhi</i>	22.71	0.28	ORN 97		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	3.60	0.18			
404063	Low discrimination				404063
<i>Citrobacter freundii</i>	55.44	0.38	ONP 88		
<i>Escherichia coli</i>	15.33	0.23	LYS 1		
<i>Yersinia rohdei</i>	12.74	0.18			
404073	Low discrimination				404073
<i>Citrobacter freundii</i>	75.35	0.36	ONP 88		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	9.48	0.19	LYS 1		
<i>Citrobacter youngae</i>	7.83	0.13			
404103	Very good identification				404103
<i>Hafnia alvei</i>	100.0	0.65	ORN 98		
404113	Low discrimination				404113
<i>Hafnia alvei</i>	76.22	0.50	ORN 98		
<i>Escherichia vulneris</i>	23.78	0.18			
404123	Good identification				404123
<i>Hafnia alvei</i>	100.0	0.46	ORN 98		
404243	Good identification				404243
				VPT	
<i>Salmonella</i> serovar <i>enteritidis</i>	95.92	0.37	H2S 95	1	
<i>Serratia odorifera</i> biovar 2	2.76	0.16	ORN 97	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.67	0.11		1	
404253	Very good identification				404253
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 2	95.56	0.57	ONP 99	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	2.67	0.33		1	
<i>Salmonella</i> serovar enteritidis	1.77	0.11		1	
404413	Very good identification				404413
<i>Klebsiella pneumoniae</i> subsp. ozaenae	99.29	0.57			
<i>Escherichia fergusonii</i>	0.36	-.04			
<i>Hafnia alvei</i>	0.36	0.09			
404433	Low discrimination				404433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	89.47	0.44		1	
<i>Serratia rubidaea</i>	10.53	0.10		99	
404443	Low discrimination				404443
<i>Klebsiella pneumoniae</i> subsp. ozaenae	85.47	0.40	CEL 92		
<i>Salmonella</i> serovar enteritidis	8.74	0.02			
<i>Salmonella</i> serovar typhi	3.17	-.13			
404453	Very good identification				404453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	98.10	0.62		1	
<i>Serratia odorifera</i> biovar 2	1.64	0.18		99	
<i>Salmonella enterica</i> subsp. houtenae	0.26	-.09		1	
404473	Good identification				404473
<i>Klebsiella pneumoniae</i> subsp. ozaenae	100.0	0.50			
404603	Good identification				404603
<i>Klebsiella pneumoniae</i> subsp. ozaenae	100.0	0.37	CEL 92		
404613	Very good identification				404613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	97.53	0.59		1	
<i>Serratia odorifera</i> biovar 2	2.47	0.18		99	
404633	Good identification				404633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	97.65	0.46		1	
<i>Serratia rubidaea</i>	2.35	-.03		99	
404643	Low discrimination				404643
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	83.19	0.42	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	13.06	0.18		99	
<i>Salmonella</i> serovar enteritidis	3.75	-.04		1	
404653	Low discrimination				404653
				VPT	
<i>Serratia odorifera</i> biovar 2	57.47	0.59	ONP 99	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	42.53	0.64		1	
404673	Acceptable identification				404673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	94.01	0.52		1	
<i>Serratia odorifera</i> biovar 2	5.13	0.18		99	
<i>Klebsiella pneumoniae</i> subsp. rhinoscleromatis	0.86	-.09		1	
406003	Acceptable identification				406003

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	93.59	0.46	ORN 98		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.51	0.16	ESL 10		
<i>Salmonella</i> serovar <i>enteritidis</i>	1.90	-.10			
406053	Acceptable identification				406053
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	91.47	0.44	ADO 97	1	
<i>Serratia odorifera</i> biovar 2	6.73	0.12		99	
<i>Salmonella</i> serovar <i>enteritidis</i>	1.80	-.10		1	
406103	Good identification				406103
<i>Hafnia alvei</i>	100.0	0.46	ORN 98		
406213	Low discrimination				406213
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	89.95	0.40	ADO 97	1	
<i>Serratia odorifera</i> biovar 2	10.05	0.12		99	
406253	Low discrimination				406253
				VPT	
<i>Serratia odorifera</i> biovar 2	85.63	0.54	ONP 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	14.37	0.45		1	
406403	Good identification				406403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.47	CEL 92		
406413	Very good identification				406413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.88	0.69		1	
<i>Serratia rubidaea</i>	0.12	-.07		99	
406433	Low discrimination				406433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	68.44	0.57		1	
<i>Serratia rubidaea</i>	31.56	0.34		99	
406443	Good identification				406443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.53	CEL 92		
406452	Good identification				406452
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.40	TRE 98		
406453	Very good identification				406453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.72	0.75		1	
<i>Serratia odorifera</i> biovar 2	0.28	0.14		99	
406463	Low discrimination				406463
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	67.38	0.40	CEL 92	1	
<i>Serratia marcescens</i>	32.63	0.19		98	
406473	Very good identification				406473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.53	0.62		1	
<i>Serratia rubidaea</i>	0.25	-.07		99	
<i>Serratia marcescens</i>	0.22	-.07		98	
406513	Low discrimination				406513
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	62.90	0.38	MAL 3	1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia rubidaea</i>	37.10	0.18		99	
406533	Very good identification				406533
				VPT	
<i>Serratia rubidaea</i>	99.57	0.59	ONP 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.43	0.26		1	
406553	Good identification				406553
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.44	MAL 3		
406603	Good identification				406603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.49	CEL 92		
406612	Good identification				406612
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.36	TRE 98		
406613	Very good identification				406613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.58	0.71		1	
<i>Serratia odorifera biovar 2</i>	0.42	0.14		99	
406623	Acceptable identification				406623
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.53	0.37	CEL 92	1	
<i>Serratia rubidaea</i>	6.48	-.03		99	
406633	Good identification				406633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	91.38	0.59		1	
<i>Serratia rubidaea</i>	8.62	0.22		99	
406643	Very good identification				406643
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.45	0.55	CEL 92	1	
<i>Serratia odorifera biovar 2</i>	2.55	0.14		99	
406651	Low discrimination				406651
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	59.18	0.35	MAN 99	1	
<i>Serratia odorifera biovar 2</i>	40.82	0.24		99	
406652	Low discrimination				406652
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	89.97	0.42	TRE 98	1	
<i>Serratia odorifera biovar 2</i>	10.03	0.14		99	
406653	Low discrimination				406653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	81.62	0.76		1	
<i>Serratia odorifera biovar 2</i>	18.38	0.55		99	
406673	Good identification				406673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.87	0.64		1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	2.47	0.10		98	
<i>Serratia odorifera biovar 1</i>	1.55	0.14		50	
406713	Low discrimination				406713
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	89.23	0.40	MAL 3	1	
<i>Serratia rubidaea</i>	10.77	0.05		99	
406733	Good identification				406733

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Serratia rubidaea</i>	97.35	0.47	ONP 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.04	0.27		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.43	-0.9		98	
406753	Low discrimination				406753
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	85.87	0.45	MAL 3	1	
<i>Serratia odorifera</i> biovar 2	6.32	0.14		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	4.31	0.00		1	
407653	Low discrimination				407653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.62	0.35	PHE 1	1	
<i>Serratia odorifera</i> biovar 2	18.38	0.14		99	
410000	Low discrimination				410000
<i>Shigella dysenteriae</i> (group A)	55.89	0.38	LYS 1		
<i>Edwardsiella tarda</i>	24.60	0.18	TRE 90		
<i>Shigella flexneri</i> (group B)	14.85	0.26			
410001	Low discrimination				410001
<i>Shigella dysenteriae</i> (group A)	80.21	0.57	LYS 1		
<i>Escherichia coli</i>	9.66	0.45			
<i>Shigella flexneri</i> (group B)	4.81	0.33			
410002	Low discrimination				410002
<i>Shigella flexneri</i> (group B)	71.98	0.53	LYS 1		
<i>Escherichia coli</i>	15.46	0.45			
<i>Shigella boydii</i> (group C)	12.19	0.34			
410003	Low discrimination				410003
<i>Escherichia coli</i>	57.45	0.72	SOR 88		
<i>Shigella flexneri</i> (group B)	28.59	0.59			
<i>Shigella boydii</i> (group C)	13.52	0.49			
410013	Low discrimination				410013
<i>Escherichia coli</i>	53.57	0.37	CEL 2		
<i>Escherichia fergusonii</i>	18.27	0.22	SOR 88		
<i>Shigella flexneri</i> (group B)	13.20	0.18			
410021	Low discrimination				410021
<i>Escherichia coli</i>	85.81	0.42	SOR 88		
<i>Shigella dysenteriae</i> (group A)	10.80	0.16	MAN 95		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	3.40	0.08			
410022	Acceptable identification				410022
<i>Escherichia coli</i>	92.38	0.42	SOR 88		
<i>Shigella flexneri</i> (group B)	6.52	0.12	TRE 95		
<i>Shigella boydii</i> (group C)	1.10	-0.8			
410023	Very good identification				410023
<i>Escherichia coli</i>	98.90	0.68	SOR 88		
<i>Shigella flexneri</i> (group B)	0.75	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella boydii</i> (group C)	0.35	0.08			
410041	Low discrimination				410041
<i>Escherichia coli</i>	65.40	0.63	MAN 95		
<i>Shigella dysenteriae</i> (group A)	31.74	0.50			
<i>Shigella flexneri</i> (group B)	1.81	0.25			
410042	Low discrimination				410042
<i>Escherichia coli</i>	73.50	0.63	TRE 95		
<i>Shigella flexneri</i> (group B)	19.07	0.45			
<i>Shigella boydii</i> (group C)	5.96	0.31			
410043	Good identification				410043
<i>Escherichia coli</i>	94.25	0.90			
<i>Shigella flexneri</i> (group B)	2.61	0.51			
<i>Shigella boydii</i> (group C)	2.28	0.47			
410053	Good identification				410053
<i>Escherichia coli</i>	94.85	0.55	CEL 2		
<i>Yersinia kristensenii</i>	1.99	0.11			
<i>Shigella flexneri</i> (group B)	1.30	0.10			
410061	Very good identification				410061
<i>Escherichia coli</i>	99.27	0.60	MAN 95		
<i>Shigella dysenteriae</i> (group A)	0.73	0.09			
410062	Very good identification				410062
<i>Escherichia coli</i>	99.61	0.60	TRE 95		
<i>Shigella flexneri</i> (group B)	0.39	0.04			
410063	Very good identification				410063
<i>Escherichia coli</i>	99.80	0.86			
<i>Yersinia rohdei</i>	0.07	0.18			
<i>Citrobacter freundii</i>	0.04	0.19			
410073	Good identification				410073
<i>Escherichia coli</i>	97.37	0.51	CEL 2		
<i>Citrobacter freundii</i>	1.47	0.17			
<i>Yersinia rohdei</i>	1.16	0.08			
410143	Acceptable identification				410143
<i>Escherichia coli</i>	94.29	0.48	MAL 1		
<i>Shigella flexneri</i> (group B)	2.61	0.10			
<i>Shigella boydii</i> (group C)	2.28	0.06			
410163	Good identification				410163
<i>Escherichia coli</i>	100.0	0.45	MAL 1		
410243	Acceptable identification				410243
<i>Escherichia coli</i>	94.29	0.48	INO 1		
<i>Shigella flexneri</i> (group B)	2.61	0.10			
<i>Shigella boydii</i> (group C)	2.28	0.06			

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
410263	Good identification					410263
<i>Escherichia coli</i>		100.0	0.45	INO 1		
410403	Low discrimination					410403
<i>Escherichia coli</i>		81.09	0.45	ADO 5		
<i>Shigella flexneri</i> (group B)		7.75	0.18	SOR 88		
<i>Escherichia fergusonii</i>		7.50	0.18			
410413	Good identification					410413
<i>Escherichia fergusonii</i>		96.26	0.45	ORN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		2.62	0.23			
<i>Escherichia coli</i>		1.12	0.11			
410423	Good identification					410423
<i>Escherichia coli</i>		100.0	0.42	ADO 5		
410441	Acceptable identification					410441
<i>Escherichia coli</i>		91.48	0.37	ADO 5		
<i>Shigella dysenteriae</i> (group A)		8.52	0.09	MAN 95		
410442	Good identification					410442
<i>Escherichia coli</i>		95.26	0.37	ADO 5		
<i>Shigella flexneri</i> (group B)		4.74	0.04	TRE 95		
410443	Very good identification					410443
<i>Escherichia coli</i>		98.75	0.63	ADO 5		
<i>Shigella flexneri</i> (group B)		0.53	0.10			
<i>Shigella boydii</i> (group C)		0.46	0.06			
410463	Very good identification					410463
<i>Escherichia coli</i>		100.0	0.60	ADO 5		
410513	Good identification					410513
<i>Escherichia fergusonii</i>		100.0	0.39	ORN 99		
411001	Very good identification					411001
<i>Morganella morganii</i> subsp. <i>sibonii</i>		97.68	0.56	URE 97		
<i>Shigella dysenteriae</i> (group A)		1.49	0.16			
<i>Providencia stuartii</i>		0.65	0.10			
411043	Acceptable identification					411043
<i>Escherichia coli</i>		94.29	0.48	PHE 1		
<i>Shigella flexneri</i> (group B)		2.61	0.10			
<i>Shigella boydii</i> (group C)		2.28	0.06			
411063	Good identification					411063
<i>Escherichia coli</i>		100.0	0.45	PHE 1		
411201	Acceptable identification					411201
<i>Providencia stuartii</i>		92.62	0.36	LYS 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>		7.38	0.15	SCI 93		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
411221	Good identification					411221
<i>Providencia stuartii</i>		100.0	0.36	LYS 1		
412003	Very good identification					412003
<i>Escherichia coli</i>		97.12	0.59	SOR 88		
<i>Shigella flexneri</i> (group B)		1.95	0.18			
<i>Shigella boydii</i> (group C)		0.92	0.08			
412023	Very good identification					412023
<i>Escherichia coli</i>		100.0	0.56	SOR 88		
412041	Good identification					412041
<i>Escherichia coli</i>		98.08	0.51	MAN 95		
<i>Shigella dysenteriae</i> (group A)		1.92	0.09			
412042	Good identification					412042
<i>Escherichia coli</i>		98.96	0.51	TRE 95		
<i>Shigella flexneri</i> (group B)		1.04	0.04			
412043	Very good identification					412043
<i>Escherichia coli</i>		99.76	0.77			
<i>Shigella flexneri</i> (group B)		0.11	0.10			
<i>Shigella boydii</i> (group C)		0.10	0.06			
412053	Good identification					412053
<i>Escherichia coli</i>		98.48	0.42	CEL 2		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		1.52	0.10			
412061	Good identification					412061
<i>Escherichia coli</i>		100.0	0.47	MAN 95		
412062	Good identification					412062
<i>Escherichia coli</i>		100.0	0.47	TRE 95		
412063	Very good identification					412063
<i>Escherichia coli</i>		100.0	0.73			
412073	Good identification					412073
<i>Escherichia coli</i>		100.0	0.39	CEL 2		
412143	Good identification					412143
<i>Escherichia coli</i>		100.0	0.36	MAL 1		
412243	Good identification					412243
<i>Escherichia coli</i>		100.0	0.36	INO 1		
412413	Low discrimination					412413
<i>Escherichia fergusonii</i>		88.66	0.43	ORN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		11.35	0.36			
412443	Good identification					412443

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	98.34	0.51	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.66	0.19			
412453	Low discrimination				412453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	87.13	0.41	IND 1		
<i>Escherichia coli</i>	9.17	0.16			
<i>Escherichia fergusonii</i>	3.70	0.02			
412463	Good identification				412463
<i>Escherichia coli</i>	99.37	0.47	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.63	0.07			
412513	Acceptable identification				412513
<i>Escherichia fergusonii</i>	92.84	0.38	ORN 99		
<i>Leclercia adecarboxylata</i>	7.16	0.12			
412613	Acceptable identification				412613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.93	0.37	IND 1		
<i>Escherichia fergusonii</i>	6.07	0.02			
412653	Low discrimination				412653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	77.19	0.43	IND 1	1	
<i>Serratia odorifera biovar 2</i>	22.81	0.24		99	
413043	Good identification				413043
<i>Escherichia coli</i>	100.0	0.36	PHE 1		
414043	Low discrimination				414043
<i>Escherichia coli</i>	89.18	0.48	SCI 1		
<i>Shigella flexneri (group B)</i>	2.47	0.10			
<i>Shigella boydii (group C)</i>	2.16	0.06			
414063	Low discrimination				414063
<i>Escherichia coli</i>	86.59	0.45	SCI 1		
<i>Citrobacter freundii</i>	13.41	0.32			
414253	Very good identification				414253
<i>Serratia odorifera biovar 2</i>	100.0	0.57	ONP 99		
414653	Very good identification				414653
				VPT	
<i>Serratia odorifera biovar 2</i>	99.26	0.59	ONP 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.74	0.23		1	
415201	Very good identification				415201
<i>Providencia stuartii</i>	100.0	0.59	LYS 1		
415203	Good identification				415203
<i>Providencia stuartii</i>	100.0	0.39	LYS 1		
415221	Very good identification				415221
<i>Providencia stuartii</i>	100.0	0.59	LYS 1		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
415223	Good identification					415223
<i>Providencia stuartii</i>		100.0	0.39	LYS 1		
415400	Very good identification					415400
<i>Providencia alcalifaciens</i>		100.0	0.59	LYS 1		
415420	Good identification					415420
<i>Providencia alcalifaciens</i>		100.0	0.43	LYS 1		
416043	Good identification					416043
<i>Escherichia coli</i>		100.0	0.36	SCI 1		
416253	Very good identification					416253
<i>Serratia odorifera biovar 2</i>		100.0	0.54	ONP 99		
416653	Very good identification					416653
					VPT	
<i>Serratia odorifera biovar 2</i>		95.71	0.55	ONP 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		4.29	0.35		1	
416773	Good identification					416773
<i>Klebsiella oxytoca</i>		99.39	0.39	ONP 99		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		0.42	-.09	URE 90		
<i>Enterobacter aerogenes</i>		0.18	-.17			
420000	Low discrimination					420000
<i>Salmonella enterica subsp. enterica</i>		87.01	0.46	SOR 90		
<i>Edwardsiella tarda</i>		11.85	0.18	MAN 98		
<i>Hafnia alvei</i>		0.60	0.18			
420001	Low discrimination					420001
<i>Hafnia alvei</i>		66.51	0.59	MAN 99		
<i>Morganella morganii subsp. sibonii</i>		24.20	0.38			
<i>Shigella dysenteriae (group A)</i>		3.37	0.18			
420002	Very good identification					420002
<i>Salmonella enterica subsp. enterica</i>		98.49	0.80	SOR 90		
<i>Hafnia alvei</i>		1.36	0.59			
<i>Escherichia coli</i>		0.06	0.24			
420003	Very good identification					420003
<i>Hafnia alvei</i>		95.53	1.00			
<i>Shigella sonnei</i>		1.82	0.39			
<i>Escherichia coli</i>		0.86	0.51			
420011	Good identification					420011
<i>Hafnia alvei</i>		95.10	0.43	MAN 99		
<i>Yokenella regensburgei</i>		2.92	-.10			
<i>Morganella morganii subsp. sibonii</i>		1.98	-.03			
420012	Low discrimination					420012
<i>Salmonella enterica subsp. enterica</i>		80.06	0.39	CEL 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	19.35	0.43	SOR 90		
<i>Yokenella regensburgei</i>	0.59	-.10			
420013	Very good identification				420013
<i>Hafnia alvei</i>	95.20	0.85			
<i>Yokenella regensburgei</i>	2.92	0.31			
<i>Escherichia fergusonii</i>	0.72	0.28			
420021	Low discrimination				420021
<i>Hafnia alvei</i>	67.17	0.39	SUC 10		
<i>Escherichia coli</i>	18.79	0.21	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	14.04	0.13			
420022	Low discrimination				420022
<i>Salmonella enterica subsp. enterica</i>	83.70	0.39	SUC 1		
<i>Hafnia alvei</i>	12.74	0.39	SOR 90		
<i>Escherichia coli</i>	3.56	0.21			
420023	Good identification				420023
<i>Hafnia alvei</i>	94.53	0.80	SUC 10		
<i>Escherichia coli</i>	5.07	0.47			
<i>Shigella sonnei</i>	0.16	-.02			
420033	Very good identification				420033
<i>Hafnia alvei</i>	98.59	0.65	SUC 10		
<i>Escherichia coli</i>	0.61	0.12			
<i>Escherichia hermannii</i>	0.33	-.02			
420040	Very good identification				420040
<i>Salmonella enterica subsp. enterica</i>	99.87	0.65	MAN 98		
<i>Escherichia coli</i>	0.14	0.16			
420041	Low discrimination				420041
<i>Escherichia coli</i>	48.07	0.42	IND 92		
<i>Salmonella serovar paratyphi</i>	22.70	0.18	MAN 95		
<i>Salmonella enterica subsp. enterica</i>	18.86	0.24			
420042	Excellent identification				420042
<i>Salmonella enterica subsp. enterica</i>	99.91	1.00			
<i>Escherichia coli</i>	0.05	0.42			
<i>Salmonella serovar paratyphi</i>	0.03	0.18			
420043	Low discrimination				420043
<i>Salmonella serovar paratyphi</i>	47.13	0.59	LYS 1		
<i>Salmonella enterica subsp. enterica</i>	19.39	0.59			
<i>Escherichia coli</i>	19.16	0.68			
420052	Very good identification				420052
<i>Salmonella enterica subsp. enterica</i>	99.64	0.59	CEL 1		
<i>Salmonella serovar paratyphi</i>	0.13	-.09			
<i>Yersinia kristensenii</i>	0.12	-.01			
420061	Good identification				420061

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	95.32	0.38	IND 92		
<i>Yersinia rohdei</i>	4.68	0.08	MAN 95		
420062	Very good identification				420062
<i>Salmonella enterica subsp. enterica</i>	96.49	0.59	SUC 1		
<i>Escherichia coli</i>	3.35	0.38			
<i>Yersinia rohdei</i>	0.16	0.08			
420063	Low discrimination				420063
<i>Escherichia coli</i>	74.11	0.65	IND 92		
<i>Yersinia rohdei</i>	18.94	0.49			
<i>Salmonella serovar paratyphi</i>	2.76	0.18			
420073	Low discrimination				420073
<i>Yersinia rohdei</i>	67.06	0.39	LYS 1		
<i>Escherichia coli</i>	16.07	0.30			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	8.53	0.23			
420101	Very good identification				420101
<i>Hafnia alvei</i>	99.63	0.59	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	0.37	-.03			
420102	Low discrimination				420102
<i>Hafnia alvei</i>	57.79	0.59	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	42.21	0.39			
420103	Excellent identification				420103
<i>Hafnia alvei</i>	99.95	1.00			
<i>Shigella sonnei</i>	0.02	-.02			
<i>Escherichia coli</i>	0.01	0.10			
420111	Good identification				420111
<i>Hafnia alvei</i>	100.0	0.43	MAN 99		
420112	Good identification				420112
<i>Hafnia alvei</i>	95.99	0.43	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	4.01	-.02			
420113	Very good identification				420113
<i>Hafnia alvei</i>	98.94	0.85			
<i>Escherichia vulneris</i>	0.63	0.18			
<i>Escherichia fergusonii</i>	0.40	0.22			
420121	Good identification				420121
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
420122	Acceptable identification				420122
<i>Hafnia alvei</i>	93.78	0.39	SUC 10		
<i>Salmonella enterica subsp. enterica</i>	6.23	-.02	TRE 99		
420123	Very good identification				420123

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	99.95	0.80	SUC 10		
<i>Escherichia coli</i>	0.05	0.06			
420133	Very good identification				420133
<i>Hafnia alvei</i>	99.50	0.65	SUC 10		
<i>Escherichia vulneris</i>	0.50	-.04			
420142	Very good identification				420142
<i>Salmonella enterica subsp. enterica</i>	99.79	0.59	MAL 1		
<i>Hafnia alvei</i>	0.15	0.18			
<i>Escherichia coli</i>	0.05	0.01			
420143	Low discrimination				420143
<i>Hafnia alvei</i>	67.01	0.59	SOR 1		
<i>Salmonella serovar paratyphi</i>	10.82	0.18			
<i>Salmonella enterica subsp. salamae</i>	9.05	0.18			
420153	Acceptable identification				420153
<i>Hafnia alvei</i>	91.46	0.43	SOR 1		
<i>Salmonella serovar paratyphi</i>	4.40	-.09			
<i>Yersinia kristensenii</i>	4.14	-.01			
420163	Low discrimination				420163
<i>Hafnia alvei</i>	66.92	0.39	SUC 10		
<i>Escherichia coli</i>	26.34	0.24	SOR 1		
<i>Yersinia rohdei</i>	6.73	0.08			
420202	Good identification				420202
<i>Salmonella enterica subsp. enterica</i>	98.64	0.39	INO 1		
<i>Hafnia alvei</i>	1.36	0.18	SOR 90		
420203	Low discrimination				420203
<i>Hafnia alvei</i>	89.03	0.59	INO 1		
<i>Salmonella serovar enteritidis</i>	7.06	0.16			
<i>Shigella sonnei</i>	1.70	-.02			
420213	Acceptable identification				420213
<i>Hafnia alvei</i>	94.85	0.43	INO 1		
<i>Yokenella regensburgei</i>	2.91	-.10			
<i>Salmonella serovar enteritidis</i>	2.24	-.11			
420223	Acceptable identification				420223
<i>Hafnia alvei</i>	94.91	0.39	INO 1		
<i>Escherichia coli</i>	5.09	0.06	SUC 10		
420242	Very good identification				420242
<i>Salmonella enterica subsp. enterica</i>	99.72	0.59	INO 1		
<i>Salmonella serovar enteritidis</i>	0.23	0.01			
<i>Escherichia coli</i>	0.05	0.01			
420243	Identification to the genus				420243
<i>Salmonella serovar enteritidis</i>	82.96	0.42	H2S 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar paratyphi</i>	8.89	0.18	SCI 95		
<i>Salmonella enterica subsp. enterica</i>	3.66	0.18			
420303	Very good identification				420303
<i>Hafnia alvei</i>	100.0	0.59	INO 1		
420313	Good identification				420313
<i>Hafnia alvei</i>	100.0	0.43	INO 1		
420323	Good identification				420323
<i>Hafnia alvei</i>	100.0	0.39	INO 1		
420402	Good identification				420402
<i>Salmonella enterica subsp. enterica</i>	98.64	0.39	ADO 1		
<i>Hafnia alvei</i>	1.36	0.18	SOR 90		
420403	Low discrimination				420403
<i>Hafnia alvei</i>	84.72	0.59	ADO 1		
<i>Escherichia fergusonii</i>	7.83	0.25			
<i>Escherichia coli</i>	3.95	0.24			
420413	Low discrimination				420413
<i>Escherichia fergusonii</i>	87.35	0.51	IND 98		
<i>Hafnia alvei</i>	8.78	0.43			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.61	0.33			
420423	Low discrimination				420423
<i>Hafnia alvei</i>	78.14	0.39	ADO 1		
<i>Escherichia coli</i>	21.86	0.21	SUC 10		
420442	Very good identification				420442
<i>Salmonella enterica subsp. enterica</i>	99.73	0.59	ADO 1		
<i>Escherichia coli</i>	0.27	0.16			
420443	Low discrimination				420443
<i>Escherichia coli</i>	53.77	0.42	IND 92		
<i>Salmonella serovar paratyphi</i>	25.39	0.18	ADO 5		
<i>Salmonella enterica subsp. enterica</i>	10.44	0.18			
420453	Low discrimination				420453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	72.45	0.39	ORN 3		
<i>Escherichia fergusonii</i>	9.54	0.10			
<i>Salmonella enterica subsp. houtenae</i>	5.40	-.02			
420463	Acceptable identification				420463
				VPT	
<i>Escherichia coli</i>	92.10	0.38	IND 92	1	
<i>Yersinia rohdei</i>	4.52	0.08	ADO 5	1	
<i>Serratia marcescens</i>	3.38	-.01		98	
420503	Very good identification				420503
<i>Hafnia alvei</i>	95.26	0.59	ADO 1		
<i>Escherichia fergusonii</i>	4.74	0.19			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
420513	Low discrimination				420513
<i>Escherichia fergusonii</i>	84.28	0.46	IND 98		
<i>Hafnia alvei</i>	15.73	0.43			
420523	Good identification				420523
<i>Hafnia alvei</i>	100.0	0.39	ADO 1		
420613	Low discrimination				420613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	83.33	0.35	ORN 3		
<i>Escherichia fergusonii</i>	16.67	0.10			
420653	Good identification				420653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	ORN 3		
421001	Very good identification				421001
<i>Morganella morganii subsp. sibonii</i>	99.79	0.61	URE 97		
<i>Hafnia alvei</i>	0.21	0.18			
421002	Good identification				421002
<i>Salmonella enterica subsp. enterica</i>	98.64	0.39	PHE 1		
<i>Hafnia alvei</i>	1.36	0.18	SOR 90		
421003	Good identification				421003
<i>Hafnia alvei</i>	91.51	0.59	PHE 1		
<i>Morganella morganii subsp. sibonii</i>	4.47	0.20			
<i>Shigella sonnei</i>	1.75	-.02			
421013	Good identification				421013
<i>Hafnia alvei</i>	97.02	0.43	PHE 1		
<i>Yokenella regensburgei</i>	2.98	-.10			
421021	Good identification				421021
<i>Morganella morganii subsp. sibonii</i>	100.0	0.36	URE 97		
421023	Acceptable identification				421023
<i>Hafnia alvei</i>	94.91	0.39	PHE 1		
<i>Escherichia coli</i>	5.09	0.06	SUC 10		
421042	Very good identification				421042
<i>Salmonella enterica subsp. enterica</i>	99.95	0.59	PHE 1		
<i>Escherichia coli</i>	0.05	0.01			
421103	Very good identification				421103
<i>Hafnia alvei</i>	100.0	0.59	PHE 1		
421113	Good identification				421113
<i>Hafnia alvei</i>	100.0	0.43	PHE 1		
421123	Good identification				421123
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
422001	Low discrimination				422001
<i>Hafnia alvei</i>	87.88	0.39	ESL 10		
<i>Escherichia coli</i>	9.22	0.12	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	2.91	-.03			
422002	Low discrimination				422002
<i>Salmonella enterica subsp. enterica</i>	85.61	0.39	ESL 1		
<i>Hafnia alvei</i>	13.03	0.39	SOR 90		
<i>Escherichia coli</i>	1.37	0.12			
422003	Very good identification				422003
<i>Hafnia alvei</i>	97.51	0.80	ESL 10		
<i>Escherichia coli</i>	1.96	0.38			
<i>Shigella sonnei</i>	0.17	-.02			
422013	Low discrimination				422013
<i>Hafnia alvei</i>	61.33	0.65	ESL 10		
<i>Yokenella regensburgei</i>	34.37	0.37			
<i>Escherichia fergusonii</i>	3.56	0.27			
422023	Low discrimination				422023
<i>Hafnia alvei</i>	89.22	0.61	ESL 10		
<i>Escherichia coli</i>	10.78	0.35	SUC 10		
422033	Acceptable identification				422033
<i>Hafnia alvei</i>	93.35	0.45	ESL 10		
<i>Yokenella regensburgei</i>	4.76	-.04	SUC 10		
<i>Escherichia hermannii</i>	1.90	-.06			
422042	Very good identification				422042
<i>Salmonella enterica subsp. enterica</i>	98.72	0.59	ESL 1		
<i>Escherichia coli</i>	1.28	0.30			
422043	Low discrimination				422043
<i>Escherichia coli</i>	76.74	0.56	IND 92		
<i>Salmonella serovar paratyphi</i>	7.63	0.18			
<i>Salmonella serovar enteritidis</i>	6.96	0.21			
422063	Low discrimination				422063
				VPT	
<i>Escherichia coli</i>	80.22	0.52	IND 92	1	
<i>Serratia marcescens</i>	17.65	0.29		98	
<i>Hafnia alvei</i>	0.92	0.20		85	
422101	Good identification				422101
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
422102	Acceptable identification				422102
<i>Hafnia alvei</i>	93.78	0.39	ESL 10		
<i>Salmonella enterica subsp. enterica</i>	6.23	-.02	TRE 99		
422103	Very good identification				422103

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	100.0	0.80	ESL 10		
422113	Very good identification				422113
<i>Hafnia alvei</i>	95.13	0.65	ESL 10		
<i>Escherichia fergusonii</i>	2.97	0.21			
<i>Escherichia vulneris</i>	1.36	0.05			
422123	Very good identification				422123
<i>Hafnia alvei</i>	100.0	0.61	ESL 10		
422133	Low discrimination				422133
<i>Hafnia alvei</i>	85.35	0.45	ESL 10		
<i>Kluyvera ascorbata</i>	14.65	0.09	SUC 10		
422143	Low discrimination				422143
<i>Hafnia alvei</i>	73.42	0.39	ESL 10		
<i>Salmonella enterica subsp. salamae</i>	15.74	0.02	SOR 1		
<i>Escherichia coli</i>	10.84	0.15			
422203	Good identification				422203
<i>Hafnia alvei</i>	96.38	0.39	ESL 10		
<i>Salmonella serovar enteritidis</i>	3.62	-.11	INO 1		
422263	Good identification				422263
				VPT	
<i>Serratia marcescens</i>	98.49	0.39	ONP 95	98	
<i>Escherichia coli</i>	1.51	0.11	SCI 98	1	
422303	Good identification				422303
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
422403	Low discrimination				422403
<i>Hafnia alvei</i>	49.00	0.39	ESL 10		
<i>Escherichia fergusonii</i>	34.73	0.23	ADO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	11.13	0.24			
422413	Low discrimination				422413
<i>Escherichia fergusonii</i>	82.35	0.50	IND 98		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	15.97	0.46			
<i>Hafnia alvei</i>	1.08	0.24			
422453	Good identification				422453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.27	0.51	ORN 3		
<i>Escherichia fergusonii</i>	2.73	0.09			
422473	Acceptable identification				422473
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	94.16	0.39	ORN 3	1	
<i>Serratia marcescens</i>	5.84	-.01		98	
422503	Low discrimination				422503
<i>Hafnia alvei</i>	72.38	0.39	ESL 10		
<i>Escherichia fergusonii</i>	27.62	0.18	ADO 1		
422513	Good identification				422513

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	96.57	0.44	IND 98		
<i>Hafnia alvei</i>	2.35	0.24			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.08	0.15			
422613	Good identification				422613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.91	0.47	ORN 3		
<i>Escherichia fergusonii</i>	4.09	0.09			
422633	Good identification				422633
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.35	ORN 3		
422653	Very good identification				422653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.53	ORN 3		
422663	Good identification				422663
				VPT	
<i>Serratia marcescens</i>	97.08	0.35	ONP 95	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.92	0.19	SCI 98	1	
422673	Low discrimination				422673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	60.14	0.41	ORN 3	1	
<i>Enterobacter aerogenes</i>	16.91	0.06		98	
<i>Serratia odorifera biovar 1</i>	13.79	0.14		50	
423003	Good identification				423003
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
423103	Good identification				423103
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
424000	Good identification				424000
<i>Salmonella enterica subsp. enterica</i>	97.99	0.36	SOR 90		
<i>Hafnia alvei</i>	2.01	0.18	MAN 98		
424001	Very good identification				424001
<i>Hafnia alvei</i>	96.44	0.59	MAN 99		
<i>Salmonella serovar enteritidis</i>	2.73	0.06			
<i>Salmonella enterica subsp. enterica</i>	0.48	-0.05			
424002	Very good identification				424002
<i>Salmonella enterica subsp. enterica</i>	95.91	0.71	SOR 90		
<i>Hafnia alvei</i>	3.98	0.59			
<i>Salmonella serovar enteritidis</i>	0.11	0.06			
424003	Very good identification				424003
<i>Hafnia alvei</i>	96.82	1.00			
<i>Salmonella serovar enteritidis</i>	2.74	0.47			
<i>Salmonella enterica subsp. enterica</i>	0.24	0.30			
424011	Low discrimination				424011
<i>Hafnia alvei</i>	73.93	0.43	MAN 99		
<i>Yokenella regensburgei</i>	26.07	0.12			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
424013	Low discrimination				424013
<i>Hafnia alvei</i>	73.08	0.85			
<i>Yokenella regensburgei</i>	25.78	0.53			
<i>Salmonella serovar enteritidis</i>	0.62	0.21			
424021	Good identification				424021
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
424023	Very good identification				424023
				VPT	
<i>Hafnia alvei</i>	99.63	0.80	SUC 10	85	
<i>Salmonella serovar enteritidis</i>	0.26	0.06		1	
<i>Serratia marcescens</i>	0.06	-.04		98	
424033	Very good identification				424033
<i>Hafnia alvei</i>	96.89	0.65	SUC 10		
<i>Yokenella regensburgei</i>	3.11	0.12			
424040	Very good identification				424040
<i>Salmonella enterica subsp. enterica</i>	99.88	0.55	MAN 98		
<i>Salmonella serovar enteritidis</i>	0.12	-.09			
424042	Very good identification				424042
<i>Salmonella enterica subsp. enterica</i>	99.70	0.90			
<i>Salmonella serovar enteritidis</i>	0.25	0.33			
<i>Salmonella enterica subsp. houtenae</i>	0.04	0.18			
424043	Identification to the genus				424043
<i>Salmonella serovar enteritidis</i>	78.10	0.74	H2S 95		
<i>Salmonella enterica subsp. houtenae</i>	13.74	0.59			
<i>Salmonella enterica subsp. enterica</i>	3.22	0.49			
424052	Acceptable identification				424052
<i>Salmonella enterica subsp. enterica</i>	94.53	0.49	CEL 1		
<i>Salmonella enterica subsp. houtenae</i>	4.08	0.18			
<i>Salmonella serovar enteritidis</i>	1.22	0.06			
424053	Low discrimination				424053
<i>Salmonella enterica subsp. houtenae</i>	72.81	0.59	H2S 99		
<i>Salmonella serovar enteritidis</i>	21.79	0.47			
<i>Citrobacter braakii</i>	3.04	0.45			
424062	Good identification				424062
				VPT	
<i>Salmonella enterica subsp. enterica</i>	99.47	0.49	SUC 1	1	
<i>Serratia marcescens</i>	0.28	-.04		98	
<i>Salmonella serovar enteritidis</i>	0.25	-.09		1	
424063	Low discrimination				424063
				VPT	
<i>Serratia marcescens</i>	41.76	0.38	ONP 95	98	
<i>Salmonella serovar enteritidis</i>	36.50	0.33	ESL 95	1	
<i>Hafnia alvei</i>	7.55	0.39		85	
424101	Very good identification				424101

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	100.0	0.59	MAN 99		
424102	Low discrimination				424102
<i>Hafnia alvei</i>	80.42	0.59	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	19.58	0.30			
424103	Excellent identification				424103
<i>Hafnia alvei</i>	99.82	1.00			
<i>Salmonella enterica subsp. salamae</i>	0.14	0.18			
<i>Salmonella serovar enteritidis</i>	0.03	0.06			
424111	Good identification				424111
<i>Hafnia alvei</i>	100.0	0.43	MAN 99		
424112	Good identification				424112
<i>Hafnia alvei</i>	100.0	0.43	TRE 99		
424113	Very good identification				424113
<i>Hafnia alvei</i>	99.56	0.85			
<i>Yokenella regensburgei</i>	0.36	0.12			
<i>Escherichia fergusonii</i>	0.08	0.08			
424121	Good identification				424121
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
424122	Good identification				424122
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
424123	Very good identification				424123
<i>Hafnia alvei</i>	100.0	0.80	SUC 10		
424133	Very good identification				424133
<i>Hafnia alvei</i>	99.54	0.65	SUC 10		
<i>Kluyvera ascorbata</i>	0.46	-.04			
424142	Acceptable identification				424142
<i>Salmonella enterica subsp. enterica</i>	92.99	0.49	MAL 1		
<i>Salmonella enterica subsp. salamae</i>	5.73	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	0.62	-.04			
424143	Low discrimination				424143
<i>Salmonella enterica subsp. salamae</i>	80.16	0.59	H2S 99		
<i>Salmonella enterica subsp. diarizonae</i>	8.70	0.37			
<i>Hafnia alvei</i>	6.00	0.59			
424153	Low discrimination				424153
<i>Hafnia alvei</i>	38.97	0.43	SOR 1		
<i>Salmonella enterica subsp. salamae</i>	29.82	0.18			
<i>Salmonella enterica subsp. houtenae</i>	20.86	0.18			
424203	Low discrimination				424203

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar enteritidis</i>	60.11	0.42	H2S 95		
<i>Hafnia alvei</i>	39.90	0.59	SOR 95		
424213	Low discrimination				424213
<i>Hafnia alvei</i>	55.49	0.43	INO 1		
<i>Salmonella serovar enteritidis</i>	24.94	0.16			
<i>Yokenella regensburgei</i>	19.57	0.12			
424223	Low discrimination				424223
				VPT	
<i>Hafnia alvei</i>	76.66	0.39	INO 1	85	
<i>Serratia marcescens</i>	12.84	0.06	SUC 10	98	
<i>Salmonella serovar enteritidis</i>	10.50	0.01		1	
424242	Identification to the genus				424242
<i>Salmonella enterica subsp. enterica</i>	88.34	0.49	INO 1		
<i>Salmonella serovar enteritidis</i>	11.66	0.27			
424243	Very good identification				424243
<i>Salmonella serovar enteritidis</i>	99.33	0.68	H2S 95		
<i>Salmonella enterica subsp. houtenae</i>	0.33	0.18			
<i>Salmonella enterica subsp. salamae</i>	0.13	0.06			
424253	Acceptable identification				424253
				VPT	
<i>Salmonella serovar enteritidis</i>	92.40	0.42	H2S 95	1	
<i>Salmonella enterica subsp. houtenae</i>	5.79	0.18	CEL 5	1	
<i>Serratia odorifera biovar 2</i>	1.56	0.16		99	
424263	Low discrimination				424263
				VPT	
<i>Serratia marcescens</i>	86.44	0.47	ONP 95	98	
<i>Salmonella serovar enteritidis</i>	13.56	0.27	ESL 95	1	
424303	Very good identification				424303
<i>Hafnia alvei</i>	97.82	0.59	INO 1		
<i>Salmonella serovar enteritidis</i>	1.49	0.01			
<i>Salmonella enterica subsp. salamae</i>	0.70	-.09			
424313	Good identification				424313
<i>Hafnia alvei</i>	100.0	0.43	INO 1		
424323	Good identification				424323
<i>Hafnia alvei</i>	100.0	0.39	INO 1		
424403	Very good identification				424403
<i>Hafnia alvei</i>	95.04	0.59	ADO 1		
<i>Salmonella serovar enteritidis</i>	2.69	0.06			
<i>Escherichia fergusonii</i>	1.80	0.11			
424413	Low discrimination				424413
<i>Escherichia fergusonii</i>	56.70	0.37	IND 98		
<i>Hafnia alvei</i>	27.81	0.43			
<i>Yokenella regensburgei</i>	9.81	0.12			
424423	Good identification				424423

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	96.41	0.39	ADO 1		
<i>Serratia marcescens</i>	3.59	-.07	SUC 10		
424442	Good identification				424442
<i>Salmonella enterica subsp. enterica</i>	99.53	0.49	ADO 1		
<i>Salmonella serovar enteritidis</i>	0.25	-.09			
<i>Salmonella enterica subsp. houtenae</i>	0.23	-.09			
424503	Very good identification				424503
<i>Hafnia alvei</i>	98.99	0.59	ADO 1		
<i>Escherichia fergusonii</i>	1.01	0.05			
424523	Good identification				424523
<i>Hafnia alvei</i>	100.0	0.39	ADO 1		
424663	Good identification				424663
<i>Serratia marcescens</i>	100.0	0.44	ONP 95		
425003	Very good identification				425003
<i>Hafnia alvei</i>	97.25	0.59	PHE 1		
<i>Salmonella serovar enteritidis</i>	2.75	0.06			
425013	Low discrimination				425013
<i>Hafnia alvei</i>	73.93	0.43	PHE 1		
<i>Yokenella regensburgei</i>	26.07	0.12			
425023	Good identification				425023
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
425042	Good identification				425042
<i>Salmonella enterica subsp. enterica</i>	99.75	0.49	PHE 1		
<i>Salmonella serovar enteritidis</i>	0.25	-.09			
425103	Very good identification				425103
<i>Hafnia alvei</i>	100.0	0.59	PHE 1		
425113	Good identification				425113
<i>Hafnia alvei</i>	100.0	0.43	PHE 1		
425123	Good identification				425123
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
426001	Good identification				426001
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
426003	Very good identification				426003
<i>Hafnia alvei</i>	97.57	0.80	ESL 10		
<i>Salmonella serovar enteritidis</i>	1.31	0.21			
<i>Yokenella regensburgei</i>	1.12	0.18			
426013	Low discrimination				426013

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yokenella regensburgei</i>	86.36	0.59	ONP 99		
<i>Hafnia alvei</i>	13.40	0.65			
<i>Escherichia fergusonii</i>	0.16	0.12			
426023	Good identification				426023
<i>Hafnia alvei</i>	91.20	0.61	ESL 10		
<i>Serratia marcescens</i>	8.80	0.23	SUC 10		
426033	Low discrimination				426033
<i>Hafnia alvei</i>	53.54	0.45	ESL 10		
<i>Yokenella regensburgei</i>	31.37	0.18	SUC 10		
<i>Kluyvera ascorbata</i>	9.19	0.09			
426042	Good identification				426042
<i>Salmonella enterica subsp. enterica</i>	98.73	0.49	ESL 1		
<i>Salmonella serovar enteritidis</i>	1.27	0.06			
426043	Low discrimination				426043
				VPT	
<i>Salmonella serovar enteritidis</i>	84.90	0.47	H2S 95	1	
<i>Salmonella enterica subsp. salamae</i>	3.77	0.17	ESL 5	1	
<i>Serratia marcescens</i>	3.58	0.23		98	
426063	Very good identification				426063
				VPT	
<i>Serratia marcescens</i>	99.56	0.64	ONP 95	98	
<i>Salmonella serovar enteritidis</i>	0.24	0.06		1	
<i>Hafnia alvei</i>	0.11	0.20		85	
426073	Acceptable identification				426073
				VPT	
<i>Serratia marcescens</i>	90.77	0.38	ONP 95	98	
<i>Serratia odorifera biovar 1</i>	5.58	0.14	CEL 5	50	
<i>Kluyvera ascorbata</i>	3.65	0.05		1	
426101	Good identification				426101
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
426102	Good identification				426102
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
426103	Very good identification				426103
<i>Hafnia alvei</i>	99.78	0.80	ESL 10		
<i>Salmonella enterica subsp. salamae</i>	0.22	0.02			
426113	Good identification				426113
<i>Hafnia alvei</i>	92.52	0.65	ESL 10		
<i>Yokenella regensburgei</i>	6.02	0.18			
<i>Kluyvera ascorbata</i>	0.86	0.02			
426123	Very good identification				426123
				VPT	
<i>Hafnia alvei</i>	98.98	0.61	ESL 10	85	
<i>Kluyvera ascorbata</i>	0.73	-.04	SUC 10	1	
<i>Serratia marcescens</i>	0.30	-.08		98	
426133	Low discrimination				426133

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Kluyvera ascorbata</i>	80.19	0.37	ONP 99	1	
<i>Hafnia alvei</i>	19.47	0.45	IND 92	85	
<i>Cronobacter sakazakii</i>	0.35	-.06		99	
426143	Acceptable identification				426143
<i>Salmonella enterica subsp. salamae</i>	93.73	0.43	H2S 99		
<i>Hafnia alvei</i>	4.42	0.39			
<i>Salmonella serovar enteritidis</i>	1.12	0.06			
426203	Low discrimination				426203
				VPT	
<i>Hafnia alvei</i>	57.28	0.39	ESL 10	85	
<i>Salmonella serovar enteritidis</i>	40.88	0.16	INO 1	1	
<i>Serratia marcescens</i>	1.84	-.09		98	
426243	Low discrimination				426243
				VPT	
<i>Salmonella serovar enteritidis</i>	80.70	0.42	H2S 95	1	
<i>Serratia marcescens</i>	18.95	0.33	ESL 5	98	
<i>Salmonella enterica subsp. salamae</i>	0.35	-.09		1	
426263	Very good identification				426263
				VPT	
<i>Serratia marcescens</i>	99.85	0.74	ONP 95	98	
<i>Serratia odorifera biovar 1</i>	0.11	0.14		50	
<i>Salmonella serovar enteritidis</i>	0.04	0.01		1	
426273	Identification to the genus				426273
<i>Serratia odorifera biovar 1</i>	66.76	0.55	ONP 99		
<i>Serratia marcescens</i>	32.92	0.47			
<i>Enterobacter aerogenes</i>	0.32	-.02			
426303	Good identification				426303
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
426363	Good identification				426363
<i>Serratia marcescens</i>	99.68	0.43	ONP 95		
<i>Enterobacter aerogenes</i>	0.32	-.17	MAL 3		
426403	Low discrimination				426403
<i>Hafnia alvei</i>	80.48	0.39	ESL 10		
<i>Escherichia fergusonii</i>	11.68	0.09	ADO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	7.83	0.16			
426413	Low discrimination				426413
<i>Escherichia fergusonii</i>	53.13	0.35	IND 98		
<i>Yokenella regensburgei</i>	21.91	0.18			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	21.56	0.38			
426453	Good identification				426453
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.21	0.44	ORN 3	1	
<i>Salmonella enterica subsp. houtenae</i>	2.07	-.09		1	
<i>Serratia marcescens</i>	1.72	-.07		98	
426463	Very good identification				426463

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Serratia marcescens</i>	99.94	0.60	ONP 95	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.06	0.09		1	
426503	Acceptable identification				426503
<i>Hafnia alvei</i>	92.75	0.39	ESL 10		
<i>Escherichia fergusonii</i>	7.25	0.04	ADO 1		
426613	Good identification				426613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.40	ORN 3		
426653	Low discrimination				426653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	77.96	0.45	ORN 3	1	
<i>Serratia odorifera biovar 1</i>	10.43	0.14		50	
<i>Serratia odorifera biovar 2</i>	5.74	0.14		99	
426663	Very good identification				426663
<i>Serratia marcescens</i>	99.77	0.70	ONP 95		
<i>Serratia odorifera biovar 1</i>	0.16	0.14			
<i>Enterobacter aerogenes</i>	0.04	-0.09			
426673	Low discrimination				426673
<i>Serratia odorifera biovar 1</i>	63.18	0.55	ONP 99		
<i>Serratia marcescens</i>	20.77	0.44			
<i>Enterobacter aerogenes</i>	14.86	0.33			
426763	Low discrimination				426763
<i>Serratia marcescens</i>	81.06	0.39	ONP 95		
<i>Enterobacter aerogenes</i>	18.95	0.18	MAL 3		
426773	Very good identification				426773
<i>Enterobacter aerogenes</i>	99.50	0.59	ONP 99		
<i>Serratia marcescens</i>	0.23	0.13			
<i>Serratia odorifera biovar 1</i>	0.23	0.14			
427003	Good identification				427003
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
427103	Good identification				427103
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
430000	Very good identification				430000
<i>Edwardsiella tarda</i>	99.61	0.59	H2S 99		
<i>Escherichia coli</i>	0.14	0.20			
<i>Morganella morganii subsp. morganii</i>	0.14	0.04			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
430001	Low discrimination				430001
<i>Escherichia coli</i>	46.38	0.46	SOR 88		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	31.48	0.38	MAN 95		
<i>Edwardsiella tarda</i>	17.38	0.18			
430002	Low discrimination				430002
<i>Salmonella enterica</i> subsp. <i>enterica</i>	48.31	0.39	IND 1		
<i>Escherichia coli</i>	35.46	0.46	SOR 90		
<i>Edwardsiella tarda</i>	13.29	0.18			
430003	Low discrimination				430003
<i>Escherichia coli</i>	87.36	0.72	SOR 88		
<i>Hafnia alvei</i>	8.58	0.59			
<i>Escherichia fergusonii</i>	2.92	0.36			
430013	Identification to the genus				430013
<i>Escherichia fergusonii</i>	84.50	0.63	ADO 93		
<i>Escherichia hermannii</i>	10.38	0.41			
<i>Escherichia coli</i>	2.71	0.38			
430021	Acceptable identification				430021
<i>Escherichia coli</i>	93.90	0.42	SOR 88		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	6.10	0.13	MAN 95		
430022	Good identification				430022
<i>Escherichia coli</i>	97.98	0.42	SOR 88		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	2.02	-.02	TRE 95		
430023	Very good identification				430023
<i>Escherichia coli</i>	98.06	0.69	SOR 88		
<i>Hafnia alvei</i>	1.61	0.39			
<i>Escherichia hermannii</i>	0.29	0.08			
430033	Identification to the genus				430033
<i>Escherichia hermannii</i>	74.43	0.39	ONP 98		
<i>Escherichia coli</i>	15.85	0.34	LYS 6		
<i>Escherichia fergusonii</i>	7.48	0.22			
430040	Low discrimination				430040
<i>Escherichia coli</i>	38.18	0.38	TRE 95		
<i>Edwardsiella tarda</i>	37.07	0.18	MAN 95		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	24.75	0.24			
430041	Very good identification				430041
<i>Escherichia coli</i>	99.46	0.64	MAN 95		
<i>Shigella dysenteriae</i> (group A)	0.45	0.09			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.09	-.03			
430042	Low discrimination				430042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	62.52	0.59	IND 1		
<i>Escherichia coli</i>	37.39	0.64			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Shigella flexneri</i> (group B)	0.09	0.04			
430043	Very good identification				430043
<i>Escherichia coli</i>	99.54	0.90			
<i>Salmonella serovar paratyphi</i>	0.22	0.18			
<i>Salmonella enterica subsp. enterica</i>	0.09	0.18			
430053	Low discrimination				430053
<i>Escherichia coli</i>	75.88	0.55	CEL 2		
<i>Yersinia kristensenii</i>	16.85	0.33			
<i>Escherichia fergusonii</i>	3.26	0.22			
430061	Very good identification				430061
<i>Escherichia coli</i>	100.0	0.60	MAN 95		
430062	Very good identification				430062
<i>Escherichia coli</i>	97.53	0.60	TRE 95		
<i>Salmonella enterica subsp. enterica</i>	2.47	0.18			
430063	Very good identification				430063
<i>Escherichia coli</i>	99.95	0.87			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.03	0.13			
<i>Yersinia rohdei</i>	0.02	0.08			
430073	Low discrimination				430073
<i>Escherichia coli</i>	85.62	0.52	CEL 2		
<i>Citrobacter farmeri</i>	8.86	0.18			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	3.95	0.23			
430103	Low discrimination				430103
<i>Hafnia alvei</i>	77.73	0.59	IND 1		
<i>Escherichia fergusonii</i>	14.27	0.31			
<i>Escherichia coli</i>	8.00	0.31			
430113	Good identification				430113
<i>Escherichia fergusonii</i>	94.98	0.57	ADO 93		
<i>Hafnia alvei</i>	4.81	0.43			
<i>Escherichia hermannii</i>	0.22	-0.01			
430123	Low discrimination				430123
<i>Hafnia alvei</i>	61.83	0.39	IND 1		
<i>Escherichia coli</i>	38.17	0.28	SUC 10		
430143	Good identification				430143
<i>Escherichia coli</i>	98.68	0.49	MAL 1		
<i>Hafnia alvei</i>	1.32	0.18			
430163	Good identification				430163
<i>Escherichia coli</i>	100.0	0.46	MAL 1		
430243	Good identification				430243
<i>Escherichia coli</i>	98.02	0.49	INO 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar enteritidis</i>	1.98	0.01			
430263	Good identification				430263
<i>Escherichia coli</i>	98.69	0.46	INO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.32	0.05			
430403	Identification to the genus				430403
<i>Escherichia fergusonii</i>	89.24	0.60	CEL 95		
<i>Escherichia coli</i>	10.56	0.46			
<i>Hafnia alvei</i>	0.20	0.18			
430411	Good identification				430411
<i>Escherichia fergusonii</i>	100.0	0.45	MAN 99		
430412	Good identification				430412
<i>Escherichia fergusonii</i>	100.0	0.51	TRE 98		
430413	Very good identification				430413
<i>Escherichia fergusonii</i>	99.98	0.86			
<i>Escherichia coli</i>	0.01	0.11			
<i>Escherichia hermannii</i>	0.01	-0.1			
430423	Identification to the genus				430423
<i>Escherichia coli</i>	88.65	0.42	ADO 5		
<i>Escherichia fergusonii</i>	11.35	0.18	SOR 88		
430433	Good identification				430433
<i>Escherichia fergusonii</i>	98.43	0.45	SUC 1		
<i>Escherichia coli</i>	0.83	0.08			
<i>Escherichia hermannii</i>	0.74	-0.2			
430441	Good identification				430441
<i>Escherichia coli</i>	100.0	0.38	ADO 5		
430442	Low discrimination				430442
<i>Escherichia coli</i>	75.71	0.38	ADO 5		
<i>Salmonella enterica subsp. enterica</i>	24.29	0.18	TRE 95		
430443	Very good identification				430443
<i>Escherichia coli</i>	98.85	0.64	ADO 5		
<i>Escherichia fergusonii</i>	1.15	0.18			
430453	Acceptable identification				430453
<i>Escherichia fergusonii</i>	91.22	0.45	SOR 1		
<i>Escherichia coli</i>	8.42	0.29			
<i>Yersinia kristensenii</i>	0.36	-0.8			
430463	Very good identification				430463
<i>Escherichia coli</i>	100.0	0.60	ADO 5		
430503	Very good identification				430503
<i>Escherichia fergusonii</i>	99.37	0.54	CEL 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	0.41	0.18			
<i>Escherichia coli</i>	0.22	0.05			
430511	Good identification				430511
<i>Escherichia fergusonii</i>	100.0	0.39	MAN 99		
430512	Good identification				430512
<i>Escherichia fergusonii</i>	100.0	0.46	TRE 98		
430513	Very good identification				430513
<i>Escherichia fergusonii</i>	100.0	0.80			
430533	Good identification				430533
<i>Escherichia fergusonii</i>	100.0	0.39	SUC 1		
430553	Good identification				430553
<i>Escherichia fergusonii</i>	100.0	0.39	SOR 1		
430613	Good identification				430613
<i>Escherichia fergusonii</i>	100.0	0.45	INO 1		
430713	Good identification				430713
<i>Escherichia fergusonii</i>	100.0	0.39	INO 1		
431001	Very good identification				431001
<i>Morganella morganii subsp. sibonii</i>	99.78	0.61	URE 97		
<i>Escherichia coli</i>	0.11	0.05			
<i>Morganella morganii subsp. morganii</i>	0.11	-.11			
431021	Good identification				431021
<i>Morganella morganii subsp. sibonii</i>	98.84	0.36	URE 97		
<i>Escherichia coli</i>	1.16	0.01	SUC 6		
431043	Good identification				431043
<i>Escherichia coli</i>	100.0	0.49	PHE 1		
431063	Good identification				431063
<i>Escherichia coli</i>	100.0	0.46	PHE 1		
431413	Good identification				431413
<i>Escherichia fergusonii</i>	100.0	0.45	PHE 1		
431513	Good identification				431513
<i>Escherichia fergusonii</i>	100.0	0.39	PHE 1		
432003	Identification to the genus				432003
<i>Escherichia coli</i>	85.90	0.60	SOR 88		
<i>Escherichia fergusonii</i>	9.80	0.35			
<i>Hafnia alvei</i>	3.75	0.39			
432013	Good identification				432013

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	90.00	0.61	ADO 93		
<i>Escherichia hermannii</i>	8.65	0.37			
<i>Escherichia coli</i>	0.85	0.25			
432023	Very good identification				432023
<i>Escherichia coli</i>	98.51	0.56	SOR 88		
<i>Escherichia hermannii</i>	0.78	0.04			
<i>Hafnia alvei</i>	0.72	0.20			
432033	Identification to the genus				432033
<i>Escherichia hermannii</i>	80.05	0.35	ONP 98		
<i>Escherichia fergusonii</i>	10.28	0.20	LYS 6		
<i>Escherichia coli</i>	6.39	0.22			
432041	Good identification				432041
<i>Escherichia coli</i>	100.0	0.52	MAN 95		
432042	Acceptable identification				432042
<i>Escherichia coli</i>	93.67	0.52	TRE 95		
<i>Salmonella enterica subsp. enterica</i>	6.33	0.18			
432043	Very good identification				432043
<i>Escherichia coli</i>	100.0	0.78			
432053	Identification to the genus				432053
<i>Escherichia coli</i>	85.52	0.43	CEL 2		
<i>Escherichia fergusonii</i>	12.51	0.20			
<i>Escherichia hermannii</i>	1.20	-.04			
432061	Good identification				432061
<i>Escherichia coli</i>	100.0	0.48	MAN 95		
432062	Good identification				432062
<i>Escherichia coli</i>	100.0	0.48	TRE 95		
432063	Very good identification				432063
<i>Escherichia coli</i>	99.96	0.74			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.04	0.03			
432073	Low discrimination				432073
<i>Escherichia coli</i>	88.86	0.39	CEL 2		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	5.47	0.13			
<i>Kluyvera ascorbata</i>	4.14	-.02			
432113	Very good identification				432113
<i>Escherichia fergusonii</i>	98.88	0.56	ADO 93		
<i>Hafnia alvei</i>	0.65	0.24			
<i>Kluyvera ascorbata</i>	0.29	-.04			
432143	Good identification				432143
<i>Escherichia coli</i>	100.0	0.37	MAL 1		
432243	Good identification				432243

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>		100.0	0.37	INO 1		
432403	Very good identification					432403
<i>Escherichia fergusonii</i>		96.64	0.58	CEL 95		
<i>Escherichia coli</i>		3.36	0.34			
432411	Good identification					432411
<i>Escherichia fergusonii</i>		100.0	0.43	MAN 99		
432412	Good identification					432412
<i>Escherichia fergusonii</i>		100.0	0.50	TRE 98		
432413	Very good identification					432413
<i>Escherichia fergusonii</i>		99.99	0.84			
<i>Escherichia hermannii</i>		0.01	-.04			
432433	Good identification					432433
<i>Escherichia fergusonii</i>		99.41	0.43	SUC 1		
<i>Escherichia hermannii</i>		0.59	-.06			
432443	Good identification					432443
<i>Escherichia coli</i>		96.19	0.52	ADO 5		
<i>Escherichia fergusonii</i>		3.82	0.17			
432453	Good identification					432453
<i>Escherichia fergusonii</i>		96.67	0.43	SOR 1		
<i>Escherichia coli</i>		2.62	0.17			
<i>Klebsiella pneumoniae subsp. ozaenae</i>		0.71	0.10			
432463	Good identification					432463
<i>Escherichia coli</i>		100.0	0.48	ADO 5		
432503	Good identification					432503
<i>Escherichia fergusonii</i>		100.0	0.53	CEL 95		
432511	Good identification					432511
<i>Escherichia fergusonii</i>		100.0	0.38	MAN 99		
432512	Good identification					432512
<i>Escherichia fergusonii</i>		100.0	0.44	TRE 98		
432513	Very good identification					432513
<i>Escherichia fergusonii</i>		100.0	0.79			
432533	Good identification					432533
<i>Escherichia fergusonii</i>		98.93	0.38	SUC 1		
<i>Kluyvera ascorbata</i>		1.07	-.11			
432553	Good identification					432553
<i>Escherichia fergusonii</i>		100.0	0.38	SOR 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
432613	Good identification				432613
<i>Escherichia fergusonii</i>	99.52	0.43	INO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.48	0.06			
432713	Good identification				432713
<i>Escherichia fergusonii</i>	100.0	0.38	INO 1		
433043	Good identification				433043
<i>Escherichia coli</i>	100.0	0.37	PHE 1		
433413	Good identification				433413
<i>Escherichia fergusonii</i>	100.0	0.43	PHE 1		
433513	Good identification				433513
<i>Escherichia fergusonii</i>	100.0	0.38	PHE 1		
434003	Low discrimination				434003
<i>Hafnia alvei</i>	83.27	0.59	IND 1		
<i>Escherichia coli</i>	8.57	0.31			
<i>Escherichia fergusonii</i>	5.82	0.22			
434013	Low discrimination				434013
<i>Escherichia fergusonii</i>	84.32	0.49	ADO 93		
<i>Hafnia alvei</i>	11.22	0.43			
<i>Yokenella regensburgei</i>	3.96	0.12			
434023	Low discrimination				434023
<i>Hafnia alvei</i>	61.83	0.39	IND 1		
<i>Escherichia coli</i>	38.17	0.28	SUC 10		
434042	Good identification				434042
<i>Salmonella enterica subsp. enterica</i>	97.98	0.49	IND 1		
<i>Escherichia coli</i>	1.78	0.23			
<i>Salmonella serovar enteritidis</i>	0.24	-.09			
434043	Low discrimination				434043
<i>Escherichia coli</i>	49.03	0.49	SCI 1		
<i>Salmonella serovar enteritidis</i>	34.90	0.33			
<i>Citrobacter braakii</i>	6.15	0.32			
434053	Low discrimination				434053
<i>Citrobacter braakii</i>	42.02	0.38	LYS 1		
<i>Citrobacter amalonaticus</i>	24.12	0.17			
<i>Salmonella enterica subsp. houtenae</i>	20.65	0.18			
434063	Good identification				434063
				VPT	
<i>Escherichia coli</i>	96.41	0.46	SCI 1	1	
<i>Citrobacter braakii</i>	1.37	0.09		1	
<i>Serratia marcescens</i>	1.19	-.04		98	
434103	Very good identification				434103

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	96.38	0.59	IND 1		
<i>Escherichia fergusonii</i>	3.62	0.17			
434113	Low discrimination				434113
<i>Escherichia fergusonii</i>	80.19	0.43	ADO 93		
<i>Hafnia alvei</i>	19.81	0.43			
434123	Good identification				434123
<i>Hafnia alvei</i>	100.0	0.39	IND 1		
434403	Good identification				434403
<i>Escherichia fergusonii</i>	98.36	0.45	CEL 95		
<i>Hafnia alvei</i>	1.07	0.18			
<i>Escherichia coli</i>	0.57	0.05			
434412	Good identification				434412
<i>Escherichia fergusonii</i>	100.0	0.37	TRE 98		
434413	Very good identification				434413
<i>Escherichia fergusonii</i>	100.0	0.72			
434503	Good identification				434503
<i>Escherichia fergusonii</i>	98.02	0.40	CEL 95		
<i>Hafnia alvei</i>	1.98	0.18			
434513	Very good identification				434513
<i>Escherichia fergusonii</i>	100.0	0.66			
436003	Low discrimination				436003
<i>Hafnia alvei</i>	56.60	0.39	IND 1		
<i>Escherichia fergusonii</i>	30.30	0.21	ESL 10		
<i>Escherichia coli</i>	13.10	0.19			
436013	Low discrimination				436013
<i>Escherichia fergusonii</i>	87.60	0.47	ADO 93		
<i>Yokenella regensburgei</i>	9.79	0.18			
<i>Hafnia alvei</i>	1.52	0.24			
436043	Low discrimination				436043
<i>Escherichia coli</i>	86.97	0.37	SCI 1		
<i>Salmonella serovar enteritidis</i>	13.03	0.06			
436103	Low discrimination				436103
<i>Hafnia alvei</i>	77.62	0.39	IND 1		
<i>Escherichia fergusonii</i>	22.38	0.15	ESL 10		
436113	Low discrimination				436113
<i>Escherichia fergusonii</i>	72.74	0.42	ADO 93		
<i>Kluyvera ascorbata</i>	24.92	0.24			
<i>Hafnia alvei</i>	2.34	0.24			
436133	Very good identification				436133

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Kluyvera ascorbata</i>	99.94	0.59	ONP 99		
<i>Escherichia fergusonii</i>	0.06	0.01			
436173	Very good identification				436173
<i>Kluyvera ascorbata</i>	100.0	0.55	ONP 99		
436273	Very good identification				436273
<i>Serratia odorifera</i> biovar 1	99.67	0.59	ONP 99		
<i>Serratia marcescens</i>	0.33	0.06			
436403	Good identification				436403
<i>Escherichia fergusonii</i>	100.0	0.44	CEL 95		
436412	Good identification				436412
<i>Escherichia fergusonii</i>	100.0	0.35	TRE 98		
436413	Very good identification				436413
<i>Escherichia fergusonii</i>	100.0	0.70			
436503	Good identification				436503
<i>Escherichia fergusonii</i>	100.0	0.38	CEL 95		
436513	Very good identification				436513
<i>Escherichia fergusonii</i>	100.0	0.65			
436673	Very good identification				436673
<i>Serratia odorifera</i> biovar 1	99.62	0.59	ONP 99		
<i>Serratia marcescens</i>	0.22	0.03			
<i>Enterobacter aerogenes</i>	0.16	-0.09			
440001	Very good identification				440001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	98.94	0.64	PHE 93		
<i>Shigella dysenteriae</i> (group A)	0.76	0.18			
<i>Hafnia alvei</i>	0.31	0.24			
440003	Low discrimination				440003
<i>Hafnia alvei</i>	80.56	0.65	ORN 98		
<i>Yersinia pseudotuberculosis</i>	11.65	0.25			
<i>Shigella boydii</i> (group C)	2.67	0.18			
440013	Acceptable identification				440013
<i>Hafnia alvei</i>	92.79	0.50	ORN 98		
<i>Escherichia vulneris</i>	5.11	0.02			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.10	0.14			
440021	Low discrimination				440021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	84.26	0.39	PHE 93		
<i>Proteus penneri</i>	15.75	0.18	SUC 6		
440023	Low discrimination				440023
<i>Hafnia alvei</i>	86.49	0.46	ORN 98		
<i>Yersinia rohdei</i>	9.75	0.15	SUC 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	2.12	0.05			
440063	Very good identification				440063
<i>Yersinia rohdei</i>	96.66	0.56	LYS 1		
<i>Escherichia coli</i>	1.56	0.23			
<i>Citrobacter freundii</i>	1.11	0.23			
440073	Good identification				440073
<i>Yersinia rohdei</i>	95.10	0.47	LYS 1		
<i>Citrobacter freundii</i>	2.57	0.21			
<i>Citrobacter youngae</i>	1.06	0.11			
440103	Very good identification				440103
<i>Hafnia alvei</i>	100.0	0.65	ORN 98		
440113	Low discrimination				440113
<i>Hafnia alvei</i>	76.22	0.50	ORN 98		
<i>Escherichia vulneris</i>	23.78	0.18			
440123	Good identification				440123
<i>Hafnia alvei</i>	100.0	0.46	ORN 98		
440413	Good identification				440413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.64	0.45	URE 10		
<i>Hafnia alvei</i>	1.36	0.09			
440453	Good identification				440453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.50	URE 10		
440473	Acceptable identification				440473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.49	0.38	URE 10		
<i>Yersinia rohdei</i>	6.52	0.06			
440613	Good identification				440613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.46	URE 10		
440653	Good identification				440653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.52	URE 10		
440673	Good identification				440673
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.59	0.40	URE 10		
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	3.41	-.09			
441000	Low discrimination				441000
<i>Morganella morganii subsp. sibonii</i>	89.54	0.46	TRE 99		
<i>Proteus penneri</i>	6.51	0.16			
<i>Morganella morganii subsp. morganii</i>	3.50	0.06			
441001	Very good identification				441001
<i>Morganella morganii subsp. sibonii</i>	99.91	0.87			
<i>Proteus penneri</i>	0.09	0.18			
441003	Good identification				441003

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.75	0.46	MAN 1		
<i>Hafnia alvei</i>	2.25	0.24			
441011	Good identification				441011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	CEL 1		
441020	Very good identification				441020
<i>Proteus penneri</i>	96.92	0.57	LYS 1		
<i>Proteus vulgaris</i>	2.22	0.33			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.86	0.21			
441021	Low discrimination				441021
<i>Proteus penneri</i>	57.93	0.59	LYS 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	41.60	0.62			
<i>Proteus vulgaris</i>	0.47	0.25			
441041	Good identification				441041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	SOR 1		
441101	Good identification				441101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	MAL 1		
441201	Good identification				441201
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	INO 1		
441401	Good identification				441401
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	ADO 1		
442003	Good identification				442003
<i>Yersinia pseudotuberculosis</i>	96.11	0.51	LYS 1		
<i>Hafnia alvei</i>	3.89	0.46			
442103	Low discrimination				442103
<i>Hafnia alvei</i>	80.02	0.46	ORN 98		
<i>Yersinia pseudotuberculosis</i>	19.98	0.10	ESL 10		
442403	Low discrimination				442403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	61.78	0.35	URE 10		
<i>Yersinia pseudotuberculosis</i>	38.22	0.10	CEL 92		
442413	Very good identification				442413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.57	URE 10		
442433	Good identification				442433
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.45	URE 10		
442443	Good identification				442443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	URE 10		
442453	Very good identification				442453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.63	URE 10		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
442473	Good identification					442473
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.50	URE 10		
442603	Good identification					442603
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.37	URE 10		
442613	Very good identification					442613
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.59	URE 10		
442633	Good identification					442633
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.46	URE 10		
442643	Good identification					442643
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.43	URE 10		
442653	Very good identification					442653
<i>Klebsiella pneumoniae subsp. ozaenae</i>		100.0	0.64	URE 10		
442673	Good identification					442673
<i>Klebsiella pneumoniae subsp. ozaenae</i>		96.21	0.52	URE 10	VPT 1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		3.79	0.01		98	
443001	Good identification					443001
<i>Morganella morganii subsp. sibonii</i>		100.0	0.46	ESL 1		
444003	Very good identification					444003
<i>Hafnia alvei</i>		100.0	0.65	ORN 98		
444013	Good identification					444013
<i>Hafnia alvei</i>		99.04	0.50	ORN 98		
<i>Klebsiella pneumoniae subsp. ozaenae</i>		0.96	0.06			
444023	Good identification					444023
<i>Hafnia alvei</i>		100.0	0.46	ORN 98		
444063	Low discrimination					444063
<i>Citrobacter freundii</i>		66.53	0.36	ONP 88		
<i>Citrobacter youngae</i>		18.80	0.22	LYS 1		
<i>Yersinia rohdei</i>		14.67	0.15			
444103	Very good identification					444103
<i>Hafnia alvei</i>		100.0	0.65	ORN 98		
444113	Good identification					444113
<i>Hafnia alvei</i>		100.0	0.50	ORN 98		
444123	Good identification					444123
<i>Hafnia alvei</i>		100.0	0.46	ORN 98		
444413	Good identification					444413

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.88	0.37	URE 10		
<i>Hafnia alvei</i>	3.12	0.09			
444453	Good identification				444453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	URE 10		
444613	Good identification				444613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.39	URE 10		
444653	Low discrimination				444653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	89.06	0.44	URE 10	1	
<i>Serratia odorifera</i> biovar 2	10.94	0.18		99	
445001	Good identification				445001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	SCI 1		
446003	Low discrimination				446003
<i>Hafnia alvei</i>	80.02	0.46	ORN 98		
<i>Yersinia pseudotuberculosis</i>	19.98	0.10	ESL 10		
446103	Good identification				446103
<i>Hafnia alvei</i>	100.0	0.46	ORN 98		
446373	Good identification				446373
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	100.0	0.39	ONP 99		
446413	Good identification				446413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.49	URE 10		
446433	Acceptable identification				446433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.19	0.37	URE 10	1	
<i>Serratia rubidaea</i>	7.81	-.01		99	
446453	Very good identification				446453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.55	URE 10		
446473	Identification to the genus				446473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	77.53	0.43	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	22.47	0.10		98	
446613	Good identification				446613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.51	URE 10		
446633	Acceptable identification				446633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.21	0.39	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	7.79	-.05		98	
446653	Very good identification				446653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.91	0.57	URE 10	1	
<i>Serratia odorifera</i> biovar 2	1.98	0.14		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.10	-.05		98	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
446673	Identification to the genus				446673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	81.63	0.36	ONP 99	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	18.12	0.44	MAL 93	1	
<i>Klebsiella oxytoca</i>	0.25	-.17		95	
446773	Very good identification				446773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.79	0.59	ONP 99	98	
<i>Klebsiella oxytoca</i>	1.12	0.18		95	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.05	0.13		1	
450001	Very good identification				450001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.30	0.64	PHE 93		
<i>Shigella dysenteriae</i> (group A)	0.62	0.16			
<i>Escherichia coli</i>	0.08	0.04			
450021	Good identification				450021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.22	0.39	PHE 93		
<i>Escherichia coli</i>	0.78	0.01	SUC 6		
450043	Acceptable identification				450043
<i>Escherichia coli</i>	93.33	0.48	URE 1		
<i>Shigella flexneri</i> (group B)	2.59	0.10			
<i>Shigella boydii</i> (group C)	2.26	0.06			
450063	Acceptable identification				450063
<i>Escherichia coli</i>	92.17	0.45	URE 1		
<i>Yersinia rohdei</i>	5.02	0.15			
<i>Citrobacter freundii</i>	2.80	0.17			
451000	Identification to the genus				451000
<i>Morganella morganii</i> subsp. <i>sibonii</i>	57.23	0.46	TRE 99		
<i>Morganella morganii</i> subsp. <i>morganii</i>	42.48	0.33			
<i>Proteus vulgaris</i>	0.29	0.02			
451001	Very good identification				451001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.98	0.87			
<i>Providencia stuartii</i>	0.01	0.02			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.01	-.09			
451003	Good identification				451003
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	MAN 1		
451011	Good identification				451011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	CEL 1		
451021	Very good identification				451021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.41	0.62	SUC 6		
<i>Proteus penneri</i>	1.37	0.18			
<i>Proteus vulgaris</i>	1.09	0.25			
451041	Good identification				451041

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	SOR 1		
451101	Good identification				451101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	MAL 1		
451201	Low discrimination				451201
<i>Morganella morganii</i> subsp. <i>sibonii</i>	85.73	0.46	INO 1		
<i>Providencia stuartii</i>	14.27	0.28			
451401	Good identification				451401
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	ADO 1		
452043	Good identification				452043
<i>Escherichia coli</i>	100.0	0.36	URE 1		
453001	Good identification				453001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	ESL 1		
455001	Low discrimination				455001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	89.57	0.46	SCI 1		
<i>Providencia stuartii</i>	10.43	0.25			
455201	Good identification				455201
<i>Providencia stuartii</i>	99.55	0.51	LYS 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.46	0.05			
455221	Good identification				455221
<i>Providencia stuartii</i>	100.0	0.51	LYS 1		
455402	Good identification				455402
<i>Providencia rettgeri</i>	99.67	0.39	LYS 1		
<i>Providencia alcalifaciens</i>	0.33	-.17	INO 90		
455602	Very good identification				455602
<i>Providencia rettgeri</i>	100.0	0.59	LYS 1		
455622	Good identification				455622
<i>Providencia rettgeri</i>	100.0	0.43	LYS 1		
456773	Very good identification				456773
<i>Klebsiella oxytoca</i>	99.11	0.59	ONP 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.89	0.18			
457602	Very good identification				457602
<i>Providencia rettgeri</i>	100.0	0.53	LYS 1		
457622	Good identification				457622
<i>Providencia rettgeri</i>	100.0	0.38	LYS 1		
460001	Good identification				460001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	92.17	0.69	PHE 93		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	7.84	0.59			
460002	Low discrimination				460002
<i>Hafnia alvei</i>	57.79	0.59	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	42.21	0.39			
460003	Excellent identification				460003
<i>Hafnia alvei</i>	99.84	1.00			
<i>Morganella morganii subsp. sibonii</i>	0.12	0.28			
<i>Shigella sonnei</i>	0.02	-.02			
460011	Low discrimination				460011
<i>Hafnia alvei</i>	59.76	0.43	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	40.24	0.28			
460012	Good identification				460012
<i>Hafnia alvei</i>	95.99	0.43	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	4.01	-.02			
460013	Very good identification				460013
<i>Hafnia alvei</i>	99.82	0.85			
<i>Yersinia kristensenii</i>	0.15	0.10			
<i>Yokenella regensburgei</i>	0.03	-.10			
460021	Low discrimination				460021
<i>Morganella morganii subsp. sibonii</i>	87.11	0.44	PHE 93		
<i>Hafnia alvei</i>	12.89	0.39	SUC 6		
460022	Acceptable identification				460022
<i>Hafnia alvei</i>	93.78	0.39	SUC 10		
<i>Salmonella enterica subsp. enterica</i>	6.23	-.02	TRE 99		
460023	Very good identification				460023
<i>Hafnia alvei</i>	99.80	0.80	SUC 10		
<i>Yersinia rohdei</i>	0.08	0.06			
<i>Morganella morganii subsp. sibonii</i>	0.07	0.03			
460033	Very good identification				460033
<i>Hafnia alvei</i>	100.0	0.65	SUC 10		
460042	Very good identification				460042
<i>Salmonella enterica subsp. enterica</i>	99.79	0.59	URE 1		
<i>Hafnia alvei</i>	0.15	0.18			
<i>Escherichia coli</i>	0.05	0.01			
460043	Low discrimination				460043
<i>Hafnia alvei</i>	71.12	0.59	SOR 1		
<i>Salmonella serovar paratyphi</i>	11.48	0.18			
<i>Salmonella enterica subsp. enterica</i>	4.72	0.18			
460053	Acceptable identification				460053
<i>Yersinia kristensenii</i>	90.55	0.51	LYS 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	6.04	0.43			
<i>Citrobacter braakii</i>	2.73	0.31			
460063	Low discrimination				460063
<i>Yersinia rohdei</i>	80.54	0.47	LYS 1		
<i>Hafnia alvei</i>	10.72	0.39			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	4.53	0.23			
460073	Low discrimination				460073
<i>Yersinia rohdei</i>	59.04	0.37	LYS 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	29.86	0.33			
<i>Yersinia kristensenii</i>	5.67	0.10			
460101	Low discrimination				460101
<i>Hafnia alvei</i>	89.38	0.59	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	10.62	0.28			
460102	Very good identification				460102
<i>Hafnia alvei</i>	99.27	0.59	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	0.73	-.02			
460103	Excellent identification				460103
<i>Hafnia alvei</i>	100.0	1.00			
460111	Good identification				460111
<i>Hafnia alvei</i>	100.0	0.43	MAN 99		
460112	Good identification				460112
<i>Hafnia alvei</i>	100.0	0.43	TRE 99		
460113	Very good identification				460113
<i>Hafnia alvei</i>	100.0	0.85			
460121	Acceptable identification				460121
<i>Hafnia alvei</i>	93.61	0.39	SUC 10		
<i>Morganella morganii subsp. sibonii</i>	6.39	0.03	MAN 99		
460122	Good identification				460122
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
460123	Very good identification				460123
<i>Hafnia alvei</i>	100.0	0.80	SUC 10		
460133	Very good identification				460133
<i>Hafnia alvei</i>	100.0	0.65	SUC 10		
460143	Very good identification				460143
<i>Hafnia alvei</i>	100.0	0.59	SOR 1		
460153	Low discrimination				460153
<i>Hafnia alvei</i>	84.78	0.43	SOR 1		
<i>Yersinia kristensenii</i>	12.84	0.10			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter sedlakii</i>	2.39	-.11			
460163	Acceptable identification				460163
<i>Hafnia alvei</i>	92.95	0.39	SUC 10		
<i>Yersinia rohdei</i>	7.05	0.06	SOR 1		
460203	Very good identification				460203
<i>Hafnia alvei</i>	100.0	0.59	INO 1		
460213	Good identification				460213
<i>Hafnia alvei</i>	97.40	0.43	INO 1		
<i>Yersinia kristensenii</i>	2.60	-.05			
460223	Good identification				460223
<i>Hafnia alvei</i>	100.0	0.39	INO 1		
460253	Good identification				460253
<i>Yersinia kristensenii</i>	100.0	0.36	LYS 1		
460303	Very good identification				460303
<i>Hafnia alvei</i>	100.0	0.59	INO 1		
460313	Good identification				460313
<i>Hafnia alvei</i>	100.0	0.43	INO 1		
460323	Good identification				460323
<i>Hafnia alvei</i>	100.0	0.39	INO 1		
460403	Very good identification				460403
<i>Hafnia alvei</i>	100.0	0.59	ADO 1		
460413	Low discrimination				460413
<i>Hafnia alvei</i>	87.24	0.43	ADO 1		
<i>Escherichia fergusonii</i>	8.77	0.10			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.99	0.14			
460423	Good identification				460423
<i>Hafnia alvei</i>	100.0	0.39	ADO 1		
460503	Very good identification				460503
<i>Hafnia alvei</i>	100.0	0.59	ADO 1		
460513	Acceptable identification				460513
<i>Hafnia alvei</i>	94.87	0.43	ADO 1		
<i>Escherichia fergusonii</i>	5.14	0.04			
460523	Good identification				460523
<i>Hafnia alvei</i>	100.0	0.39	ADO 1		
461000	Identification to the genus				461000
<i>Morganella morganii subsp. sibonii</i>	70.55	0.51	TRE 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	29.45	0.33			
461001	Very good identification				461001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.92	0.92			
<i>Proteus mirabilis</i>	0.07	0.19			
<i>Hafnia alvei</i>	0.01	0.18			
461003	Low discrimination				461003
<i>Morganella morganii</i> subsp. <i>sibonii</i>	61.22	0.51	MAN 1		
<i>Hafnia alvei</i>	38.78	0.59			
461011	Good identification				461011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	CEL 1		
461013	Acceptable identification				461013
<i>Hafnia alvei</i>	91.71	0.43	PHE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	8.29	0.10			
461021	Very good identification				461021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.01	0.67	SUC 6		
<i>Proteus penneri</i>	0.78	0.18			
<i>Proteus mirabilis</i>	0.20	0.03			
461023	Low discrimination				461023
<i>Hafnia alvei</i>	52.44	0.39	PHE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	47.56	0.26	SUC 10		
461041	Good identification				461041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	SOR 1		
461101	Good identification				461101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.36	0.51	MAL 1		
<i>Hafnia alvei</i>	0.64	0.18			
461103	Very good identification				461103
<i>Hafnia alvei</i>	98.43	0.59	PHE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.57	0.10			
461113	Good identification				461113
<i>Hafnia alvei</i>	100.0	0.43	PHE 1		
461123	Good identification				461123
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
461201	Good identification				461201
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	INO 1		
461401	Good identification				461401
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	ADO 1		
462002	Acceptable identification				462002
<i>Hafnia alvei</i>	93.78	0.39	ESL 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica subsp. enterica</i>	6.23	-.02	TRE 99		
462003	Very good identification				462003
<i>Hafnia alvei</i>	99.49	0.80	ESL 10		
<i>Yersinia pseudotuberculosis</i>	0.51	0.10			
462013	Very good identification				462013
<i>Hafnia alvei</i>	99.44	0.65	ESL 10		
<i>Yokenella regensburgei</i>	0.56	-.04			
462023	Very good identification				462023
<i>Hafnia alvei</i>	100.0	0.61	ESL 10		
462033	Good identification				462033
<i>Hafnia alvei</i>	100.0	0.45	ESL 10		
462043	Low discrimination				462043
<i>Hafnia alvei</i>	87.14	0.39	ESL 10		
<i>Escherichia coli</i>	12.86	0.15	SOR 1		
462101	Good identification				462101
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
462102	Good identification				462102
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
462103	Very good identification				462103
<i>Hafnia alvei</i>	100.0	0.80	ESL 10		
462113	Very good identification				462113
<i>Hafnia alvei</i>	100.0	0.65	ESL 10		
462123	Very good identification				462123
<i>Hafnia alvei</i>	100.0	0.61	ESL 10		
462133	Good identification				462133
<i>Hafnia alvei</i>	100.0	0.45	ESL 10		
462143	Good identification				462143
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
462203	Good identification				462203
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
462303	Good identification				462303
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
462403	Good identification				462403
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
462503	Good identification				462503

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	100.0	0.39	ESL 10		
463001	Good identification				463001
<i>Morganella morganii subsp. sibonii</i>	100.0	0.51	ESL 1		
463003	Low discrimination				463003
<i>Hafnia alvei</i>	87.45	0.39	PHE 1		
<i>Morganella morganii subsp. sibonii</i>	12.55	0.10	ESL 10		
463103	Good identification				463103
<i>Hafnia alvei</i>	100.0	0.39	PHE 1		
464001	Low discrimination				464001
<i>Hafnia alvei</i>	89.03	0.59	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	10.58	0.28			
<i>Proteus mirabilis</i>	0.39	-.11			
464002	Low discrimination				464002
<i>Hafnia alvei</i>	80.42	0.59	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	19.58	0.30			
464003	Excellent identification				464003
<i>Hafnia alvei</i>	99.97	1.00			
<i>Salmonella serovar enteritidis</i>	0.03	0.06			
464011	Good identification				464011
<i>Hafnia alvei</i>	100.0	0.43	MAN 99		
464012	Good identification				464012
<i>Hafnia alvei</i>	100.0	0.43	TRE 99		
464013	Very good identification				464013
<i>Hafnia alvei</i>	99.65	0.85			
<i>Yokenella regensburgei</i>	0.36	0.12			
464021	Acceptable identification				464021
<i>Hafnia alvei</i>	93.61	0.39	SUC 10		
<i>Morganella morganii subsp. sibonii</i>	6.39	0.03	MAN 99		
464022	Good identification				464022
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
464023	Very good identification				464023
<i>Hafnia alvei</i>	100.0	0.80	SUC 10		
464033	Very good identification				464033
<i>Hafnia alvei</i>	100.0	0.65	SUC 10		
464042	Good identification				464042
<i>Salmonella enterica subsp. enterica</i>	99.30	0.49	URE 1		
<i>Hafnia alvei</i>	0.46	0.18			
<i>Salmonella serovar enteritidis</i>	0.25	-.09			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
464043	Low discrimination				464043
<i>Hafnia alvei</i>	52.90	0.59	SOR 1		
<i>Salmonella serovar enteritidis</i>	28.41	0.33			
<i>Salmonella enterica subsp. houtenae</i>	10.10	0.24			
464053	Low discrimination				464053
<i>Citrobacter braakii</i>	33.55	0.40	LYS 1		
<i>Salmonella enterica subsp. houtenae</i>	26.76	0.24			
<i>Hafnia alvei</i>	24.74	0.43			
464063	Low discrimination				464063
				VPT	
<i>Hafnia alvei</i>	45.87	0.39	SUC 10	85	
<i>Serratia marcescens</i>	44.75	0.22	SOR 1	98	
<i>Citrobacter braakii</i>	3.66	0.11		1	
464101	Very good identification				464101
<i>Hafnia alvei</i>	100.0	0.59	MAN 99		
464102	Very good identification				464102
<i>Hafnia alvei</i>	100.0	0.59	TRE 99		
464103	Excellent identification				464103
<i>Hafnia alvei</i>	100.0	1.00			
464111	Good identification				464111
<i>Hafnia alvei</i>	100.0	0.43	MAN 99		
464112	Good identification				464112
<i>Hafnia alvei</i>	100.0	0.43	TRE 99		
464113	Very good identification				464113
<i>Hafnia alvei</i>	100.0	0.85			
464121	Good identification				464121
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
464122	Good identification				464122
<i>Hafnia alvei</i>	100.0	0.39	SUC 10		
464123	Very good identification				464123
<i>Hafnia alvei</i>	100.0	0.80	SUC 10		
464133	Very good identification				464133
<i>Hafnia alvei</i>	100.0	0.65	SUC 10		
464143	Low discrimination				464143
<i>Hafnia alvei</i>	86.57	0.59	SOR 1		
<i>Salmonella enterica subsp. salamae</i>	11.69	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	1.27	-.04			
464153	Low discrimination				464153

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	87.92	0.43	SOR 1		
<i>Citrobacter sedlakii</i>	12.08	0.04			
464163	Good identification				464163
<i>Hafnia alvei</i>	97.07	0.39	SUC 10		
<i>Serratia marcescens</i>	2.93	-.09	SOR 1		
464203	Very good identification				464203
<i>Hafnia alvei</i>	98.50	0.59	INO 1		
<i>Salmonella serovar enteritidis</i>	1.50	0.01			
464213	Good identification				464213
<i>Hafnia alvei</i>	100.0	0.43	INO 1		
464223	Good identification				464223
<i>Hafnia alvei</i>	97.13	0.39	INO 1		
<i>Serratia marcescens</i>	2.87	-.09	SUC 10		
464303	Very good identification				464303
<i>Hafnia alvei</i>	100.0	0.59	INO 1		
464313	Good identification				464313
<i>Hafnia alvei</i>	100.0	0.43	INO 1		
464323	Good identification				464323
<i>Hafnia alvei</i>	100.0	0.39	INO 1		
464403	Very good identification				464403
<i>Hafnia alvei</i>	100.0	0.59	ADO 1		
464413	Good identification				464413
<i>Hafnia alvei</i>	96.14	0.43	ADO 1		
<i>Escherichia fergusonii</i>	1.98	-.04			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.88	0.06			
464423	Good identification				464423
<i>Hafnia alvei</i>	100.0	0.39	ADO 1		
464503	Very good identification				464503
<i>Hafnia alvei</i>	100.0	0.59	ADO 1		
464513	Good identification				464513
<i>Hafnia alvei</i>	100.0	0.43	ADO 1		
464523	Good identification				464523
<i>Hafnia alvei</i>	100.0	0.39	ADO 1		
465001	Low discrimination				465001
<i>Morganella morganii subsp. sibonii</i>	87.51	0.51	SCI 1		
<i>Proteus mirabilis</i>	11.94	0.24			
<i>Hafnia alvei</i>	0.56	0.18			

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
465003	Very good identification					465003
<i>Hafnia alvei</i>		98.43	0.59	PHE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>		1.57	0.10			
465013	Good identification					465013
<i>Hafnia alvei</i>		100.0	0.43	PHE 1		
465023	Good identification					465023
<i>Hafnia alvei</i>		100.0	0.39	PHE 1		
465103	Very good identification					465103
<i>Hafnia alvei</i>		100.0	0.59	PHE 1		
465113	Good identification					465113
<i>Hafnia alvei</i>		100.0	0.43	PHE 1		
465123	Good identification					465123
<i>Hafnia alvei</i>		100.0	0.39	PHE 1		
466001	Good identification					466001
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		
466002	Good identification					466002
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		
466003	Very good identification					466003
<i>Hafnia alvei</i>		100.0	0.80	ESL 10		
466013	Good identification					466013
<i>Hafnia alvei</i>		93.89	0.65	ESL 10		
<i>Yokenella regensburgei</i>		6.11	0.18			
466023	Very good identification					466023
<i>Hafnia alvei</i>		98.33	0.61	ESL 10		
<i>Serratia marcescens</i>		1.67	0.07	SUC 10		
466033	Good identification					466033
<i>Hafnia alvei</i>		100.0	0.45	ESL 10		
466043	Low discrimination					466043
<i>Hafnia alvei</i>		69.37	0.39	ESL 10	VPT 85	
<i>Salmonella serovar enteritidis</i>		17.64	0.06	SOR 1	1	
<i>Serratia marcescens</i>		12.99	0.07		98	
466063	Good identification					466063
<i>Serratia marcescens</i>		99.40	0.48	ONP 95		
<i>Hafnia alvei</i>		0.60	0.20			
466101	Good identification					466101
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
466102	Good identification					466102
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		
466103	Very good identification					466103
<i>Hafnia alvei</i>		100.0	0.80	ESL 10		
466113	Very good identification					466113
<i>Hafnia alvei</i>		100.0	0.65	ESL 10		
466123	Very good identification					466123
<i>Hafnia alvei</i>		100.0	0.61	ESL 10		
466133	Good identification					466133
<i>Hafnia alvei</i>		96.01	0.45	ESL 10		
<i>Kluyvera ascorbata</i>		4.00	-.04	SUC 10		
466143	Low discrimination					466143
<i>Hafnia alvei</i>		82.34	0.39	ESL 10		
<i>Salmonella enterica subsp. salamae</i>		17.66	0.02	SOR 1		
466203	Good identification					466203
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		
466263	Very good identification					466263
<i>Serratia marcescens</i>		100.0	0.58	ONP 95		
466303	Good identification					466303
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		
466403	Good identification					466403
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		
466463	Good identification					466463
<i>Serratia marcescens</i>		100.0	0.45	ONP 95		
466503	Good identification					466503
<i>Hafnia alvei</i>		100.0	0.39	ESL 10		
466663	Very good identification					466663
<i>Serratia marcescens</i>		100.0	0.55	ONP 95		
467003	Good identification					467003
<i>Hafnia alvei</i>		100.0	0.39	PHE 1		
467103	Good identification					467103
<i>Hafnia alvei</i>		100.0	0.39	PHE 1		
470001	Very good identification					470001
<i>Morganella morganii subsp. sibonii</i>		99.81	0.69	PHE 93		
<i>Hafnia alvei</i>		0.09	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.06	-0.09			
470003	Low discrimination				470003
<i>Hafnia alvei</i>	81.62	0.59	IND 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	9.70	0.28			
<i>Escherichia coli</i>	8.40	0.31			
470013	Low discrimination				470013
<i>Hafnia alvei</i>	67.51	0.43	IND 1		
<i>Escherichia fergusonii</i>	25.03	0.22			
<i>Yersinia kristensenii</i>	4.38	0.03			
470021	Good identification				470021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.52	0.44	PHE 93		
<i>Escherichia coli</i>	0.48	0.01	SUC 6		
470023	Low discrimination				470023
<i>Hafnia alvei</i>	59.33	0.39	IND 1		
<i>Escherichia coli</i>	36.62	0.28	SUC 10		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	4.05	0.03			
470043	Acceptable identification				470043
<i>Escherichia coli</i>	94.86	0.49	URE 1		
<i>Citrobacter braakii</i>	2.43	0.18			
<i>Yersinia kristensenii</i>	1.44	0.03			
470053	Acceptable identification				470053
<i>Yersinia kristensenii</i>	94.16	0.44	LYS 1		
<i>Citrobacter braakii</i>	3.26	0.24			
<i>Escherichia coli</i>	1.28	0.14			
470063	Acceptable identification				470063
<i>Escherichia coli</i>	90.09	0.46	URE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.40	0.23			
<i>Yersinia rohdei</i>	1.51	0.06			
470103	Very good identification				470103
<i>Hafnia alvei</i>	100.0	0.59	IND 1		
470113	Low discrimination				470113
<i>Hafnia alvei</i>	83.36	0.43	IND 1		
<i>Escherichia fergusonii</i>	16.64	0.16			
470123	Good identification				470123
<i>Hafnia alvei</i>	100.0	0.39	IND 1		
470413	Good identification				470413
<i>Escherichia fergusonii</i>	100.0	0.45	URE 1		
470513	Good identification				470513
<i>Escherichia fergusonii</i>	100.0	0.39	URE 1		
471000	Identification to the genus				471000

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>morganii</i>	88.80	0.59	LYS 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	11.20	0.51			
471001	Very good identification				471001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.92	0.92			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.08	0.18			
471003	Good identification				471003
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.36	0.51	MAN 1		
<i>Hafnia alvei</i>	0.64	0.18			
471011	Good identification				471011
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	CEL 1		
471021	Very good identification				471021
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.67	SUC 6		
471041	Good identification				471041
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	SOR 1		
471101	Good identification				471101
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	MAL 1		
471201	Good identification				471201
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	INO 1		
471401	Good identification				471401
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	ADO 1		
472003	Low discrimination				472003
<i>Hafnia alvei</i>	81.20	0.39	IND 1		
<i>Escherichia coli</i>	18.80	0.19	ESL 10		
472043	Good identification				472043
<i>Escherichia coli</i>	100.0	0.37	URE 1		
472103	Good identification				472103
<i>Hafnia alvei</i>	100.0	0.39	IND 1		
472413	Good identification				472413
<i>Escherichia fergusonii</i>	100.0	0.43	URE 1		
472513	Good identification				472513
<i>Escherichia fergusonii</i>	100.0	0.38	URE 1		
473001	Good identification				473001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.51	ESL 1		
474003	Very good identification				474003
<i>Hafnia alvei</i>	100.0	0.59	IND 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
474013	Low discrimination				474013
<i>Hafnia alvei</i>	89.11	0.43	IND 1		
<i>Escherichia fergusonii</i>	6.77	0.07			
<i>Citrobacter amalonaticus</i>	4.13	-.07			
474023	Good identification				474023
<i>Hafnia alvei</i>	100.0	0.39	IND 1		
474103	Very good identification				474103
<i>Hafnia alvei</i>	100.0	0.59	IND 1		
474113	Good identification				474113
<i>Hafnia alvei</i>	96.07	0.43	IND 1		
<i>Escherichia fergusonii</i>	3.93	0.02			
474123	Good identification				474123
<i>Hafnia alvei</i>	100.0	0.39	IND 1		
475001	Good identification				475001
<i>Morganella morganii subsp. sibonii</i>	99.72	0.51	SCI 1		
<i>Proteus mirabilis</i>	0.28	-.11			
476003	Good identification				476003
<i>Hafnia alvei</i>	100.0	0.39	IND 1		
476103	Good identification				476103
<i>Hafnia alvei</i>	100.0	0.39	IND 1		
500001	Acceptable identification				500001
<i>Shigella dysenteriae (group A)</i>	91.82	0.51	LYS 1		
<i>Escherichia coli</i>	5.51	0.33			
<i>Shigella boydii (group C)</i>	0.97	0.08			
500003	Low discrimination				500003
<i>Escherichia coli</i>	33.71	0.60	IND 92		
<i>Escherichia vulneris</i>	26.71	0.43	SOR 88		
<i>Hafnia alvei</i>	22.72	0.63			
500011	Good identification				500011
<i>Escherichia vulneris</i>	98.62	0.43	MAN 99		
<i>Shigella dysenteriae (group A)</i>	1.10	0.10			
<i>Yokenella regensburgei</i>	0.28	-.10			
500012	Good identification				500012
<i>Escherichia vulneris</i>	99.42	0.43	TRE 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.30	0.11			
<i>Yokenella regensburgei</i>	0.28	-.10			
500013	Very good identification				500013
<i>Escherichia vulneris</i>	99.38	0.85			
<i>Yokenella regensburgei</i>	0.28	0.31			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	0.15	0.48			
500023	Low discrimination				500023
<i>Escherichia coli</i>	80.21	0.56	IND 92		
<i>Hafnia alvei</i>	9.01	0.44	SOR 88		
<i>Escherichia vulneris</i>	8.29	0.22			
500033	Very good identification				500033
<i>Escherichia vulneris</i>	99.06	0.63	SUC 8		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.43	0.33			
<i>Escherichia coli</i>	0.20	0.21			
500041	Low discrimination				500041
<i>Escherichia coli</i>	50.02	0.51	IND 92		
<i>Shigella dysenteriae (group A)</i>	48.75	0.44	MAN 95		
<i>Shigella boydii (group C)</i>	0.91	0.06			
500042	Low discrimination				500042
<i>Escherichia coli</i>	84.02	0.51	IND 92		
<i>Shigella boydii (group C)</i>	8.71	0.21	TRE 95		
<i>Salmonella enterica subsp. enterica</i>	5.89	0.18			
500043	Good identification				500043
<i>Escherichia coli</i>	92.04	0.78	IND 92		
<i>Salmonella serovar typhi</i>	3.05	0.28			
<i>Shigella boydii (group C)</i>	2.85	0.37			
500053	Low discrimination				500053
<i>Escherichia vulneris</i>	58.33	0.43	SOR 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	16.18	0.51			
<i>Escherichia coli</i>	11.02	0.43			
500061	Acceptable identification				500061
<i>Escherichia coli</i>	93.64	0.48	IND 92		
<i>Yersinia rohdei</i>	4.98	0.18	MAN 95		
<i>Shigella dysenteriae (group A)</i>	1.38	0.03			
500062	Acceptable identification				500062
<i>Escherichia coli</i>	94.96	0.48	IND 92		
<i>Yersinia rohdei</i>	5.05	0.18	TRE 95		
500063	Low discrimination				500063
<i>Escherichia coli</i>	76.55	0.74	IND 92		
<i>Yersinia rohdei</i>	21.20	0.59			
<i>Citrobacter freundii</i>	1.71	0.43			
500073	Low discrimination				500073
<i>Yersinia rohdei</i>	56.65	0.49	LYS 1		
<i>Escherichia coli</i>	12.53	0.39			
<i>Citrobacter freundii</i>	10.76	0.41			
500103	Low discrimination				500103

Code	ID	T	tests	Differentiation tests	Code
Taxon	score	index	against		
<i>Escherichia vulneris</i>	86.70	0.59	CEL 99		
<i>Hafnia alvei</i>	13.02	0.63			
<i>Escherichia coli</i>	0.20	0.19			
500111	Very good identification				500111
<i>Escherichia vulneris</i>	100.0	0.59	MAN 99		
500112	Very good identification				500112
<i>Escherichia vulneris</i>	100.0	0.59	TRE 99		
500113	Excellent identification				500113
<i>Escherichia vulneris</i>	99.97	1.00			
<i>Hafnia alvei</i>	0.03	0.48			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.00	0.15			
500123	Low discrimination				500123
<i>Escherichia vulneris</i>	81.23	0.37	CEL 99		
<i>Hafnia alvei</i>	15.58	0.44	SUC 8		
<i>Pantoea agglomerans</i>	1.79	0.05			
500131	Good identification				500131
<i>Escherichia vulneris</i>	100.0	0.37	SUC 8		
500132	Good identification				500132
<i>Escherichia vulneris</i>	100.0	0.37	SUC 8		
500133	Very good identification				500133
				VPT	
<i>Escherichia vulneris</i>	99.92	0.78	SUC 8	1	
<i>Hafnia alvei</i>	0.03	0.28		85	
<i>Serratia rubidaea</i>	0.03	0.08		99	
500143	Low discrimination				500143
<i>Escherichia coli</i>	53.02	0.36	IND 92		
<i>Escherichia vulneris</i>	32.46	0.18	MAL 1		
<i>Hafnia alvei</i>	4.87	0.22			
500153	Very good identification				500153
<i>Escherichia vulneris</i>	99.75	0.59	SOR 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.15	0.20			
<i>Citrobacter youngae</i>	0.07	0.09			
500173	Good identification				500173
<i>Escherichia vulneris</i>	96.61	0.37	SUC 8		
<i>Citrobacter freundii</i>	1.85	0.19	SOR 1		
<i>Yersinia rohdei</i>	1.13	0.08			
500213	Low discrimination				500213
				VPT	
<i>Escherichia vulneris</i>	81.60	0.43	INO 1	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	14.89	0.47		1	
<i>Serratia odorifera biovar 2</i>	3.28	0.26		99	
500243	Low discrimination				500243
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	53.79	0.36	IND 92	1	
<i>Serratia odorifera</i> biovar 2	23.10	0.26	INO 1	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	16.96	0.31		1	
500251	Good identification				500251
				VPT	
<i>Serratia odorifera</i> biovar 2	97.29	0.36	SCI 97	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	2.71	0.12	MAN 97	1	
500253	Good identification				500253
				VPT	
<i>Serratia odorifera</i> biovar 2	91.50	0.67	SCI 97	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	7.80	0.53		1	
<i>Yersinia kristensenii</i>	0.34	0.11		1	
500273	Low discrimination				500273
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	60.10	0.41	ADO 97	1	
<i>Serratia odorifera</i> biovar 2	28.48	0.26		99	
<i>Yersinia enterocolitica</i> ssp. enterocolitica	7.34	0.15		2	
500313	Very good identification				500313
<i>Escherichia vulneris</i>	99.90	0.59	INO 1		
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.10	0.16			
500333	Good identification				500333
				VPT	
<i>Escherichia vulneris</i>	99.37	0.37	INO 1	1	
<i>Serratia rubidaea</i>	0.63	-.04	SUC 8	99	
500403	Low discrimination				500403
<i>Klebsiella pneumoniae</i> subsp. ozaenae	81.85	0.55	CEL 92		
<i>Escherichia coli</i>	12.95	0.33			
<i>Escherichia vulneris</i>	1.97	0.02			
500411	Low discrimination				500411
<i>Klebsiella pneumoniae</i> subsp. ozaenae	82.84	0.36	MAN 99		
<i>Escherichia vulneris</i>	17.16	0.02			
500412	Acceptable identification				500412
<i>Klebsiella pneumoniae</i> subsp. ozaenae	90.70	0.42	TRE 98		
<i>Escherichia vulneris</i>	9.30	0.02			
500413	Low discrimination				500413
<i>Klebsiella pneumoniae</i> subsp. ozaenae	82.17	0.77			
<i>Escherichia vulneris</i>	17.02	0.43			
<i>Escherichia fergusonii</i>	0.76	0.24			
500423	Low discrimination				500423
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	68.02	0.42	CEL 92	1	
<i>Escherichia coli</i>	28.70	0.30		1	
<i>Serratia rubidaea</i>	3.28	0.00		99	
500433	Low discrimination				500433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	87.89	0.64		1	
<i>Escherichia vulneris</i>	6.33	0.22		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia rubidaea</i>	5.78	0.25		99	
500443	Low discrimination				500443
<i>Klebsiella pneumoniae subsp. ozaenae</i>	61.26	0.60	CEL 92		
<i>Escherichia coli</i>	38.27	0.51			
<i>Salmonella serovar typhi</i>	0.24	-.13			
500451	Good identification				500451
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	MAN 99		
500452	Good identification				500452
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.47	TRE 98		
500453	Very good identification				500453
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.24	0.82		1	
<i>Serratia odorifera biovar 2</i>	0.54	0.28		99	
<i>Escherichia coli</i>	0.11	0.16		1	
500463	Low discrimination				500463
<i>Escherichia coli</i>	60.49	0.48	IND 92		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	36.30	0.48	ADO 5		
<i>Yersinia rohdei</i>	3.21	0.18			
500472	Good identification				500472
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.35	TRE 98		
500473	Very good identification				500473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.45	0.70			
<i>Escherichia coli</i>	0.29	0.13			
<i>Yersinia rohdei</i>	0.26	0.08			
500513	Very good identification				500513
<i>Escherichia vulneris</i>	96.82	0.59	ADO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.55	0.46			
<i>Escherichia fergusonii</i>	0.41	0.19			
500533	Low discrimination				500533
				VPT	
<i>Serratia rubidaea</i>	70.10	0.49	ESL 94	99	
<i>Escherichia vulneris</i>	27.79	0.37	SCI 95	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.11	0.33		1	
500553	Low discrimination				500553
<i>Klebsiella pneumoniae subsp. ozaenae</i>	82.89	0.51	MAL 3		
<i>Escherichia vulneris</i>	17.11	0.18			
500573	Low discrimination				500573
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	77.42	0.39	MAL 3	1	
<i>Serratia rubidaea</i>	14.02	0.08		99	
<i>Escherichia vulneris</i>	5.56	-.04		1	
500603	Very good identification				500603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.57	CEL 92		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
500611	Good identification					500611
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.37	MAN 99		
500612	Good identification					500612
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.44	TRE 98		
500613	Very good identification					500613
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		99.01	0.78		1	
<i>Serratia odorifera</i> biovar 2		0.82	0.28		99	
<i>Escherichia vulneris</i>		0.17	0.02		1	
500623	Good identification					500623
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.44	CEL 92		
500633	Very good identification					500633
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		98.67	0.66		1	
<i>Serratia rubidaea</i>		1.33	0.12		99	
500643	Good identification					500643
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		94.64	0.62	CEL 92	1	
<i>Serratia odorifera</i> biovar 2		4.87	0.28		99	
<i>Escherichia coli</i>		0.49	0.10		1	
500651	Low discrimination					500651
					VPT	
<i>Serratia odorifera</i> biovar 2		57.58	0.38	SCI 97	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		42.42	0.43	MAN 97	1	
500652	Low discrimination					500652
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		82.01	0.49	TRE 98	1	
<i>Serratia odorifera</i> biovar 2		17.99	0.28		99	
500653	Low discrimination					500653
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		69.28	0.84		1	
<i>Serratia odorifera</i> biovar 2		30.72	0.69		99	
500663	Good identification					500663
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		97.64	0.50	CEL 92	1	
<i>Escherichia coli</i>		1.35	0.06		1	
<i>Serratia marcescens</i>		1.02	-.06		98	
500672	Good identification					500672
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		100.0	0.37	TRE 98		
500673	Very good identification					500673
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		98.15	0.72		1	
<i>Serratia odorifera</i> biovar 2		1.76	0.28		99	
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>		0.10	-.09		1	
500713	Low discrimination					500713
					VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		75.14	0.47	MAL 3	1	
<i>Escherichia vulneris</i>		23.57	0.18		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia rubidaea</i>	1.29	-.04		99	
500733	Low discrimination				500733
				VPT	
<i>Serratia rubidaea</i>	86.00	0.37	ESL 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	12.63	0.35	SCI 95	1	
<i>Escherichia vulneris</i>	1.38	-.04		1	
500753	Low discrimination				500753
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	83.69	0.53	MAL 3	1	
<i>Serratia odorifera biovar 2</i>	12.12	0.28		99	
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	4.20	0.08		1	
500773	Low discrimination				500773
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	51.07	0.41	MAL 3	1	
<i>Klebsiella pneumoniae subsp. rhinoscleromatis</i>	30.74	0.18		1	
<i>Enterobacter aerogenes</i>	11.25	0.04		98	
501013	Good identification				501013
<i>Escherichia vulneris</i>	99.72	0.43	PHE 1		
<i>Yokenella regensburgei</i>	0.28	-.10			
501043	Acceptable identification				501043
<i>Escherichia coli</i>	93.98	0.36	IND 92		
<i>Salmonella serovar typhi</i>	3.12	-.13	PHE 1		
<i>Shigella boydii (group C)</i>	2.91	-.04			
501113	Very good identification				501113
<i>Escherichia vulneris</i>	100.0	0.59	PHE 1		
501133	Good identification				501133
<i>Escherichia vulneris</i>	100.0	0.37	PHE 1		
501413	Low discrimination				501413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	82.84	0.36	PHE 1		
<i>Escherichia vulneris</i>	17.16	0.02			
501453	Good identification				501453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	PHE 1		
501613	Good identification				501613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.37	PHE 1		
501653	Low discrimination				501653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	69.28	0.43	PHE 1	1	
<i>Serratia odorifera biovar 2</i>	30.72	0.28		99	
502013	Very good identification				502013
<i>Escherichia vulneris</i>	95.43	0.72			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.30	0.58			
<i>Yokenella regensburgei</i>	2.16	0.37			
502023	Low discrimination				502023

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	77.91	0.44	IND 92		
<i>Escherichia vulneris</i>	8.05	0.09	SOR 88		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	4.81	0.24			
502033	Acceptable identification				502033
				VPT	
<i>Escherichia vulneris</i>	92.20	0.50	SUC 8	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	6.40	0.46		1	
<i>Serratia rubidaea</i>	0.54	0.08		99	
502041	Good identification				502041
<i>Escherichia coli</i>	96.21	0.39	IND 92		
<i>Shigella dysenteriae (group A)</i>	3.79	0.03	MAN 95		
502042	Good identification				502042
<i>Escherichia coli</i>	98.41	0.39	IND 92		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.59	0.07	TRE 95		
502043	Very good identification				502043
<i>Escherichia coli</i>	95.34	0.65	IND 92		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.97	0.42			
<i>Citrobacter youngae</i>	0.19	0.11			
502053	Low discrimination				502053
<i>Klebsiella pneumoniae subsp. ozaenae</i>	76.88	0.64	ADO 97		
<i>Escherichia vulneris</i>	17.33	0.31			
<i>Escherichia coli</i>	3.27	0.30			
502061	Good identification				502061
<i>Escherichia coli</i>	100.0	0.35	IND 92		
502062	Good identification				502062
<i>Escherichia coli</i>	100.0	0.35	IND 92		
502063	Very good identification				502063
				VPT	
<i>Escherichia coli</i>	95.80	0.61	IND 92	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.50	0.29		1	
<i>Serratia marcescens</i>	1.46	0.14		98	
502073	Low discrimination				502073
<i>Klebsiella pneumoniae subsp. ozaenae</i>	70.86	0.51	ADO 97		
<i>Serratia ficaria</i>	12.01	0.16			
<i>Escherichia coli</i>	8.05	0.27			
502103	Acceptable identification				502103
<i>Escherichia vulneris</i>	92.67	0.47	CEL 99		
<i>Hafnia alvei</i>	6.18	0.44			
<i>Pantoea agglomerans</i>	0.71	0.05			
502111	Good identification				502111
<i>Escherichia vulneris</i>	100.0	0.47	MAN 99		
502112	Good identification				502112

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia vulneris</i>	100.0	0.47	TRE 99		
502113	Very good identification				502113
<i>Escherichia vulneris</i>	99.96	0.88			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.01	0.27			
<i>Hafnia alvei</i>	0.01	0.28			
502123	Low discrimination				502123
				VPT	
<i>Pantoea agglomerans</i>	87.88	0.47	LYS 1	64	
<i>Escherichia vulneris</i>	10.07	0.25		1	
<i>Serratia rubidaea</i>	1.03	0.08		99	
502133	Good identification				502133
				VPT	
<i>Escherichia vulneris</i>	91.94	0.66	SUC 8	1	
<i>Pantoea agglomerans</i>	6.37	0.44		64	
<i>Serratia rubidaea</i>	1.48	0.33		99	
502153	Good identification				502153
<i>Escherichia vulneris</i>	97.64	0.47	SOR 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.36	0.32			
502203	Low discrimination				502203
<i>Klebsiella pneumoniae subsp. ozaenae</i>	87.27	0.38	ADO 97		
<i>Yersinia pseudotuberculosis</i>	4.87	-.09	CEL 92		
<i>Escherichia coli</i>	4.38	0.06			
502213	Low discrimination				502213
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	72.10	0.60	ADO 97	1	
<i>Escherichia vulneris</i>	24.69	0.31		1	
<i>Serratia odorifera biovar 2</i>	2.64	0.22		99	
502233	Low discrimination				502233
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	86.88	0.47	ADO 97	1	
<i>Escherichia vulneris</i>	10.35	0.09		1	
<i>Serratia rubidaea</i>	1.49	-.04		99	
502243	Low discrimination				502243
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	70.16	0.44	ADO 97	1	
<i>Serratia odorifera biovar 2</i>	15.93	0.22	CEL 92	99	
<i>Escherichia coli</i>	13.91	0.24		1	
502253	Low discrimination				502253
				VPT	
<i>Serratia odorifera biovar 2</i>	66.11	0.64	SCI 97	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	33.82	0.65		1	
<i>Escherichia vulneris</i>	0.06	-.10		1	
502273	Low discrimination				502273
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	74.22	0.53	ADO 97	1	
<i>Serratia ficaria</i>	12.58	0.18		75	
<i>Serratia odorifera biovar 2</i>	5.86	0.22		99	
502313	Good identification				502313

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia vulneris</i>	98.43	0.47	INO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.57	0.29			
502403	Very good identification				502403
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.55	0.67	CEL 92		
<i>Escherichia coli</i>	0.98	0.21			
<i>Yersinia pseudotuberculosis</i>	0.21	-.09			
502411	Good identification				502411
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.72	0.48	MAN 99		
<i>Escherichia vulneris</i>	1.28	-.10			
502412	Very good identification				502412
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.36	0.54	TRE 98		
<i>Escherichia vulneris</i>	0.64	-.10			
502413	Very good identification				502413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.44	0.89			
<i>Escherichia vulneris</i>	1.27	0.31			
<i>Escherichia fergusonii</i>	0.19	0.23			
502423	Low discrimination				502423
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	82.28	0.55	CEL 92	1	
<i>Serratia rubidaea</i>	15.55	0.25		99	
<i>Escherichia coli</i>	2.17	0.17		1	
502431	Low discrimination				502431
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.53	0.36	MAN 99	1	
<i>Serratia rubidaea</i>	20.47	0.08		99	
502432	Low discrimination				502432
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	88.70	0.42	TRE 98	1	
<i>Serratia rubidaea</i>	11.30	0.08		99	
502433	Low discrimination				502433
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.21	0.77		1	
<i>Serratia rubidaea</i>	20.39	0.49		99	
<i>Escherichia vulneris</i>	0.36	0.09		1	
502442	Acceptable identification				502442
<i>Klebsiella pneumoniae subsp. ozaenae</i>	90.85	0.38	CEL 92		
<i>Escherichia coli</i>	9.15	0.12	TRE 98		
502443	Very good identification				502443
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.24	0.73	CEL 92		
<i>Escherichia coli</i>	3.76	0.39			
502451	Very good identification				502451
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.54	MAN 99		
502452	Very good identification				502452
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.60	TRE 98		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
502453	Excellent identification				502453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.90	0.95		1	
<i>Serratia odorifera</i> biovar 2	0.09	0.24		99	
<i>Escherichia coli</i>	0.01	0.04		1	
502463	Low discrimination				502463
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	88.95	0.60	CEL 92	1	
<i>Escherichia coli</i>	9.26	0.35		1	
<i>Serratia marcescens</i>	1.79	0.11		98	
502471	Good identification				502471
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	MAN 99		
502472	Good identification				502472
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.47	TRE 98		
502473	Very good identification				502473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.80	0.82		1	
<i>Serratia rubidaea</i>	0.14	0.08		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.04	-.11		98	
502503	Low discrimination				502503
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	65.91	0.36	MAL 3	1	
<i>Escherichia vulneris</i>	18.16	0.05	CEL 92	1	
<i>Serratia rubidaea</i>	15.93	0.08		99	
502513	Low discrimination				502513
				VPT	
<i>Escherichia vulneris</i>	63.05	0.47	ADO 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	26.58	0.58		1	
<i>Serratia rubidaea</i>	8.75	0.33		99	
502523	Good identification				502523
				VPT	
<i>Serratia rubidaea</i>	98.12	0.49	SCI 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.03	0.24	CEL 94	1	
<i>Pantoea agglomerans</i>	0.86	0.05		64	
502533	Very good identification				502533
				VPT	
<i>Serratia rubidaea</i>	98.42	0.74	SCI 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.76	0.46		1	
<i>Escherichia vulneris</i>	0.62	0.25		1	
502543	Good identification				502543
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.42	MAL 3		
502553	Very good identification				502553
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.55	0.64	MAL 3	1	
<i>Escherichia vulneris</i>	1.27	0.05		1	
<i>Serratia rubidaea</i>	0.18	-.09		99	
502573	Low discrimination				502573
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	49.01	0.51	MAL 3	1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia rubidaea</i>	34.76	0.33		99	
<i>Enterobacter aerogenes</i>	8.51	0.13		98	
502603	Very good identification				502603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.69	CEL 92		
502611	Good identification				502611
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.50	MAN 99		
502612	Very good identification				502612
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.56	TRE 98		
502613	Very good identification				502613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.84	0.91		1	
<i>Serratia odorifera biovar 2</i>	0.14	0.24		99	
<i>Serratia rubidaea</i>	0.01	-.04		99	
502623	Very good identification				502623
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.28	0.57	CEL 92	1	
<i>Serratia rubidaea</i>	3.72	0.12		99	
502631	Acceptable identification				502631
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.00	0.37	MAN 99	1	
<i>Serratia rubidaea</i>	5.00	-.04		99	
502632	Good identification				502632
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.46	0.44	TRE 98	1	
<i>Serratia rubidaea</i>	2.54	-.04		99	
502633	Good identification				502633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.00	0.78		1	
<i>Serratia rubidaea</i>	5.00	0.37		99	
502642	Good identification				502642
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.40	CEL 92		
502643	Very good identification				502643
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.15	0.75	CEL 92	1	
<i>Serratia odorifera biovar 2</i>	0.85	0.24		99	
502651	Low discrimination				502651
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	81.55	0.55	MAN 99	1	
<i>Serratia odorifera biovar 2</i>	18.45	0.34		99	
502652	Very good identification				502652
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.47	0.62	TRE 98	1	
<i>Serratia odorifera biovar 2</i>	3.53	0.24		99	
502653	Good identification				502653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.12	0.96		1	
<i>Serratia odorifera biovar 2</i>	6.88	0.65		99	
502663	Very good identification				502663

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.30	0.62	CEL 92	1	
<i>Serratia marcescens</i>	4.71	0.21		98	
502671	Good identification				502671
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	MAN 99		
502672	Good identification				502672
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.49	TRE 98		
502673	Very good identification				502673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.49	0.84		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.56	0.16		98	
<i>Enterobacter aerogenes</i>	0.43	0.13		98	
502703	Good identification				502703
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.29	0.38	MAL 3	1	
<i>Serratia rubidaea</i>	4.71	-.04	CEL 92	99	
502713	Good identification				502713
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	92.00	0.60	MAL 3	1	
<i>Serratia rubidaea</i>	6.20	0.20		99	
<i>Escherichia vulneris</i>	1.80	0.05		1	
502723	Good identification				502723
				VPT	
<i>Serratia rubidaea</i>	95.14	0.37	SCI 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.86	0.26	CEL 94	1	
502733	Very good identification				502733
				VPT	
<i>Serratia rubidaea</i>	96.05	0.61	SCI 95	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.60	0.47		1	
<i>Enterobacter aerogenes</i>	0.18	-.02		98	
502743	Good identification				502743
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.44	MAL 3		
502753	Very good identification				502753
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.92	0.65	MAL 3	1	
<i>Serratia odorifera</i> biovar 2	2.32	0.24		99	
<i>Enterobacter aerogenes</i>	0.65	-.02		98	
502773	Low discrimination				502773
				VPT	
<i>Enterobacter aerogenes</i>	41.45	0.39	ORN 98	98	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	37.65	0.39	SCI 95	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	15.37	0.53		1	
503113	Good identification				503113
<i>Escherichia vulneris</i>	100.0	0.47	PHE 1		
503413	Good identification				503413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.72	0.48	PHE 1		
<i>Escherichia vulneris</i>	1.28	-.10			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
503433	Low discrimination				503433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	79.53	0.36	PHE 1	1	
<i>Serratia rubidaea</i>	20.47	0.08		99	
503453	Very good identification				503453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.54	PHE 1		
503473	Good identification				503473
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.41	PHE 1		
503613	Good identification				503613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.50	PHE 1		
503633	Acceptable identification				503633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.00	0.37	PHE 1	1	
<i>Serratia rubidaea</i>	5.00	-.04		99	
503653	Good identification				503653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.12	0.55	PHE 1	1	
<i>Serratia odorifera</i> biovar 2	6.88	0.24		99	
503673	Good identification				503673
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.43	PHE 1		
504003	Good identification				504003
<i>Hafnia alvei</i>	92.53	0.63	ORN 98		
<i>Yokenella regensburgei</i>	3.48	0.12			
<i>Escherichia coli</i>	1.39	0.19			
504013	Low discrimination				504013
<i>Yokenella regensburgei</i>	72.06	0.53	ORN 99		
<i>Escherichia vulneris</i>	22.73	0.43			
<i>Hafnia alvei</i>	3.41	0.48			
504023	Low discrimination				504023
<i>Hafnia alvei</i>	87.05	0.44	ORN 98		
<i>Escherichia coli</i>	7.83	0.15	SUC 10		
<i>Citrobacter freundii</i>	5.13	0.15			
504043	Low discrimination				504043
<i>Citrobacter youngae</i>	41.29	0.46	LYS 1		
<i>Escherichia coli</i>	15.21	0.36			
<i>Salmonella bongori</i>	15.17	0.18			
504053	Low discrimination				504053
				VPT	
<i>Serratia odorifera</i> biovar 2	72.14	0.57	INO 99	99	
<i>Citrobacter youngae</i>	11.54	0.44		1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.60	0.44		1	
504063	Low discrimination				504063
<i>Citrobacter freundii</i>	72.11	0.56	LYS 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	8.83	0.34			
<i>Escherichia coli</i>	8.16	0.33			
504073	Low discrimination				504073
<i>Citrobacter freundii</i>	71.15	0.54	LYS 1		
<i>Citrobacter youngae</i>	9.07	0.33			
<i>Serratia ficaria</i>	7.73	0.16			
504103	Good identification				504103
<i>Hafnia alvei</i>	93.10	0.63	ORN 98		
<i>Escherichia vulneris</i>	6.26	0.18			
<i>Citrobacter werkmanii</i>	0.64	-0.04			
504113	Very good identification				504113
<i>Escherichia vulneris</i>	96.81	0.59	SCI 1		
<i>Hafnia alvei</i>	2.57	0.48			
<i>Yokenella regensburgei</i>	0.55	0.12			
504123	Low discrimination				504123
<i>Hafnia alvei</i>	59.76	0.44	ORN 98		
<i>Pantoea agglomerans</i>	27.47	0.18	SUC 10		
<i>Serratia rubidaea</i>	9.63	0.10			
504133	Low discrimination				504133
				VPT	
<i>Escherichia vulneris</i>	62.44	0.37	SCI 1	1	
<i>Serratia rubidaea</i>	30.22	0.34	SUC 8	99	
<i>Pantoea agglomerans</i>	4.33	0.16		64	
504213	Good identification				504213
				VPT	
<i>Serratia odorifera biovar 2</i>	91.52	0.57	SOR 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	5.51	0.40		1	
<i>Yokenella regensburgei</i>	2.26	0.12		1	
504243	Very good identification				504243
				VPT	
<i>Serratia odorifera biovar 2</i>	97.22	0.57	CEL 99	99	
<i>Citrobacter youngae</i>	1.00	0.20		1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.95	0.24		1	
504251	Very good identification				504251
<i>Serratia odorifera biovar 2</i>	100.0	0.67	MAN 97		
504252	Very good identification				504252
				VPT	
<i>Serratia odorifera biovar 2</i>	99.77	0.57	TRE 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.23	0.11		1	
504253	Excellent identification				504253
				VPT	
<i>Serratia odorifera biovar 2</i>	99.88	0.98		99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.11	0.45		1	
<i>Citrobacter youngae</i>	0.01	0.18		1	
504273	Identification to the genus				504273
<i>Serratia odorifera biovar 2</i>	85.62	0.57	SUC 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 1	6.68	0.29			
<i>Serratia ficaria</i>	3.79	0.18			
504353	Very good identification				504353
				VPT	
<i>Serratia odorifera</i> biovar 2	99.66	0.57	MAL 1	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.35	0.14		1	
504403	Good identification				504403
<i>Klebsiella pneumoniae</i> subsp. ozaenae	95.44	0.47	CEL 92		
<i>Hafnia alvei</i>	4.56	0.22			
504413	Very good identification				504413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	96.17	0.69		1	
<i>Yokenella regensburgei</i>	1.49	0.12		1	
<i>Serratia odorifera</i> biovar 2	0.75	0.18		99	
504433	Low discrimination				504433
				VPT	
<i>Serratia rubidaea</i>	74.45	0.51	ESL 94	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	25.55	0.57	MAL 94	1	
504443	Acceptable identification				504443
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	93.43	0.53	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	4.48	0.18		99	
<i>Escherichia coli</i>	1.38	0.10		1	
504452	Low discrimination				504452
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	83.03	0.40	TRE 98	1	
<i>Serratia odorifera</i> biovar 2	16.97	0.18		99	
504453	Low discrimination				504453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	70.75	0.75		1	
<i>Serratia odorifera</i> biovar 2	29.21	0.59		99	
<i>Citrobacter youngae</i>	0.04	0.03		1	
504463	Low discrimination				504463
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	62.89	0.40	CEL 92	1	
<i>Serratia marcescens</i>	30.45	0.19		98	
<i>Citrobacter freundii</i>	4.19	0.15		1	
504473	Very good identification				504473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	95.71	0.62		1	
<i>Serratia odorifera</i> biovar 2	1.60	0.18		99	
<i>Serratia rubidaea</i>	1.52	0.10		99	
504523	Good identification				504523
<i>Serratia rubidaea</i>	100.0	0.51	ESL 94		
504533	Very good identification				504533
				VPT	
<i>Serratia rubidaea</i>	99.91	0.75	ESL 94	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.07	0.26		1	
<i>Escherichia vulneris</i>	0.02	-0.04		1	
504553	Low discrimination				504553

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	86.57	0.44	MAL 3	1	
<i>Serratia odorifera</i> biovar 2	11.68	0.18		99	
<i>Serratia rubidaea</i>	1.76	-.07		99	
504603	Acceptable identification				504603
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.21	0.49	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	6.79	0.18		99	
504612	Low discrimination				504612
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.30	0.36	TRE 98	1	
<i>Serratia odorifera</i> biovar 2	23.70	0.18		99	
504613	Low discrimination				504613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	61.39	0.71		1	
<i>Serratia odorifera</i> biovar 2	38.52	0.59		99	
<i>Serratia rubidaea</i>	0.09	-.03		99	
504623	Low discrimination				504623
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	69.57	0.37	CEL 92	1	
<i>Serratia rubidaea</i>	30.43	0.14		99	
504633	Low discrimination				504633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	61.68	0.59		1	
<i>Serratia rubidaea</i>	36.76	0.38		99	
<i>Serratia odorifera</i> biovar 2	1.56	0.18		99	
504643	Low discrimination				504643
				VPT	
<i>Serratia odorifera</i> biovar 2	79.53	0.59	CEL 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	20.47	0.55		1	
504651	Very good identification				504651
				VPT	
<i>Serratia odorifera</i> biovar 2	99.03	0.69	MAN 97	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.97	0.35		1	
504652	Good identification				504652
				VPT	
<i>Serratia odorifera</i> biovar 2	94.30	0.59	TRE 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.70	0.42		1	
504653	Very good identification				504653
				VPT	
<i>Serratia odorifera</i> biovar 2	97.10	1.00		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.90	0.76		1	
504673	Low discrimination				504673
				VPT	
<i>Serratia odorifera</i> biovar 2	54.31	0.59	SUC 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	40.18	0.64		1	
<i>Serratia odorifera</i> biovar 1	3.47	0.29		50	
504713	Low discrimination				504713
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	50.83	0.40	MAL 3	1	
<i>Serratia rubidaea</i>	38.75	0.22		99	
<i>Serratia odorifera</i> biovar 2	10.42	0.18		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
504723	Good identification				504723
				VPT	
<i>Serratia rubidaea</i>	99.55	0.38	ESL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.45	0.06	CEL 94	1	
504733	Very good identification				504733
				VPT	
<i>Serratia rubidaea</i>	99.54	0.63	ESL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.33	0.27		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.07	-.09		98	
504753	Good identification				504753
				VPT	
<i>Serratia odorifera</i> biovar 2	91.21	0.59	MAL 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	8.35	0.45		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.24	-.09		98	
505253	Very good identification				505253
<i>Serratia odorifera</i> biovar 2	100.0	0.57	PHE 1		
505653	Very good identification				505653
				VPT	
<i>Serratia odorifera</i> biovar 2	97.10	0.59	PHE 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.90	0.35		1	
506003	Low discrimination				506003
<i>Hafnia alvei</i>	49.47	0.44	ORN 98		
<i>Yokenella regensburgei</i>	34.04	0.18	ESL 10		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	11.65	0.29			
506013	Good identification				506013
<i>Yokenella regensburgei</i>	92.34	0.59	ORN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	3.67	0.50			
<i>Escherichia vulneris</i>	3.59	0.31			
506053	Low discrimination				506053
				VPT	
<i>Serratia odorifera</i> biovar 2	59.02	0.54	INO 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	32.42	0.56		1	
<i>Yokenella regensburgei</i>	4.44	0.18		1	
506063	Acceptable identification				506063
				VPT	
<i>Serratia marcescens</i>	93.36	0.49	ORN 99	98	
<i>Serratia ficaria</i>	3.81	0.16		75	
<i>Escherichia coli</i>	1.26	0.20		1	
506073	Good identification				506073
				VPT	
<i>Serratia ficaria</i>	94.81	0.57	LYS 1	75	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.42	0.44		1	
<i>Serratia marcescens</i>	1.24	0.23		98	
506103	Low discrimination				506103
<i>Hafnia alvei</i>	61.11	0.44	ORN 98		
<i>Pantoea agglomerans</i>	28.09	0.18	ESL 10		
<i>Escherichia vulneris</i>	9.25	0.05			
506113	Low discrimination				506113

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Escherichia vulneris</i>	89.24	0.47	SCI 1	1	
<i>Yokenella regensburgei</i>	4.10	0.18		1	
<i>Serratia rubidaea</i>	2.38	0.18		99	
506123	Good identification				506123
<i>Pantoea agglomerans</i>	94.43	0.59	LYS 1		
<i>Serratia rubidaea</i>	5.24	0.34			
<i>Hafnia alvei</i>	0.23	0.24			
506133	Low discrimination				506133
				VPT	
<i>Serratia rubidaea</i>	48.39	0.59	ADO 99	99	
<i>Pantoea agglomerans</i>	43.76	0.57		64	
<i>Kluyvera ascorbata</i>	5.92	0.37		1	
506213	Low discrimination				506213
				VPT	
<i>Serratia odorifera biovar 2</i>	69.32	0.54	SOR 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	25.06	0.52		1	
<i>Yokenella regensburgei</i>	5.21	0.18		1	
506233	Low discrimination				506233
				VPT	
<i>Cronobacter sakazakii</i>	53.69	0.38	LYS 1	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	15.84	0.40	ORN 91	1	
<i>Serratia rubidaea</i>	12.07	0.22		99	
506243	Good identification				506243
				VPT	
<i>Serratia odorifera biovar 2</i>	91.01	0.54	CEL 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	5.31	0.36		1	
<i>Serratia marcescens</i>	3.67	0.18		98	
506251	Very good identification				506251
				VPT	
<i>Serratia odorifera biovar 2</i>	99.78	0.64	MAN 97	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.22	0.17		1	
506252	Very good identification				506252
				VPT	
<i>Serratia odorifera biovar 2</i>	98.65	0.54	TRE 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.35	0.23		1	
506253	Excellent identification				506253
				VPT	
<i>Serratia odorifera biovar 2</i>	99.23	0.95		99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.67	0.58		1	
<i>Serratia ficaria</i>	0.07	0.18		75	
506263	Very good identification				506263
<i>Serratia marcescens</i>	97.05	0.59	ORN 99		
<i>Serratia ficaria</i>	1.61	0.18			
<i>Serratia odorifera biovar 1</i>	0.55	0.14			
506273	Low discrimination				506273
<i>Serratia ficaria</i>	62.05	0.59	LYS 1		
<i>Serratia odorifera biovar 1</i>	20.99	0.55			
<i>Serratia odorifera biovar 2</i>	9.44	0.54			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
506333	Low discrimination				506333
<i>Serratia rubidaea</i>	86.28	0.47	ADO 99		
<i>Cronobacter sakazakii</i>	5.38	0.25			
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	4.22	0.13			
506353	Good identification				506353
				VPT	
<i>Serratia odorifera biovar 2</i>	92.79	0.54	MAL 1	99	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	4.90	0.13		98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.93	0.27		1	
506373	Good identification				506373
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	90.47	0.54	URE 95		
<i>Enterobacter aerogenes</i>	7.10	0.30	ADO 90		
<i>Serratia ficaria</i>	1.15	0.18			
506403	Very good identification				506403
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.93	0.60	CEL 92	1	
<i>Serratia rubidaea</i>	2.07	0.10		99	
506411	Good identification				506411
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.20	0.40	MAN 99	1	
<i>Serratia rubidaea</i>	2.80	-.07		99	
506412	Good identification				506412
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.59	0.47	TRE 98	1	
<i>Serratia rubidaea</i>	1.41	-.07		99	
506413	Very good identification				506413
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.23	0.82		1	
<i>Serratia rubidaea</i>	2.77	0.34		99	
<i>Yokenella regensburgei</i>	0.76	0.18		1	
506423	Low discrimination				506423
				VPT	
<i>Serratia rubidaea</i>	88.93	0.51	MAL 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	10.62	0.47	CEL 94	1	
<i>Serratia marcescens</i>	0.46	0.04		98	
506433	Good identification				506433
				VPT	
<i>Serratia rubidaea</i>	91.94	0.75	MAL 94	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	8.06	0.69		1	
506443	Very good identification				506443
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.64	0.65	CEL 92	1	
<i>Serratia odorifera biovar 2</i>	0.79	0.14		99	
<i>Serratia marcescens</i>	0.57	0.04		98	
506451	Low discrimination				506451
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	82.60	0.46	MAN 99	1	
<i>Serratia odorifera biovar 2</i>	17.41	0.24		99	
506452	Good identification				506452
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.71	0.52	TRE 98	1	
<i>Serratia odorifera</i> biovar 2	3.29	0.14		99	
506453	Good identification				506453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.55	0.87		1	
<i>Serratia odorifera</i> biovar 2	6.44	0.55		99	
<i>Serratia rubidaea</i>	0.02	-0.7		99	
506463	Low discrimination				506463
				VPT	
<i>Serratia marcescens</i>	68.55	0.46	ORN 99	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	29.80	0.53		1	
<i>Serratia rubidaea</i>	1.36	0.10		99	
506472	Good identification				506472
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.02	0.40	TRE 98	1	
<i>Serratia rubidaea</i>	2.98	-0.7		99	
506473	Low discrimination				506473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	87.13	0.75		1	
<i>Serratia rubidaea</i>	5.41	0.34		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	3.66	0.24		98	
506513	Good identification				506513
				VPT	
<i>Serratia rubidaea</i>	93.16	0.59	SUC 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.38	0.50		1	
<i>Escherichia vulneris</i>	0.36	0.05		1	
506523	Very good identification				506523
				VPT	
<i>Serratia rubidaea</i>	99.79	0.75	CEL 94	99	
<i>Pantoea agglomerans</i>	0.18	0.18		64	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.02	0.16		1	
506531	Very good identification				506531
<i>Serratia rubidaea</i>	100.0	0.59	MAN 99		
506532	Very good identification				506532
<i>Serratia rubidaea</i>	100.0	0.59	TRE 99		
506533	Excellent identification				506533
				VPT	
<i>Serratia rubidaea</i>	99.96	1.00		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.02	0.38		1	
<i>Pantoea agglomerans</i>	0.01	0.16		64	
506553	Low discrimination				506553
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	85.70	0.56	MAL 3	1	
<i>Serratia rubidaea</i>	6.81	0.18		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	3.90	0.06		98	
506573	Low discrimination				506573
<i>Serratia rubidaea</i>	53.84	0.59	SOR 1		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	30.85	0.47			
<i>Enterobacter aerogenes</i>	13.17	0.39			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
506603	Very good identification				506603
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.38	0.61	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	1.20	0.14		99	
<i>Serratia rubidaea</i>	0.43	-.03		99	
506611	Low discrimination				506611
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	75.75	0.42	MAN 99	1	
<i>Serratia odorifera</i> biovar 2	24.25	0.24		99	
506612	Good identification				506612
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.08	0.49	TRE 98	1	
<i>Serratia odorifera</i> biovar 2	4.92	0.14		99	
506613	Good identification				506613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	90.05	0.83		1	
<i>Serratia odorifera</i> biovar 2	9.42	0.55		99	
<i>Serratia rubidaea</i>	0.53	0.22		99	
506623	Low discrimination				506623
				VPT	
<i>Serratia rubidaea</i>	60.78	0.38	MAL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	35.47	0.49	CEL 94	1	
<i>Serratia marcescens</i>	3.76	0.14		98	
506633	Low discrimination				506633
				VPT	
<i>Serratia rubidaea</i>	69.41	0.63	MAL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	29.73	0.71		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.36	0.10		98	
506643	Low discrimination				506643
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	60.18	0.67	CEL 92	1	
<i>Serratia odorifera</i> biovar 2	38.97	0.55		99	
<i>Serratia marcescens</i>	0.86	0.14		98	
506651	Good identification				506651
				VPT	
<i>Serratia odorifera</i> biovar 2	94.47	0.65	MAN 97	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.53	0.48		1	
506652	Low discrimination				506652
				VPT	
<i>Serratia odorifera</i> biovar 2	73.40	0.55	TRE 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	26.60	0.54		1	
506653	Low discrimination				506653
				VPT	
<i>Serratia odorifera</i> biovar 2	84.75	0.96		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	15.20	0.89		1	
<i>Serratia odorifera</i> biovar 1	0.02	0.14		50	
506663	Low discrimination				506663
				VPT	
<i>Serratia marcescens</i>	81.77	0.55	ORN 99	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	14.48	0.55		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2.22	0.16		98	
506671	Low discrimination				506671

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	33.95	0.35	MAN 99	1	
<i>Serratia odorifera</i> biovar 2	23.41	0.24		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	22.13	0.10		98	
506672	Low discrimination				506672
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	57.69	0.42	TRE 98	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	18.62	0.10		98	
<i>Serratia odorifera</i> biovar 1	11.70	0.14		50	
506673	Low discrimination				506673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	39.42	0.76		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	25.71	0.51		98	
<i>Serratia odorifera</i> biovar 1	16.15	0.55		50	
506713	Low discrimination				506713
				VPT	
<i>Serratia rubidaea</i>	73.93	0.47	SUC 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	24.76	0.52		1	
<i>Serratia odorifera</i> biovar 2	0.85	0.14		99	
506723	Very good identification				506723
				VPT	
<i>Serratia rubidaea</i>	99.71	0.63	CEL 94	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.14	-.02		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.12	0.18		1	
506731	Good identification				506731
<i>Serratia rubidaea</i>	99.37	0.47	MAN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.44	-.09			
<i>Enterobacter aerogenes</i>	0.19	-.17			
506732	Good identification				506732
<i>Serratia rubidaea</i>	99.37	0.47	TRE 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.44	-.09			
<i>Enterobacter aerogenes</i>	0.19	-.17			
506733	Very good identification				506733
<i>Serratia rubidaea</i>	99.28	0.88			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.44	0.33			
<i>Enterobacter aerogenes</i>	0.19	0.24			
506743	Low discrimination				506743
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	70.79	0.36	MAL 3	1	
<i>Serratia odorifera</i> biovar 2	14.97	0.14	CEL 92	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	11.75	-.02		98	
506753	Low discrimination				506753
				VPT	
<i>Serratia odorifera</i> biovar 2	47.13	0.55	MAL 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	25.89	0.58		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	18.31	0.33		98	
506763	Low discrimination				506763
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	71.63	0.39	URE 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter aerogenes</i>	15.14	0.24	CEL 98		
<i>Serratia marcescens</i>	6.15	0.24			
506773	Low discrimination				506773
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	67.65	0.74	URE 95		
<i>Enterobacter aerogenes</i>	28.88	0.65			
<i>Klebsiella oxytoca</i>	1.62	0.39			
507123	Good identification				507123
<i>Pantoea agglomerans</i>	99.44	0.38	LYS 1		
<i>Serratia rubidaea</i>	0.56	-.07	PHE 9		
507133	Low discrimination				507133
<i>Pantoea agglomerans</i>	84.40	0.36	LYS 1		
<i>Serratia rubidaea</i>	9.53	0.18	PHE 9		
<i>Cronobacter sakazakii</i>	4.90	0.15			
507233	Good identification				507233
<i>Cronobacter sakazakii</i>	100.0	0.38	LYS 1		
507253	Very good identification				507253
				VPT	
<i>Serratia odorifera biovar 2</i>	99.33	0.54	PHE 1	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.67	0.17		1	
507413	Good identification				507413
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.20	0.40	PHE 1	1	
<i>Serratia rubidaea</i>	2.80	-.07		99	
507453	Acceptable identification				507453
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.56	0.46	PHE 1	1	
<i>Serratia odorifera biovar 2</i>	6.44	0.14		99	
507533	Very good identification				507533
<i>Serratia rubidaea</i>	99.91	0.59	PHE 1		
<i>Pantoea agglomerans</i>	0.09	-.05			
507613	Acceptable identification				507613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	90.53	0.42	PHE 1	1	
<i>Serratia odorifera biovar 2</i>	9.47	0.14		99	
507653	Low discrimination				507653
				VPT	
<i>Serratia odorifera biovar 2</i>	84.79	0.55	PHE 1	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	15.21	0.48		1	
507673	Low discrimination				507673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	40.30	0.35	PHE 1	1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	26.28	0.10		98	
<i>Serratia odorifera biovar 1</i>	16.50	0.14		50	
507733	Good identification				507733
<i>Serratia rubidaea</i>	99.37	0.47	PHE 1		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.44	-.09			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Enterobacter aerogenes</i>	0.19	-.17			
510001	Low discrimination				510001
<i>Shigella dysenteriae</i> (group A)	54.14	0.50	LYS 1		
<i>Escherichia coli</i>	45.63	0.55			
<i>Shigella boydii</i> (group C)	0.23	-.02			
510002	Very good identification				510002
<i>Escherichia coli</i>	95.70	0.55	SOR 88		
<i>Shigella boydii</i> (group C)	2.80	0.14	TRE 95		
<i>Shigella flexneri</i> (group B)	1.50	0.12			
510003	Very good identification				510003
<i>Escherichia coli</i>	98.67	0.82	SOR 88		
<i>Shigella boydii</i> (group C)	0.86	0.30			
<i>Shigella flexneri</i> (group B)	0.17	0.18			
510013	Low discrimination				510013
<i>Escherichia vulneris</i>	60.02	0.43	IND 1		
<i>Escherichia coli</i>	17.78	0.47			
<i>Escherichia hermannii</i>	12.16	0.34			
510021	Good identification				510021
<i>Escherichia coli</i>	98.23	0.52	SOR 88		
<i>Shigella dysenteriae</i> (group A)	1.77	0.09	MAN 95		
510022	Good identification				510022
<i>Escherichia coli</i>	100.0	0.52	SOR 88		
510023	Very good identification				510023
<i>Escherichia coli</i>	99.95	0.78	SOR 88		
<i>Escherichia hermannii</i>	0.05	0.02			
510033	Identification to the genus				510033
<i>Escherichia coli</i>	43.86	0.43	CEL 2		
<i>Escherichia hermannii</i>	36.82	0.33	SOR 88		
<i>Escherichia vulneris</i>	19.32	0.22			
510040	Low discrimination				510040
<i>Escherichia coli</i>	87.23	0.47	TRE 95		
<i>Shigella dysenteriae</i> (group A)	12.77	0.22	MAN 95		
510041	Good identification				510041
<i>Escherichia coli</i>	93.47	0.73	MAN 95		
<i>Shigella dysenteriae</i> (group A)	6.48	0.42			
<i>Shigella boydii</i> (group C)	0.05	-.04			
510042	Very good identification				510042
<i>Escherichia coli</i>	99.61	0.73	TRE 95		
<i>Shigella boydii</i> (group C)	0.30	0.11			
<i>Shigella flexneri</i> (group B)	0.09	0.04			
510043	Excellent identification				510043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	99.87	0.99			
<i>Shigella boydii</i> (group C)	0.09	0.27			
<i>Citrobacter youngae</i>	0.02	0.21			
510051	Good identification				510051
<i>Escherichia coli</i>	96.68	0.38	CEL 2		
<i>Shigella dysenteriae</i> (group A)	3.32	0.01	MAN 95		
510052	Good identification				510052
<i>Escherichia coli</i>	100.0	0.38	CEL 2		
510053	Good identification				510053
				VPT	
<i>Escherichia coli</i>	94.68	0.65	CEL 2	1	
<i>Serratia odorifera</i> biovar 2	1.75	0.26		99	
<i>Yersinia kristensenii</i>	1.54	0.19		1	
510060	Good identification				510060
<i>Escherichia coli</i>	100.0	0.43	TRE 95		
510061	Very good identification				510061
<i>Escherichia coli</i>	99.90	0.69	MAN 95		
<i>Shigella dysenteriae</i> (group A)	0.11	0.01			
510062	Very good identification				510062
<i>Escherichia coli</i>	100.0	0.69	TRE 95		
510063	Excellent identification				510063
<i>Escherichia coli</i>	99.86	0.96			
<i>Citrobacter freundii</i>	0.10	0.37			
<i>Yersinia rohdei</i>	0.02	0.18			
510073	Good identification				510073
<i>Escherichia coli</i>	91.05	0.61	CEL 2		
<i>Citrobacter farmeri</i>	3.40	0.18			
<i>Citrobacter freundii</i>	3.35	0.35			
510103	Low discrimination				510103
<i>Escherichia coli</i>	67.53	0.40	MAL 1		
<i>Escherichia vulneris</i>	26.37	0.18	SOR 88		
<i>Hafnia alvei</i>	3.96	0.22			
510113	Very good identification				510113
<i>Escherichia vulneris</i>	98.38	0.59	IND 1		
<i>Escherichia fergusonii</i>	1.54	0.30			
<i>Escherichia coli</i>	0.05	0.06			
510123	Good identification				510123
<i>Escherichia coli</i>	95.15	0.37	MAL 1		
<i>Escherichia vulneris</i>	4.85	-.04	SOR 88		
510133	Good identification				510133

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia vulneris</i>	98.36	0.37	IND 1		
<i>Leclercia adecarboxylata</i>	0.46	-.05	SUC 8		
<i>Kluyvera ascorbata</i>	0.44	-.11			
510143	Very good identification				510143
<i>Escherichia coli</i>	100.0	0.58	MAL 1		
510163	Very good identification				510163
<i>Escherichia coli</i>	99.18	0.55	MAL 1		
<i>Citrobacter freundii</i>	0.82	0.15			
510203	Good identification				510203
<i>Escherichia coli</i>	100.0	0.40	INO 1		
510223	Good identification				510223
<i>Escherichia coli</i>	100.0	0.37	INO 1		
510243	Very good identification				510243
				VPT	
<i>Escherichia coli</i>	96.40	0.58	INO 1	1	
<i>Serratia odorifera biovar 2</i>	3.60	0.26		99	
510251	Good identification				510251
<i>Serratia odorifera biovar 2</i>	100.0	0.36	SCI 97		
510253	Very good identification				510253
				VPT	
<i>Serratia odorifera biovar 2</i>	99.21	0.67	SCI 97	99	
<i>Escherichia coli</i>	0.55	0.23		1	
<i>Yersinia kristensenii</i>	0.16	0.03		1	
510263	Very good identification				510263
<i>Escherichia coli</i>	99.52	0.55	INO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.48	0.05			
510403	Identification to the genus				510403
<i>Escherichia coli</i>	86.50	0.55	ADO 5		
<i>Escherichia fergusonii</i>	13.02	0.33	SOR 88		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.48	0.14			
510413	Very good identification				510413
<i>Escherichia fergusonii</i>	96.62	0.59	ORN 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.16	0.36			
<i>Escherichia coli</i>	0.69	0.20			
510423	Good identification				510423
<i>Escherichia coli</i>	100.0	0.52	ADO 5		
510441	Good identification				510441
<i>Escherichia coli</i>	98.69	0.47	ADO 5		
<i>Shigella dysenteriae (group A)</i>	1.31	0.01	MAN 95		
510442	Good identification				510442
<i>Escherichia coli</i>	100.0	0.47	ADO 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
510443	Very good identification				510443
<i>Escherichia coli</i>	99.86	0.73	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.14	0.19			
510453	Low discrimination				510453
				VPT	
<i>Escherichia coli</i>	41.42	0.38	ADO 5	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	32.81	0.41	CEL 2	1	
<i>Serratia odorifera biovar 2</i>	17.78	0.28		99	
510461	Good identification				510461
<i>Escherichia coli</i>	100.0	0.43	ADO 5		
510462	Good identification				510462
<i>Escherichia coli</i>	100.0	0.43	ADO 5		
510463	Very good identification				510463
<i>Escherichia coli</i>	99.95	0.69	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.05	0.07			
510513	Good identification				510513
<i>Escherichia fergusonii</i>	94.15	0.53	ORN 99		
<i>Escherichia vulneris</i>	4.58	0.18			
<i>Leclercia adecarboxylata</i>	1.27	0.12			
510613	Low discrimination				510613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	45.59	0.37	IND 1	1	
<i>Serratia odorifera biovar 2</i>	37.54	0.28		99	
<i>Escherichia fergusonii</i>	16.88	0.18		1	
510651	Good identification				510651
<i>Serratia odorifera biovar 2</i>	100.0	0.38	SCI 97		
510653	Very good identification				510653
				VPT	
<i>Serratia odorifera biovar 2</i>	97.77	0.69	SCI 97	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.23	0.43		1	
511003	Good identification				511003
<i>Escherichia coli</i>	100.0	0.40	PHE 1		
511023	Good identification				511023
<i>Escherichia coli</i>	100.0	0.37	PHE 1		
511043	Very good identification				511043
<i>Escherichia coli</i>	100.0	0.58	PHE 1		
511063	Very good identification				511063
<i>Escherichia coli</i>	100.0	0.55	PHE 1		
512001	Good identification				512001
<i>Escherichia coli</i>	95.43	0.43	SOR 88		
<i>Shigella dysenteriae (group A)</i>	4.57	0.09	MAN 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
512002	Good identification				512002
<i>Escherichia coli</i>	100.0	0.43	SOR 88		
512003	Very good identification				512003
<i>Escherichia coli</i>	99.52	0.69	SOR 88		
<i>Escherichia fergusonii</i>	0.20	0.08			
<i>Escherichia hermannii</i>	0.12	0.00			
512021	Good identification				512021
<i>Escherichia coli</i>	100.0	0.39	SOR 88		
512022	Good identification				512022
<i>Escherichia coli</i>	100.0	0.39	SOR 88		
512023	Very good identification				512023
<i>Escherichia coli</i>	99.86	0.66	SOR 88		
<i>Escherichia hermannii</i>	0.14	-.02			
512041	Very good identification				512041
<i>Escherichia coli</i>	99.72	0.61	MAN 95		
<i>Shigella dysenteriae (group A)</i>	0.28	0.01			
512042	Very good identification				512042
<i>Escherichia coli</i>	100.0	0.61	TRE 95		
512043	Very good identification				512043
<i>Escherichia coli</i>	100.0	0.87			
512053	Acceptable identification				512053
				VPT	
<i>Escherichia coli</i>	93.06	0.52	CEL 2	1	
<i>Serratia odorifera biovar 2</i>	4.59	0.22		99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.92	0.22		1	
512061	Very good identification				512061
<i>Escherichia coli</i>	100.0	0.57	MAN 95		
512062	Very good identification				512062
<i>Escherichia coli</i>	100.0	0.57	TRE 95		
512063	Very good identification				512063
<i>Escherichia coli</i>	99.99	0.83			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.02	0.03			
512073	Good identification				512073
<i>Escherichia coli</i>	95.53	0.49	CEL 2		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.12	0.13			
<i>Kluyvera ascorbata</i>	1.61	-.02			
512113	Low discrimination				512113
<i>Escherichia vulneris</i>	87.75	0.47	IND 1		
<i>Leclercia adecarboxylata</i>	7.31	0.30			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	4.67	0.29			
512133	Low discrimination				512133
<i>Leclercia adecarboxylata</i>	39.35	0.36	LYS 1		
<i>Kluyvera ascorbata</i>	37.66	0.31	ADO 93		
<i>Escherichia vulneris</i>	21.18	0.25			
512143	Good identification				512143
<i>Escherichia coli</i>	100.0	0.46	MAL 1		
512163	Good identification				512163
<i>Escherichia coli</i>	100.0	0.42	MAL 1		
512243	Acceptable identification				512243
				VPT	
<i>Escherichia coli</i>	90.94	0.46	INO 1	1	
<i>Serratia odorifera biovar 2</i>	9.06	0.22		99	
512253	Very good identification				512253
				VPT	
<i>Serratia odorifera biovar 2</i>	99.28	0.64	SCI 97	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.51	0.24		1	
<i>Escherichia coli</i>	0.21	0.11		1	
512263	Good identification				512263
<i>Escherichia coli</i>	100.0	0.42	INO 1		
512403	Low discrimination				512403
<i>Escherichia coli</i>	62.44	0.43	ADO 5		
<i>Escherichia fergusonii</i>	32.02	0.31	SOR 88		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	5.55	0.26			
512413	Low discrimination				512413
<i>Escherichia fergusonii</i>	85.35	0.58	ORN 99		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	8.95	0.48			
<i>Leclercia adecarboxylata</i>	5.41	0.30			
512423	Good identification				512423
<i>Escherichia coli</i>	95.11	0.39	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.17	0.14	SOR 88		
<i>Leclercia adecarboxylata</i>	1.73	-0.05			
512433	Low discrimination				512433
<i>Leclercia adecarboxylata</i>	73.46	0.36	LYS 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	15.65	0.36	MAL 93		
<i>Escherichia fergusonii</i>	6.03	0.16			
512443	Very good identification				512443
<i>Escherichia coli</i>	97.80	0.61	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.20	0.32			
512453	Low discrimination				512453
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	81.89	0.54	IND 1	1	
<i>Serratia odorifera biovar 2</i>	7.40	0.24		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	6.46	0.26		1	
512463	Very good identification				512463
<i>Escherichia coli</i>	99.16	0.57	ADO 5		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.84	0.19			
512473	Low discrimination				512473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.41	0.41	IND 1		
<i>Escherichia coli</i>	16.71	0.22			
<i>Leclercia adecarboxylata</i>	2.03	-.05			
512513	Low discrimination				512513
<i>Leclercia adecarboxylata</i>	60.47	0.53	LYS 1		
<i>Escherichia fergusonii</i>	38.67	0.52			
<i>Escherichia vulneris</i>	0.55	0.05			
512533	Good identification				512533
				VPT	
<i>Leclercia adecarboxylata</i>	93.57	0.59	LYS 1	1	
<i>Serratia rubidaea</i>	6.05	0.33		99	
<i>Escherichia fergusonii</i>	0.31	0.11		1	
512613	Low discrimination				512613
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	82.23	0.50	IND 1	1	
<i>Serratia odorifera biovar 2</i>	11.28	0.24		99	
<i>Escherichia fergusonii</i>	6.48	0.16		1	
512633	Acceptable identification				512633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	91.62	0.37	IND 1	1	
<i>Serratia rubidaea</i>	4.82	-.04		99	
<i>Leclercia adecarboxylata</i>	3.56	-.05		1	
512653	Low discrimination				512653
				VPT	
<i>Serratia odorifera biovar 2</i>	87.97	0.65	SCI 97	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	12.03	0.55		1	
512673	Low discrimination				512673
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	40.11	0.43	IND 1	1	
<i>Klebsiella oxytoca</i>	37.47	0.19		95	
<i>Serratia odorifera biovar 2</i>	11.86	0.24		99	
512773	Very good identification				512773
<i>Klebsiella oxytoca</i>	99.59	0.54	URE 90		
<i>Enterobacter aerogenes</i>	0.18	-.02	SCI 95		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.17	-.02			
513043	Good identification				513043
<i>Escherichia coli</i>	100.0	0.46	PHE 1		
513063	Good identification				513063
<i>Escherichia coli</i>	100.0	0.42	PHE 1		
514003	Acceptable identification				514003

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	93.40	0.40	SCI 1		
<i>Hafnia alvei</i>	5.47	0.22	SOR 88		
<i>Escherichia fergusonii</i>	1.13	-.05			
514023	Good identification				514023
<i>Escherichia coli</i>	97.27	0.37	SCI 1		
<i>Citrobacter freundii</i>	2.73	0.08	SOR 88		
514043	Good identification				514043
<i>Escherichia coli</i>	90.77	0.58	SCI 1		
<i>Citrobacter youngae</i>	3.78	0.31			
<i>Citrobacter freundii</i>	2.83	0.31			
514053	Low discrimination				514053
				VPT	
<i>Serratia odorifera biovar 2</i>	87.94	0.57	INO 99	99	
<i>Citrobacter amalonaticus</i>	3.85	0.17		1	
<i>Citrobacter youngae</i>	2.48	0.29		1	
514063	Low discrimination				514063
<i>Escherichia coli</i>	71.68	0.55	SCI 1		
<i>Citrobacter freundii</i>	27.13	0.49			
<i>Citrobacter youngae</i>	1.19	0.19			
514073	Low discrimination				514073
				VPT	
<i>Citrobacter freundii</i>	81.05	0.47	LYS 1	1	
<i>Escherichia coli</i>	5.56	0.20		1	
<i>Serratia odorifera biovar 2</i>	4.99	0.16		99	
514213	Very good identification				514213
<i>Serratia odorifera biovar 2</i>	100.0	0.57	SOR 99		
514243	Very good identification				514243
				VPT	
<i>Serratia odorifera biovar 2</i>	98.99	0.57	CEL 99	99	
<i>Escherichia coli</i>	0.83	0.17		1	
<i>Citrobacter youngae</i>	0.18	0.04		1	
514251	Very good identification				514251
<i>Serratia odorifera biovar 2</i>	100.0	0.67	MAN 97		
514252	Very good identification				514252
<i>Serratia odorifera biovar 2</i>	100.0	0.57	TRE 99		
514253	Excellent identification				514253
				VPT	
<i>Serratia odorifera biovar 2</i>	100.0	0.98		99	
<i>Citrobacter youngae</i>	0.00	0.03		1	
514273	Identification to the genus				514273
				VPT	
<i>Serratia odorifera biovar 2</i>	89.40	0.57	SUC 1	99	
<i>Serratia odorifera biovar 1</i>	10.46	0.33		50	
<i>Citrobacter freundii</i>	0.15	0.06		1	
514353	Very good identification				514353

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 2	100.0	0.57	MAL 1		
514413	Acceptable identification				514413
				VPT	
<i>Escherichia fergusonii</i>	92.38	0.45	ORN 99	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	4.32	0.28		1	
<i>Serratia odorifera</i> biovar 2	3.31	0.18		99	
514453	Very good identification				514453
				VPT	
<i>Serratia odorifera</i> biovar 2	97.34	0.59	INO 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.38	0.34		1	
<i>Escherichia fergusonii</i>	0.28	0.04		1	
514513	Good identification				514513
				VPT	
<i>Escherichia fergusonii</i>	99.01	0.39	ORN 99	1	
<i>Serratia rubidaea</i>	0.99	-.07		99	
514613	Very good identification				514613
				VPT	
<i>Serratia odorifera</i> biovar 2	98.14	0.59	SOR 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.58	0.30		1	
<i>Escherichia fergusonii</i>	0.28	0.04		1	
514643	Very good identification				514643
				VPT	
<i>Serratia odorifera</i> biovar 2	99.74	0.59	CEL 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.26	0.14		1	
514651	Very good identification				514651
<i>Serratia odorifera</i> biovar 2	100.0	0.69	MAN 97		
514652	Very good identification				514652
<i>Serratia odorifera</i> biovar 2	100.0	0.59	TRE 99		
514653	Excellent identification				514653
				VPT	
<i>Serratia odorifera</i> biovar 2	99.97	1.00		99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.03	0.35		1	
514673	Identification to the genus				514673
<i>Serratia odorifera</i> biovar 2	89.63	0.59	SUC 1		
<i>Serratia odorifera</i> biovar 1	8.58	0.33			
<i>Klebsiella oxytoca</i>	1.12	0.05			
514753	Very good identification				514753
<i>Serratia odorifera</i> biovar 2	99.39	0.59	MAL 1		
<i>Klebsiella oxytoca</i>	0.62	-.02			
514773	Good identification				514773
<i>Klebsiella oxytoca</i>	97.62	0.39	URE 90		
<i>Serratia odorifera</i> biovar 2	1.61	0.18	ESL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.42	-.09			
515201	Good identification				515201
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
515221	Good identification				515221

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Providencia stuartii</i>	100.0	0.39	ONP 10		
515253	Very good identification				515253
<i>Serratia odorifera biovar 2</i>	100.0	0.57	PHE 1		
515653	Very good identification				515653
<i>Serratia odorifera biovar 2</i>	100.0	0.59	PHE 1		
516043	Good identification				516043
				VPT	
<i>Escherichia coli</i>	96.03	0.46	SCI 1	1	
<i>Serratia odorifera biovar 2</i>	3.12	0.12		99	
<i>Citrobacter youngae</i>	0.84	0.04		1	
516053	Very good identification				516053
				VPT	
<i>Serratia odorifera biovar 2</i>	97.65	0.54	INO 99	99	
<i>Citrobacter amalonaticus</i>	0.63	-.04		1	
<i>Escherichia coli</i>	0.62	0.11		1	
516063	Acceptable identification				516063
				VPT	
<i>Escherichia coli</i>	92.57	0.42	SCI 1	1	
<i>Serratia marcescens</i>	6.02	0.08		98	
<i>Citrobacter freundii</i>	1.42	0.08		1	
516133	Very good identification				516133
				VPT	
<i>Kluyvera ascorbata</i>	98.56	0.59	ORN 99	1	
<i>Serratia rubidaea</i>	0.71	0.18		99	
<i>Pantoea agglomerans</i>	0.64	0.16		64	
516173	Very good identification				516173
				VPT	
<i>Kluyvera ascorbata</i>	99.37	0.55	ORN 99	1	
<i>Klebsiella oxytoca</i>	0.56	0.05		95	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.07	-.13		98	
516213	Very good identification				516213
				VPT	
<i>Serratia odorifera biovar 2</i>	99.64	0.54	SOR 99	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.36	0.11		1	
516243	Very good identification				516243
				VPT	
<i>Serratia odorifera biovar 2</i>	99.69	0.54	CEL 99	99	
<i>Escherichia coli</i>	0.31	0.05		1	
516251	Very good identification				516251
<i>Serratia odorifera biovar 2</i>	100.0	0.64	MAN 97		
516252	Very good identification				516252
<i>Serratia odorifera biovar 2</i>	100.0	0.54	TRE 99		
516253	Excellent identification				516253
				VPT	
<i>Serratia odorifera biovar 2</i>	99.96	0.95		99	
<i>Serratia odorifera biovar 1</i>	0.03	0.18		50	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.01	0.17		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
516273	Identification to the genus				516273
<i>Serratia odorifera</i> biovar 1	75.27	0.59	ORN 99		
<i>Serratia odorifera</i> biovar 2	22.58	0.54			
<i>Serratia ficaria</i>	1.50	0.18			
516353	Very good identification				516353
<i>Serratia odorifera</i> biovar 2	98.88	0.54	MAL 1		
<i>Klebsiella oxytoca</i>	1.12	-.02			
516373	Low discrimination				516373
				VPT	
<i>Klebsiella oxytoca</i>	88.81	0.39	URE 90	95	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	4.17	0.13	ADO 99	98	
<i>Kluyvera ascorbata</i>	3.23	0.14		1	
516413	Low discrimination				516413
				VPT	
<i>Escherichia fergusonii</i>	79.76	0.43	ORN 99	1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	17.50	0.40		1	
<i>Serratia odorifera</i> biovar 2	2.24	0.14		99	
516453	Low discrimination				516453
				VPT	
<i>Serratia odorifera</i> biovar 2	86.93	0.55	INO 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	12.76	0.46		1	
<i>Escherichia fergusonii</i>	0.32	0.02		1	
516513	Low discrimination				516513
				VPT	
<i>Escherichia fergusonii</i>	78.51	0.38	ORN 99	1	
<i>Serratia rubidaea</i>	14.44	0.18		99	
<i>Leclercia adecarboxylata</i>	6.06	0.12		1	
516533	Very good identification				516533
				VPT	
<i>Serratia rubidaea</i>	97.25	0.59	IND 1	99	
<i>Kluyvera ascorbata</i>	1.38	0.18		1	
<i>Leclercia adecarboxylata</i>	0.80	0.18		1	
516573	Acceptable identification				516573
				VPT	
<i>Klebsiella oxytoca</i>	94.97	0.46	URE 90	95	
<i>Serratia rubidaea</i>	1.83	0.18	INO 98	99	
<i>Kluyvera ascorbata</i>	1.71	0.14		1	
516613	Good identification				516613
				VPT	
<i>Serratia odorifera</i> biovar 2	90.89	0.55	SOR 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	8.78	0.42		1	
<i>Escherichia fergusonii</i>	0.33	0.02		1	
516643	Very good identification				516643
				VPT	
<i>Serratia odorifera</i> biovar 2	98.46	0.55	CEL 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.54	0.26		1	
516651	Very good identification				516651
				VPT	
<i>Serratia odorifera</i> biovar 2	99.94	0.65	MAN 97	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.06	0.07		1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
516652	Very good identification				516652
				VPT	
<i>Serratia odorifera</i> biovar 2	99.64	0.55	TRE 99	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.37	0.13		1	
516653	Excellent identification				516653
				VPT	
<i>Serratia odorifera</i> biovar 2	99.77	0.96		99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.18	0.48		1	
<i>Serratia odorifera</i> biovar 1	0.03	0.18		50	
516673	Low discrimination				516673
<i>Serratia odorifera</i> biovar 1	48.13	0.59	ORN 99		
<i>Klebsiella oxytoca</i>	32.77	0.46			
<i>Serratia odorifera</i> biovar 2	17.65	0.55			
516733	Low discrimination				516733
<i>Klebsiella oxytoca</i>	50.84	0.39	URE 90		
<i>Serratia rubidaea</i>	48.85	0.47	SOR 99		
<i>Klebsiella pneumoniae</i> subsp. pneumoniae	0.22	-.09			
516753	Low discrimination				516753
				VPT	
<i>Serratia odorifera</i> biovar 2	51.81	0.55	MAL 1	99	
<i>Klebsiella oxytoca</i>	47.62	0.39		95	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.29	0.17		1	
516763	Good identification				516763
<i>Klebsiella oxytoca</i>	98.97	0.39	URE 90		
<i>Klebsiella pneumoniae</i> subsp. pneumoniae	0.85	-.02	CEL 99		
<i>Enterobacter aerogenes</i>	0.18	-.17			
516771	Good identification				516771
<i>Klebsiella oxytoca</i>	99.39	0.39	URE 90		
<i>Klebsiella pneumoniae</i> subsp. pneumoniae	0.42	-.09	MAN 99		
<i>Enterobacter aerogenes</i>	0.18	-.17			
516772	Good identification				516772
<i>Klebsiella oxytoca</i>	99.39	0.39	URE 90		
<i>Klebsiella pneumoniae</i> subsp. pneumoniae	0.42	-.09	TRE 99		
<i>Enterobacter aerogenes</i>	0.18	-.17			
516773	Very good identification				516773
<i>Klebsiella oxytoca</i>	99.34	0.80	URE 90		
<i>Klebsiella pneumoniae</i> subsp. pneumoniae	0.42	0.33			
<i>Enterobacter aerogenes</i>	0.18	0.24			
517253	Very good identification				517253
<i>Serratia odorifera</i> biovar 2	100.0	0.54	PHE 1		
517653	Very good identification				517653
				VPT	
<i>Serratia odorifera</i> biovar 2	99.82	0.55	PHE 1	99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.18	0.07		1	
517773	Good identification				517773

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella oxytoca</i>	99.39	0.39	URE 90		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.42	-.09	PHE 1		
<i>Enterobacter aerogenes</i>	0.18	-.17			
520001	Low discrimination				520001
<i>Hafnia alvei</i>	70.50	0.57	MAN 99		
<i>Shigella sonnei</i>	14.80	0.18			
<i>Escherichia coli</i>	12.05	0.34			
520002	Low discrimination				520002
<i>Hafnia alvei</i>	43.86	0.57	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	39.15	0.39			
<i>Shigella sonnei</i>	9.21	0.18			
520003	Low discrimination				520003
<i>Hafnia alvei</i>	79.96	0.98			
<i>Shigella sonnei</i>	16.79	0.59			
<i>Escherichia coli</i>	2.62	0.60			
520013	Low discrimination				520013
<i>Yokenella regensburgei</i>	74.39	0.72	SCI 92		
<i>Hafnia alvei</i>	20.05	0.83			
<i>Escherichia vulneris</i>	2.73	0.43			
520023	Low discrimination				520023
<i>Hafnia alvei</i>	82.05	0.79	SUC 10		
<i>Escherichia coli</i>	16.15	0.57			
<i>Shigella sonnei</i>	1.57	0.18			
520033	Low discrimination				520033
<i>Hafnia alvei</i>	59.27	0.63	SUC 10		
<i>Yokenella regensburgei</i>	20.00	0.31			
<i>Escherichia hermannii</i>	12.02	0.33			
520041	Good identification				520041
<i>Escherichia coli</i>	96.91	0.52	IND 92		
<i>Salmonella bongori</i>	1.09	-.07	MAN 95		
<i>Shigella dysenteriae (group A)</i>	0.88	0.03			
520042	Low discrimination				520042
<i>Salmonella enterica subsp. enterica</i>	86.24	0.59	ONP 1		
<i>Escherichia coli</i>	13.46	0.52			
<i>Salmonella bongori</i>	0.15	-.07			
520043	Low discrimination				520043
<i>Escherichia coli</i>	86.64	0.78	IND 92		
<i>Salmonella bongori</i>	5.09	0.34			
<i>Hafnia alvei</i>	3.64	0.57			
520053	Low discrimination				520053
<i>Yersinia kristensenii</i>	49.87	0.48	LYS 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	17.19	0.49			
<i>Yokenella regensburgei</i>	14.49	0.31			
520061	Good identification				520061
<i>Escherichia coli</i>	97.54	0.48	IND 92		
<i>Yersinia rohdei</i>	1.60	0.08	MAN 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.87	0.05			
520062	Low discrimination				520062
<i>Escherichia coli</i>	89.10	0.48	IND 92		
<i>Salmonella enterica subsp. enterica</i>	8.65	0.18	TRE 95		
<i>Yersinia rohdei</i>	1.46	0.08			
520063	Low discrimination				520063
<i>Escherichia coli</i>	88.00	0.75	IND 92		
<i>Yersinia rohdei</i>	7.50	0.49			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.01	0.39			
520073	Low discrimination				520073
<i>Yersinia enterocolitica ssp. enterocolitica</i>	51.06	0.49	LYS 1		
<i>Yersinia rohdei</i>	21.13	0.39			
<i>Escherichia coli</i>	15.18	0.40			
520101	Very good identification				520101
<i>Hafnia alvei</i>	100.0	0.57	MAN 99		
520102	Very good identification				520102
<i>Hafnia alvei</i>	99.11	0.57	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	0.89	-.02			
520103	Excellent identification				520103
<i>Hafnia alvei</i>	99.59	0.98			
<i>Shigella sonnei</i>	0.21	0.18			
<i>Escherichia vulneris</i>	0.14	0.18			
520111	Low discrimination				520111
<i>Hafnia alvei</i>	54.58	0.42	MAN 99		
<i>Escherichia vulneris</i>	42.05	0.18			
<i>Yokenella regensburgei</i>	2.05	-.10			
520112	Low discrimination				520112
<i>Hafnia alvei</i>	53.85	0.42	TRE 99		
<i>Escherichia vulneris</i>	41.49	0.18			
<i>Escherichia fergusonii</i>	2.65	0.02			
520113	Low discrimination				520113
<i>Hafnia alvei</i>	54.55	0.83			
<i>Escherichia vulneris</i>	42.03	0.59			
<i>Yokenella regensburgei</i>	2.05	0.31			
520121	Good identification				520121
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
520122	Good identification				520122
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
520123	Very good identification				520123
<i>Hafnia alvei</i>	99.70	0.79	SUC 10		
<i>Escherichia coli</i>	0.20	0.16			
<i>Escherichia vulneris</i>	0.11	-.04			
520133	Low discrimination				520133
<i>Hafnia alvei</i>	61.20	0.63	SUC 10		
<i>Escherichia vulneris</i>	36.90	0.37			
<i>Kluyvera ascorbata</i>	1.43	0.09			
520143	Low discrimination				520143
<i>Hafnia alvei</i>	51.55	0.57	SOR 1		
<i>Salmonella enterica subsp. diarizonae</i>	21.45	0.24			
<i>Escherichia coli</i>	12.40	0.37			
520153	Low discrimination				520153
<i>Hafnia alvei</i>	47.81	0.42	SOR 1		
<i>Escherichia vulneris</i>	36.83	0.18			
<i>Yersinia kristensenii</i>	6.17	0.07			
520203	Low discrimination				520203
<i>Hafnia alvei</i>	80.04	0.57	INO 1		
<i>Shigella sonnei</i>	16.80	0.18			
<i>Escherichia coli</i>	2.63	0.19			
520223	Low discrimination				520223
				VPT	
<i>Hafnia alvei</i>	78.36	0.38	INO 1	85	
<i>Escherichia coli</i>	15.42	0.16	SUC 10	1	
<i>Serratia marcescens</i>	6.22	-.02		98	
520243	Low discrimination				520243
<i>Escherichia coli</i>	73.41	0.37	IND 92		
<i>Salmonella serovar enteritidis</i>	11.47	0.07	INO 1		
<i>Salmonella bongori</i>	4.31	-.07			
520263	Low discrimination				520263
				VPT	
<i>Serratia marcescens</i>	72.60	0.39	ESL 95	98	
<i>Escherichia coli</i>	13.33	0.34	SCI 98	1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	12.94	0.32		2	
520273	Low discrimination				520273
				VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	60.79	0.42	LYS 1	2	
<i>Serratia odorifera biovar 1</i>	31.30	0.29		50	
<i>Serratia marcescens</i>	5.99	0.13		98	
520303	Very good identification				520303
<i>Hafnia alvei</i>	100.0	0.57	INO 1		
520313	Low discrimination				520313

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	54.58	0.42	INO 1		
<i>Escherichia vulneris</i>	42.05	0.18			
<i>Yokenella regensburgei</i>	2.05	-.10			
520323	Good identification				520323
<i>Hafnia alvei</i>	100.0	0.38	INO 1		
520403	Low discrimination				520403
<i>Hafnia alvei</i>	50.76	0.57	ADO 1		
<i>Escherichia fergusonii</i>	28.00	0.39			
<i>Shigella sonnei</i>	10.66	0.18			
520413	Low discrimination				520413
<i>Escherichia fergusonii</i>	89.53	0.65	IND 98		
<i>Yokenella regensburgei</i>	5.59	0.31			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.03	0.46			
520443	Acceptable identification				520443
<i>Escherichia coli</i>	93.21	0.52	IND 92		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	4.26	0.29	ADO 5		
<i>Salmonella bongori</i>	1.05	-.07			
520453	Low discrimination				520453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.61	0.51	ORN 3		
<i>Escherichia fergusonii</i>	12.80	0.24			
<i>Escherichia coli</i>	3.09	0.17			
520463	Low discrimination				520463
				VPT	
<i>Escherichia coli</i>	79.00	0.48	IND 92	1	
<i>Serratia marcescens</i>	18.35	0.25	ADO 5	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.35	0.17		1	
520473	Low discrimination				520473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	77.12	0.39	ORN 3		
<i>Escherichia coli</i>	7.99	0.13			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	5.16	0.08			
520503	Low discrimination				520503
<i>Hafnia alvei</i>	77.10	0.57	ADO 1		
<i>Escherichia fergusonii</i>	22.90	0.33			
520513	Good identification				520513
<i>Escherichia fergusonii</i>	94.48	0.60	IND 98		
<i>Hafnia alvei</i>	2.95	0.42			
<i>Escherichia vulneris</i>	2.28	0.18			
520523	Good identification				520523
<i>Hafnia alvei</i>	100.0	0.38	ADO 1		
520613	Low discrimination				520613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.40	0.47	ORN 3		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	19.39	0.24			
<i>Yokenella regensburgei</i>	1.21	-.10			
520633	Good identification				520633
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.35	ORN 3		
520653	Low discrimination				520653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	86.97	0.53	ORN 3	1	
<i>Serratia odorifera biovar 2</i>	12.59	0.28		99	
<i>Yersinia kristensenii</i>	0.43	-.09		1	
520663	Good identification				520663
				VPT	
<i>Serratia marcescens</i>	95.74	0.35	ESL 95	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.88	0.19	SCI 98	1	
<i>Escherichia coli</i>	1.39	0.07		1	
520773	Good identification				520773
				VPT	
<i>Enterobacter aerogenes</i>	99.71	0.39	ESL 98	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.29	0.09	SCI 95	1	
521003	Low discrimination				521003
<i>Hafnia alvei</i>	80.04	0.57	PHE 1		
<i>Shigella sonnei</i>	16.80	0.18			
<i>Escherichia coli</i>	2.63	0.19			
521023	Low discrimination				521023
<i>Hafnia alvei</i>	83.56	0.38	PHE 1		
<i>Escherichia coli</i>	16.45	0.16	SUC 10		
521043	Low discrimination				521043
<i>Escherichia coli</i>	89.40	0.37	IND 92		
<i>Salmonella bongori</i>	5.25	-.07	PHE 1		
<i>Hafnia alvei</i>	3.75	0.16			
521103	Very good identification				521103
<i>Hafnia alvei</i>	100.0	0.57	PHE 1		
521113	Low discrimination				521113
<i>Hafnia alvei</i>	54.58	0.42	PHE 1		
<i>Escherichia vulneris</i>	42.05	0.18			
<i>Yokenella regensburgei</i>	2.05	-.10			
521123	Good identification				521123
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
522001	Low discrimination				522001
<i>Hafnia alvei</i>	66.43	0.38	ESL 10		
<i>Escherichia coli</i>	25.55	0.22	MAN 99		
<i>Yokenella regensburgei</i>	8.03	-.04			
522002	Low discrimination				522002
<i>Hafnia alvei</i>	63.03	0.38	ESL 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	24.24	0.22	TRE 99		
<i>Yokenella regensburgei</i>	7.62	-.04			
522003	Low discrimination				522003
<i>Hafnia alvei</i>	82.02	0.79	ESL 10		
<i>Yokenella regensburgei</i>	9.91	0.37			
<i>Escherichia coli</i>	6.05	0.48			
522011	Good identification				522011
<i>Yokenella regensburgei</i>	97.62	0.37	SCI 92		
<i>Hafnia alvei</i>	1.44	0.22	MAN 99		
<i>Escherichia fergusonii</i>	0.50	0.00			
522012	Good identification				522012
<i>Yokenella regensburgei</i>	97.13	0.37	SCI 92		
<i>Hafnia alvei</i>	1.43	0.22	TRE 99		
<i>Escherichia fergusonii</i>	1.00	0.06			
522013	Very good identification				522013
<i>Yokenella regensburgei</i>	97.34	0.78	SCI 92		
<i>Hafnia alvei</i>	1.44	0.63			
<i>Escherichia fergusonii</i>	0.50	0.41			
522023	Low discrimination				522023
				VPT	
<i>Hafnia alvei</i>	66.39	0.59	ESL 10	85	
<i>Escherichia coli</i>	29.40	0.44	SUC 10	1	
<i>Serratia marcescens</i>	3.04	0.14		98	
522033	Low discrimination				522033
<i>Yokenella regensburgei</i>	63.43	0.37	SCI 92		
<i>Escherichia hermannii</i>	12.52	0.29	SUC 1		
<i>Hafnia alvei</i>	10.29	0.43			
522041	Good identification				522041
<i>Escherichia coli</i>	100.0	0.40	IND 92		
522042	Low discrimination				522042
<i>Escherichia coli</i>	79.43	0.40	IND 92		
<i>Salmonella enterica subsp. enterica</i>	20.57	0.18	TRE 95		
522043	Very good identification				522043
				VPT	
<i>Escherichia coli</i>	96.56	0.66	IND 92	1	
<i>Hafnia alvei</i>	1.80	0.38		85	
<i>Serratia marcescens</i>	0.91	0.14		98	
522053	Low discrimination				522053
<i>Yokenella regensburgei</i>	82.34	0.37	SCI 92		
<i>Escherichia coli</i>	7.53	0.31	SOR 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	5.05	0.32			
522061	Low discrimination				522061
				VPT	
<i>Escherichia coli</i>	78.90	0.36	IND 92	1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia marcescens</i>	21.10	0.14	MAN 95	98	
522062	Low discrimination				522062
				VPT	
<i>Escherichia coli</i>	78.90	0.36	IND 92	1	
<i>Serratia marcescens</i>	21.10	0.14	TRE 95	98	
522063	Low discrimination				522063
				VPT	
<i>Serratia marcescens</i>	57.34	0.55	SCI 98	98	
<i>Escherichia coli</i>	41.14	0.62		1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.26	0.30		2	
522073	Low discrimination				522073
				VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	38.22	0.39	LYS 1	2	
<i>Serratia marcescens</i>	30.64	0.29		98	
<i>Kluyvera ascorbata</i>	13.09	0.18		1	
522101	Good identification				522101
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
522102	Good identification				522102
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
522103	Very good identification				522103
<i>Hafnia alvei</i>	99.33	0.79	ESL 10		
<i>Escherichia vulneris</i>	0.31	0.05			
<i>Escherichia fergusonii</i>	0.17	0.09			
522113	Low discrimination				522113
<i>Escherichia vulneris</i>	47.47	0.47	ORN 1		
<i>Hafnia alvei</i>	27.38	0.63			
<i>Yokenella regensburgei</i>	18.76	0.37			
522123	Good identification				522123
<i>Hafnia alvei</i>	94.11	0.59	ESL 10		
<i>Kluyvera ascorbata</i>	3.48	0.09	SUC 10		
<i>Pantoea agglomerans</i>	1.99	0.05			
522133	Low discrimination				522133
<i>Kluyvera ascorbata</i>	89.04	0.50	IND 92		
<i>Escherichia vulneris</i>	5.82	0.25	SCI 96		
<i>Hafnia alvei</i>	4.29	0.43			
522143	Low discrimination				522143
<i>Hafnia alvei</i>	61.53	0.38	ESL 10		
<i>Escherichia coli</i>	33.30	0.25	SOR 1		
<i>Salmonella enterica subsp. salamae</i>	2.85	-.13			
522173	Good identification				522173
				VPT	
<i>Kluyvera ascorbata</i>	95.67	0.46	IND 92	1	
<i>Enterobacter aerogenes</i>	3.66	0.13	SCI 96	98	
<i>Enterobacter cloacae subsp. cloacae</i>	0.38	0.05		99	
522203	Low discrimination				522203

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	80.86	0.38	ESL 10		
<i>Yokenella regensburgei</i>	9.77	-.04	INO 1		
<i>Escherichia coli</i>	5.97	0.07			
522213	Acceptable identification				522213
<i>Yokenella regensburgei</i>	93.92	0.37	SCI 92		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.79	0.29	INO 1		
<i>Hafnia alvei</i>	1.39	0.22			
522263	Very good identification				522263
				VPT	
<i>Serratia marcescens</i>	99.18	0.65	SCI 98	98	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.31	0.22		2	
<i>Serratia odorifera biovar 1</i>	0.28	0.14		50	
522273	Low discrimination				522273
				VPT	
<i>Serratia odorifera biovar 1</i>	79.64	0.55	SCI 99	50	
<i>Serratia marcescens</i>	15.23	0.39		98	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.71	0.32		2	
522303	Good identification				522303
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
522373	Good identification				522373
				VPT	
<i>Enterobacter aerogenes</i>	95.46	0.39	SCI 95	98	
<i>Serratia odorifera biovar 1</i>	2.03	0.14	ADO 98	50	
<i>Kluyvera ascorbata</i>	1.33	0.05		1	
522403	Low discrimination				522403
<i>Escherichia fergusonii</i>	61.79	0.38	IND 98		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	16.22	0.36	CEL 95		
<i>Hafnia alvei</i>	14.61	0.38			
522413	Low discrimination				522413
<i>Escherichia fergusonii</i>	76.30	0.64	IND 98		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	12.12	0.58			
<i>Yokenella regensburgei</i>	11.36	0.37			
522433	Low discrimination				522433
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	72.66	0.46	ORN 3	1	
<i>Escherichia fergusonii</i>	18.48	0.23		1	
<i>Serratia rubidaea</i>	6.11	0.08		99	
522443	Low discrimination				522443
				VPT	
<i>Escherichia coli</i>	53.62	0.40	IND 92	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	39.20	0.42	ADO 5	1	
<i>Serratia marcescens</i>	6.37	0.11		98	
522453	Very good identification				522453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.99	0.64	ORN 3		
<i>Escherichia fergusonii</i>	3.29	0.23			
<i>Yokenella regensburgei</i>	0.49	-.04			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
522463	Acceptable identification				522463
				VPT	
<i>Serratia marcescens</i>	93.27	0.52	SCI 98	98	
<i>Escherichia coli</i>	5.28	0.36		1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	1.45	0.29		1	
522473	Low discrimination				522473
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	54.98	0.51	ORN 3	1	
<i>Enterobacter aerogenes</i>	24.61	0.21		98	
<i>Serratia marcescens</i>	16.20	0.25		98	
522513	Very good identification				522513
<i>Escherichia fergusonii</i>	97.65	0.58	IND 98		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.89	0.27			
<i>Escherichia vulneris</i>	0.69	0.05			
522573	Good identification				522573
				VPT	
<i>Enterobacter aerogenes</i>	98.92	0.47	SCI 95	98	
<i>Kluyvera ascorbata</i>	0.53	0.05	INO 95	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.36	0.20		1	
522603	Good identification				522603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.95	0.38	ORN 3		
<i>Escherichia fergusonii</i>	3.05	-.04	CEL 92		
522613	Good identification				522613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	94.36	0.60	ORN 3		
<i>Escherichia fergusonii</i>	4.91	0.23			
<i>Yokenella regensburgei</i>	0.73	-.04			
522633	Low discrimination				522633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	78.88	0.47	ORN 3	1	
<i>Enterobacter aerogenes</i>	10.29	0.06		98	
<i>Serratia odorifera biovar 1</i>	8.40	0.14		50	
522643	Low discrimination				522643
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	71.47	0.44	ORN 3	1	
<i>Serratia marcescens</i>	28.53	0.21	CEL 92	98	
522653	Good identification				522653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	94.53	0.65	ORN 3	1	
<i>Serratia odorifera biovar 2</i>	2.28	0.24		99	
<i>Enterobacter aerogenes</i>	1.66	0.06		98	
522663	Very good identification				522663
				VPT	
<i>Serratia marcescens</i>	98.46	0.62	SCI 98	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.62	0.31		1	
<i>Enterobacter aerogenes</i>	0.50	0.06		98	
522673	Low discrimination				522673
				VPT	
<i>Enterobacter aerogenes</i>	48.46	0.47	SCI 95	98	
<i>Serratia odorifera biovar 1</i>	39.53	0.55	MAL 95	50	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.97	0.53		1	
522773	Very good identification				522773
				VPT	
<i>Enterobacter aerogenes</i>	99.90	0.74	SCI 95	98	
<i>Serratia odorifera</i> biovar 1	0.04	0.14		50	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.02	0.22		1	
523003	Low discrimination				523003
<i>Hafnia alvei</i>	83.70	0.38	PHE 1		
<i>Yokenella regensburgei</i>	10.12	-0.04	ESL 10		
<i>Escherichia coli</i>	6.18	0.07			
523013	Good identification				523013
<i>Yokenella regensburgei</i>	97.62	0.37	PHE 1		
<i>Hafnia alvei</i>	1.44	0.22	SCI 92		
<i>Escherichia fergusonii</i>	0.50	0.00			
523103	Good identification				523103
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
524001	Good identification				524001
<i>Hafnia alvei</i>	92.93	0.57	MAN 99		
<i>Yokenella regensburgei</i>	7.07	0.12			
524002	Low discrimination				524002
<i>Hafnia alvei</i>	72.80	0.57	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	21.66	0.30			
<i>Yokenella regensburgei</i>	5.54	0.12			
524003	Good identification				524003
<i>Hafnia alvei</i>	92.43	0.98			
<i>Yokenella regensburgei</i>	7.03	0.53			
<i>Salmonella bongori</i>	0.21	0.18			
524011	Good identification				524011
<i>Yokenella regensburgei</i>	97.71	0.53	MAN 99		
<i>Hafnia alvei</i>	2.29	0.42			
524012	Good identification				524012
<i>Yokenella regensburgei</i>	97.71	0.53	TRE 99		
<i>Hafnia alvei</i>	2.29	0.42			
524013	Very good identification				524013
<i>Yokenella regensburgei</i>	97.68	0.94			
<i>Hafnia alvei</i>	2.29	0.83			
<i>Escherichia fergusonii</i>	0.02	0.28			
524021	Good identification				524021
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
524022	Good identification				524022
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
524023	Very good identification				524023
				VPT	
<i>Hafnia alvei</i>	97.85	0.79	SUC 10	85	
<i>Serratia marcescens</i>	1.28	0.23		98	
<i>Yokenella regensburgei</i>	0.68	0.12		1	
524033	Low discrimination				524033
				VPT	
<i>Yokenella regensburgei</i>	78.46	0.53	SUC 1	1	
<i>Hafnia alvei</i>	20.22	0.63		85	
<i>Enterobacter cloacae subsp. cloacae</i>	0.50	0.17		99	
524042	Acceptable identification				524042
<i>Salmonella enterica subsp. enterica</i>	90.16	0.49	ONP 1		
<i>Salmonella bongori</i>	7.45	0.18			
<i>Salmonella serovar enteritidis</i>	0.45	-.02			
524043	Low discrimination				524043
<i>Salmonella bongori</i>	76.99	0.59	H2S 99		
<i>Salmonella serovar enteritidis</i>	4.66	0.39			
<i>Salmonella enterica subsp. arizonae</i>	4.31	0.33			
524053	Low discrimination				524053
<i>Yokenella regensburgei</i>	70.25	0.53	SOR 1		
<i>Citrobacter braakii</i>	21.73	0.59			
<i>Salmonella bongori</i>	2.07	0.18			
524063	Very good identification				524063
				VPT	
<i>Serratia marcescens</i>	95.31	0.64	ESL 95	98	
<i>Salmonella bongori</i>	1.48	0.18		1	
<i>Escherichia coli</i>	1.07	0.34		1	
524073	Low discrimination				524073
<i>Enterobacter cloacae subsp. cloacae</i>	40.35	0.44	LYS 1		
<i>Serratia marcescens</i>	33.29	0.38			
<i>Serratia odorifera biovar 1</i>	10.66	0.29			
524101	Very good identification				524101
<i>Hafnia alvei</i>	100.0	0.57	MAN 99		
524102	Very good identification				524102
<i>Hafnia alvei</i>	100.0	0.57	TRE 99		
524103	Excellent identification				524103
<i>Hafnia alvei</i>	99.45	0.98			
<i>Salmonella enterica subsp. arizonae</i>	0.24	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	0.21	0.18			
524111	Low discrimination				524111
<i>Hafnia alvei</i>	69.88	0.42	MAN 99		
<i>Yokenella regensburgei</i>	30.12	0.12			
524112	Low discrimination				524112

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	69.88	0.42	TRE 99		
<i>Yokenella regensburgei</i>	30.12	0.12			
524113	Low discrimination				524113
<i>Hafnia alvei</i>	69.19	0.83			
<i>Yokenella regensburgei</i>	29.83	0.53			
<i>Escherichia vulneris</i>	0.54	0.18			
524121	Good identification				524121
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
524122	Good identification				524122
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
524123	Very good identification				524123
<i>Hafnia alvei</i>	99.76	0.79	SUC 10		
<i>Kluyvera ascorbata</i>	0.10	-.04			
<i>Salmonella enterica subsp. diarizonae</i>	0.10	-.09			
524133	Low discrimination				524133
				VPT	
<i>Hafnia alvei</i>	59.38	0.63	SUC 10	85	
<i>Kluyvera ascorbata</i>	33.22	0.37		1	
<i>Enterobacter cloacae subsp. cloacae</i>	4.40	0.27		99	
524143	Identification to the genus				524143
<i>Salmonella enterica subsp. arizonae</i>	48.76	0.59	H2S 99		
<i>Salmonella enterica subsp. diarizonae</i>	42.60	0.59			
<i>Salmonella enterica subsp. salamae</i>	6.03	0.43			
524173	Low discrimination				524173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	76.86	0.53	LYS 1	99	
<i>Kluyvera ascorbata</i>	20.38	0.34		1	
<i>Enterobacter aerogenes</i>	1.25	0.04		98	
524203	Low discrimination				524203
<i>Hafnia alvei</i>	89.44	0.57	INO 1		
<i>Yokenella regensburgei</i>	6.80	0.12			
<i>Salmonella serovar enteritidis</i>	3.36	0.07			
524213	Good identification				524213
				VPT	
<i>Yokenella regensburgei</i>	97.25	0.53	INO 1	1	
<i>Hafnia alvei</i>	2.28	0.42		85	
<i>Serratia odorifera biovar 2</i>	0.40	0.16		99	
524253	Low discrimination				524253
				VPT	
<i>Serratia odorifera biovar 2</i>	88.01	0.57	ORN 1	99	
<i>Serratia odorifera biovar 1</i>	6.86	0.29		50	
<i>Yokenella regensburgei</i>	2.17	0.12		1	
524263	Very good identification				524263
				VPT	
<i>Serratia marcescens</i>	99.43	0.74	ESL 95	98	
<i>Serratia odorifera biovar 1</i>	0.56	0.29		50	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar enteritidis</i>	0.02	-.08		1	
524273	Good identification				524273
<i>Serratia odorifera biovar 1</i>	90.52	0.70	ESL 95		
<i>Serratia marcescens</i>	8.57	0.47			
<i>Enterobacter cloacae subsp. cloacae</i>	0.61	0.28			
524303	Very good identification				524303
<i>Hafnia alvei</i>	100.0	0.57	INO 1		
524313	Low discrimination				524313
<i>Hafnia alvei</i>	69.88	0.42	INO 1		
<i>Yokenella regensburgei</i>	30.12	0.12			
524323	Low discrimination				524323
<i>Hafnia alvei</i>	89.26	0.38	INO 1		
<i>Serratia marcescens</i>	10.74	0.02	SUC 10		
524363	Good identification				524363
				VPT	
<i>Serratia marcescens</i>	98.20	0.43	ESL 95	98	
<i>Salmonella enterica subsp. diarizonae</i>	0.80	-.09	MAL 3	1	
<i>Enterobacter aerogenes</i>	0.63	-.11		98	
524403	Low discrimination				524403
<i>Hafnia alvei</i>	83.18	0.57	ADO 1		
<i>Escherichia fergusonii</i>	9.40	0.25			
<i>Yokenella regensburgei</i>	6.33	0.12			
524413	Low discrimination				524413
<i>Yokenella regensburgei</i>	75.26	0.53	ADO 1		
<i>Escherichia fergusonii</i>	21.45	0.51			
<i>Hafnia alvei</i>	1.76	0.42			
524423	Low discrimination				524423
<i>Hafnia alvei</i>	53.63	0.38	ADO 1		
<i>Serratia marcescens</i>	46.37	0.19	SUC 10		
524453	Low discrimination				524453
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	61.08	0.44	ORN 3	1	
<i>Yokenella regensburgei</i>	16.46	0.12		1	
<i>Serratia odorifera biovar 2</i>	8.24	0.18		99	
524463	Very good identification				524463
				VPT	
<i>Serratia marcescens</i>	99.85	0.60	ESL 95	98	
<i>Escherichia coli</i>	0.09	0.07		1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.06	0.09		1	
524503	Good identification				524503
<i>Hafnia alvei</i>	94.27	0.57	ADO 1		
<i>Escherichia fergusonii</i>	5.74	0.19			
524513	Low discrimination				524513

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	81.47	0.46	IND 98		
<i>Hafnia alvei</i>	12.44	0.42			
<i>Yokenella regensburgei</i>	5.36	0.12			
524523	Low discrimination				524523
<i>Hafnia alvei</i>	75.45	0.38	ADO 1		
<i>Serratia rubidaea</i>	24.55	0.10	SUC 10		
524573	Identification to the genus				524573
				VPT	
<i>Enterobacter aerogenes</i>	68.95	0.39	ESL 98	98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	28.90	0.44	INO 95	99	
<i>Citrobacter koseri</i>	1.25	0.14		1	
524613	Low discrimination				524613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	57.76	0.40	ORN 3	1	
<i>Yokenella regensburgei</i>	23.66	0.12		1	
<i>Serratia odorifera</i> biovar 2	11.84	0.18		99	
524653	Low discrimination				524653
				VPT	
<i>Serratia odorifera</i> biovar 2	85.82	0.59	ORN 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	7.86	0.45		1	
<i>Serratia odorifera</i> biovar 1	5.48	0.29		50	
524663	Very good identification				524663
<i>Serratia marcescens</i>	99.06	0.70	ESL 95		
<i>Serratia odorifera</i> biovar 1	0.84	0.29			
<i>Enterobacter aerogenes</i>	0.08	-0.02			
524673	Low discrimination				524673
<i>Serratia odorifera</i> biovar 1	86.08	0.70	ESL 95		
<i>Enterobacter aerogenes</i>	7.85	0.39			
<i>Serratia marcescens</i>	5.43	0.44			
524763	Low discrimination				524763
<i>Serratia marcescens</i>	67.92	0.39	ESL 95		
<i>Enterobacter aerogenes</i>	32.08	0.24	MAL 3		
524773	Very good identification				524773
<i>Enterobacter aerogenes</i>	98.90	0.65	ESL 98		
<i>Serratia odorifera</i> biovar 1	0.58	0.29			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.39	0.28			
525003	Good identification				525003
<i>Hafnia alvei</i>	92.93	0.57	PHE 1		
<i>Yokenella regensburgei</i>	7.07	0.12			
525013	Good identification				525013
<i>Yokenella regensburgei</i>	97.71	0.53	PHE 1		
<i>Hafnia alvei</i>	2.29	0.42			
525023	Good identification				525023
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
525103	Very good identification				525103
<i>Hafnia alvei</i>	100.0	0.57	PHE 1		
525113	Low discrimination				525113
<i>Hafnia alvei</i>	69.88	0.42	PHE 1		
<i>Yokenella regensburgei</i>	30.12	0.12			
525123	Good identification				525123
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
526003	Low discrimination				526003
				VPT	
<i>Yokenella regensburgei</i>	58.07	0.59	CEL 99	1	
<i>Hafnia alvei</i>	41.77	0.79		85	
<i>Serratia marcescens</i>	0.11	0.08		98	
526011	Very good identification				526011
<i>Yokenella regensburgei</i>	99.87	0.59	MAN 99		
<i>Hafnia alvei</i>	0.13	0.22			
526012	Very good identification				526012
<i>Yokenella regensburgei</i>	99.87	0.59	TRE 99		
<i>Hafnia alvei</i>	0.13	0.22			
526013	Excellent identification				526013
<i>Yokenella regensburgei</i>	99.85	1.00			
<i>Hafnia alvei</i>	0.13	0.63			
<i>Escherichia fergusonii</i>	0.01	0.27			
526023	Low discrimination				526023
				VPT	
<i>Serratia marcescens</i>	65.40	0.49	SOR 99	98	
<i>Hafnia alvei</i>	29.19	0.59		85	
<i>Yokenella regensburgei</i>	3.69	0.18		1	
526033	Low discrimination				526033
				VPT	
<i>Yokenella regensburgei</i>	68.48	0.59	SUC 1	1	
<i>Kluyvera ascorbata</i>	20.06	0.50		1	
<i>Cronobacter sakazakii</i>	9.51	0.49		99	
526043	Low discrimination				526043
				VPT	
<i>Serratia marcescens</i>	80.14	0.49	SUC 99	98	
<i>Salmonella bongori</i>	6.48	0.18		1	
<i>Yokenella regensburgei</i>	4.52	0.18		1	
526053	Very good identification				526053
				VPT	
<i>Yokenella regensburgei</i>	97.60	0.59	SOR 1	1	
<i>Serratia marcescens</i>	0.92	0.23		98	
<i>Kluyvera ascorbata</i>	0.39	0.11		1	
526061	Good identification				526061
<i>Serratia marcescens</i>	100.0	0.49	MAN 99		
526062	Good identification				526062

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia marcescens</i>	100.0	0.49	TRE 99		
526063	Very good identification				526063
				VPT	
<i>Serratia marcescens</i>	99.95	0.90		98	
<i>Serratia odorifera</i> biovar 1	0.02	0.14		50	
<i>Escherichia coli</i>	0.02	0.21		1	
526073	Low discrimination				526073
				VPT	
<i>Serratia marcescens</i>	63.07	0.64	CEL 5	98	
<i>Serratia odorifera</i> biovar 1	20.20	0.55		50	
<i>Kluyvera ascorbata</i>	13.20	0.46		1	
526101	Good identification				526101
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
526102	Good identification				526102
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
526103	Very good identification				526103
<i>Hafnia alvei</i>	98.38	0.79	ESL 10		
<i>Yokenella regensburgei</i>	1.38	0.18			
<i>Kluyvera ascorbata</i>	0.20	0.02			
526113	Low discrimination				526113
<i>Yokenella regensburgei</i>	78.26	0.59	MAL 1		
<i>Kluyvera ascorbata</i>	11.23	0.43			
<i>Hafnia alvei</i>	9.94	0.63			
526123	Low discrimination				526123
<i>Hafnia alvei</i>	48.76	0.59	ESL 10		
<i>Kluyvera ascorbata</i>	43.33	0.37	SUC 10		
<i>Pantoea agglomerans</i>	4.12	0.18			
526131	Good identification				526131
				VPT	
<i>Kluyvera ascorbata</i>	99.57	0.37	IND 92	1	
<i>Cronobacter sakazakii</i>	0.43	-.06	MAN 99	99	
526132	Good identification				526132
				VPT	
<i>Kluyvera ascorbata</i>	99.57	0.37	IND 92	1	
<i>Cronobacter sakazakii</i>	0.43	-.06	TRE 99	99	
526133	Very good identification				526133
				VPT	
<i>Kluyvera ascorbata</i>	98.99	0.78	IND 92	1	
<i>Cronobacter sakazakii</i>	0.43	0.36		99	
<i>Hafnia alvei</i>	0.20	0.43		85	
526153	Low discrimination				526153
				VPT	
<i>Kluyvera ascorbata</i>	85.51	0.40	IND 92	1	
<i>Yokenella regensburgei</i>	9.03	0.18	SUC 98	1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	2.12	0.15		99	
526163	Good identification				526163

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Serratia marcescens</i>	91.43	0.59	MAL 3	98	
<i>Kluyvera ascorbata</i>	7.90	0.34		1	
<i>Enterobacter aerogenes</i>	0.24	-0.02		98	
526173	Good identification				526173
				VPT	
<i>Kluyvera ascorbata</i>	94.92	0.75	IND 92	1	
<i>Enterobacter aerogenes</i>	2.88	0.39		98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.55	0.46		99	
526213	Very good identification				526213
				VPT	
<i>Yokenella regensburgei</i>	98.85	0.59	INO 1	1	
<i>Cronobacter sakazakii</i>	0.42	0.18		99	
<i>Serratia odorifera</i> biovar 1	0.30	0.14		50	
526223	Very good identification				526223
<i>Serratia marcescens</i>	98.53	0.59	SOR 99		
<i>Cronobacter sakazakii</i>	0.77	0.18			
<i>Serratia odorifera</i> biovar 1	0.55	0.14			
526233	Low discrimination				526233
<i>Cronobacter sakazakii</i>	54.91	0.59	LYS 1		
<i>Serratia odorifera</i> biovar 1	39.40	0.55			
<i>Serratia marcescens</i>	3.73	0.33			
526243	Very good identification				526243
				VPT	
<i>Serratia marcescens</i>	98.74	0.59	SUC 99	98	
<i>Serratia odorifera</i> biovar 1	0.56	0.14		50	
<i>Salmonella</i> serovar enteritidis	0.45	0.07		1	
526253	Identification to the genus				526253
<i>Serratia odorifera</i> biovar 1	62.79	0.55	SUC 99		
<i>Serratia odorifera</i> biovar 2	28.25	0.54			
<i>Serratia marcescens</i>	5.94	0.33			
526261	Very good identification				526261
<i>Serratia marcescens</i>	99.44	0.59	MAN 99		
<i>Serratia odorifera</i> biovar 1	0.56	0.14			
526262	Very good identification				526262
<i>Serratia marcescens</i>	99.44	0.59	TRE 99		
<i>Serratia odorifera</i> biovar 1	0.56	0.14			
526263	Excellent identification				526263
<i>Serratia marcescens</i>	99.44	1.00			
<i>Serratia odorifera</i> biovar 1	0.56	0.55			
<i>Enterobacter aerogenes</i>	0.00	-0.02			
526271	Good identification				526271
<i>Serratia odorifera</i> biovar 1	90.96	0.55	MAN 99		
<i>Serratia marcescens</i>	8.61	0.33			
<i>Enterobacter aerogenes</i>	0.44	-0.02			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
526272	Good identification				526272
<i>Serratia odorifera</i> biovar 1	90.96	0.55	TRE 99		
<i>Serratia marcescens</i>	8.61	0.33			
<i>Enterobacter aerogenes</i>	0.44	-.02			
526273	Good identification				526273
<i>Serratia odorifera</i> biovar 1	90.89	0.96			
<i>Serratia marcescens</i>	8.60	0.74			
<i>Enterobacter aerogenes</i>	0.44	0.39			
526303	Good identification				526303
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
526333	Low discrimination				526333
				VPT	
<i>Cronobacter sakazakii</i>	46.70	0.45	LYS 1	99	
<i>Kluyvera ascorbata</i>	36.28	0.37		1	
<i>Enterobacter aerogenes</i>	13.92	0.24		98	
526363	Very good identification				526363
<i>Serratia marcescens</i>	98.17	0.69	MAL 3		
<i>Enterobacter aerogenes</i>	1.63	0.24			
<i>Serratia odorifera</i> biovar 1	0.18	0.14			
526373	Low discrimination				526373
<i>Enterobacter aerogenes</i>	85.59	0.65	ADO 98		
<i>Serratia odorifera</i> biovar 1	9.48	0.55			
<i>Serratia marcescens</i>	2.75	0.43			
526413	Low discrimination				526413
<i>Yokenella regensburgei</i>	86.13	0.59	ADO 1		
<i>Escherichia fergusonii</i>	10.30	0.50			
<i>Klebsiella pneumoniae</i> subsp. ozaenae	3.43	0.50			
526423	Good identification				526423
				VPT	
<i>Serratia marcescens</i>	96.73	0.46	SOR 99	98	
<i>Serratia rubidaea</i>	1.92	0.10		99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.70	0.16		1	
526443	Acceptable identification				526443
				VPT	
<i>Serratia marcescens</i>	94.90	0.46	SUC 99	98	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	5.10	0.34		1	
526453	Low discrimination				526453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	73.79	0.56	ORN 3	1	
<i>Yokenella regensburgei</i>	10.09	0.18		1	
<i>Serratia marcescens</i>	6.28	0.19		98	
526461	Good identification				526461
<i>Serratia marcescens</i>	100.0	0.46	MAN 99		
526462	Good identification				526462

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia marcescens</i>	100.0	0.46	TRE 99		
526463	Very good identification				526463
<i>Serratia marcescens</i>	99.93	0.87			
<i>Enterobacter aerogenes</i>	0.03	0.06			
<i>Serratia odorifera</i> biovar 1	0.03	0.14			
526473	Low discrimination				526473
<i>Serratia marcescens</i>	47.25	0.60	CEL 5		
<i>Enterobacter aerogenes</i>	27.82	0.47			
<i>Serratia odorifera</i> biovar 1	22.70	0.55			
526503	Low discrimination				526503
				VPT	
<i>Hafnia alvei</i>	65.88	0.38	ESL 10	85	
<i>Escherichia fergusonii</i>	30.73	0.18	ADO 1	1	
<i>Serratia rubidaea</i>	3.39	-.07		99	
526513	Low discrimination				526513
				VPT	
<i>Escherichia fergusonii</i>	75.73	0.44	IND 98	1	
<i>Yokenella regensburgei</i>	11.88	0.18		1	
<i>Serratia rubidaea</i>	6.90	0.18		99	
526533	Low discrimination				526533
				VPT	
<i>Serratia rubidaea</i>	80.13	0.59	ORN 1	99	
<i>Kluyvera ascorbata</i>	9.81	0.37		1	
<i>Enterobacter aerogenes</i>	9.70	0.33		98	
526563	Low discrimination				526563
				VPT	
<i>Serratia marcescens</i>	83.71	0.56	MAL 3	98	
<i>Enterobacter aerogenes</i>	16.10	0.33		98	
<i>Kluyvera ascorbata</i>	0.11	-.08		1	
526573	Very good identification				526573
				VPT	
<i>Enterobacter aerogenes</i>	98.52	0.74	INO 95	98	
<i>Kluyvera ascorbata</i>	0.67	0.34		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.36	0.36		99	
526613	Low discrimination				526613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	74.43	0.52	ORN 3		
<i>Yokenella regensburgei</i>	15.47	0.18			
<i>Serratia odorifera</i> biovar 1	4.62	0.14			
526623	Very good identification				526623
				VPT	
<i>Serratia marcescens</i>	98.52	0.55	SOR 99	98	
<i>Serratia odorifera</i> biovar 1	0.83	0.14		50	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.29	0.18		1	
526633	Low discrimination				526633
<i>Serratia odorifera</i> biovar 1	72.25	0.55	SOR 99		
<i>Enterobacter aerogenes</i>	17.00	0.33			
<i>Serratia marcescens</i>	4.56	0.29			
526643	Very good identification				526643

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Serratia marcescens</i>	96.44	0.55	SUC 99	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	2.11	0.36		1	
<i>Serratia odorifera biovar 1</i>	0.81	0.14		50	
526653	Low discrimination				526653
				VPT	
<i>Serratia odorifera biovar 1</i>	46.50	0.55	SUC 99	50	
<i>Serratia odorifera biovar 2</i>	25.58	0.55		99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	14.05	0.58		1	
526661	Very good identification				526661
<i>Serratia marcescens</i>	98.97	0.55	MAN 99		
<i>Serratia odorifera biovar 1</i>	0.83	0.14			
<i>Enterobacter aerogenes</i>	0.20	-.09			
526662	Very good identification				526662
<i>Serratia marcescens</i>	98.97	0.55	TRE 99		
<i>Serratia odorifera biovar 1</i>	0.83	0.14			
<i>Enterobacter aerogenes</i>	0.20	-.09			
526663	Very good identification				526663
<i>Serratia marcescens</i>	98.96	0.96			
<i>Serratia odorifera biovar 1</i>	0.83	0.55			
<i>Enterobacter aerogenes</i>	0.20	0.33			
526671	Low discrimination				526671
<i>Serratia odorifera biovar 1</i>	77.02	0.55	MAN 99		
<i>Enterobacter aerogenes</i>	18.12	0.33			
<i>Serratia marcescens</i>	4.86	0.29			
526672	Low discrimination				526672
<i>Serratia odorifera biovar 1</i>	76.93	0.55	TRE 99		
<i>Enterobacter aerogenes</i>	18.10	0.33			
<i>Serratia marcescens</i>	4.85	0.29			
526673	Low discrimination				526673
<i>Serratia odorifera biovar 1</i>	76.96	0.96			
<i>Enterobacter aerogenes</i>	18.11	0.74			
<i>Serratia marcescens</i>	4.86	0.70			
526733	Low discrimination				526733
<i>Enterobacter aerogenes</i>	89.82	0.59	SOR 99		
<i>Serratia rubidaea</i>	9.76	0.47			
<i>Serratia odorifera biovar 1</i>	0.20	0.14			
526753	Very good identification				526753
				VPT	
<i>Enterobacter aerogenes</i>	99.35	0.59	SUC 99	98	
<i>Serratia odorifera biovar 1</i>	0.23	0.14		50	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.21	0.27		1	
526763	Low discrimination				526763
<i>Enterobacter aerogenes</i>	54.82	0.59	CEL 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia marcescens</i>	45.01	0.65			
<i>Serratia odorifera</i> biovar 1	0.12	0.14			
526771	Very good identification				526771
<i>Enterobacter aerogenes</i>	99.68	0.59	MAN 99		
<i>Serratia odorifera</i> biovar 1	0.23	0.14			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.05	-.09			
526772	Very good identification				526772
<i>Enterobacter aerogenes</i>	99.68	0.59	TRE 99		
<i>Serratia odorifera</i> biovar 1	0.23	0.14			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.05	-.09			
526773	Excellent identification				526773
<i>Enterobacter aerogenes</i>	99.68	1.00			
<i>Serratia odorifera</i> biovar 1	0.23	0.55			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.05	0.33			
527013	Very good identification				527013
				VPT	
<i>Yokenella regensburgei</i>	99.73	0.59	PHE 1	1	
<i>Cronobacter sakazakii</i>	0.14	0.08		99	
<i>Hafnia alvei</i>	0.13	0.22		85	
527033	Acceptable identification				527033
				VPT	
<i>Cronobacter sakazakii</i>	91.40	0.49	LYS 1	99	
<i>Yokenella regensburgei</i>	6.65	0.18		1	
<i>Kluyvera ascorbata</i>	1.95	0.09		1	
527063	Good identification				527063
<i>Serratia marcescens</i>	100.0	0.49	PHE 1		
527103	Good identification				527103
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
527133	Low discrimination				527133
				VPT	
<i>Kluyvera ascorbata</i>	69.62	0.37	IND 92	1	
<i>Cronobacter sakazakii</i>	29.87	0.36	PHE 1	99	
<i>Pantoea agglomerans</i>	0.51	-.05		64	
527233	Very good identification				527233
<i>Cronobacter sakazakii</i>	99.21	0.59	LYS 1		
<i>Serratia odorifera</i> biovar 1	0.72	0.14			
<i>Serratia marcescens</i>	0.07	-.09			
527263	Very good identification				527263
<i>Serratia marcescens</i>	99.44	0.59	PHE 1		
<i>Serratia odorifera</i> biovar 1	0.56	0.14			
527273	Identification to the genus				527273
<i>Serratia odorifera</i> biovar 1	89.81	0.55	PHE 1		
<i>Serratia marcescens</i>	8.50	0.33			
<i>Cronobacter sakazakii</i>	1.26	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
527333	Good identification				527333
				VPT	
<i>Cronobacter sakazakii</i>	98.93	0.45	LYS 1	99	
<i>Kluyvera ascorbata</i>	0.78	-.04		1	
<i>Enterobacter aerogenes</i>	0.30	-.17		98	
527463	Good identification				527463
<i>Serratia marcescens</i>	100.0	0.46	PHE 1		
527663	Very good identification				527663
<i>Serratia marcescens</i>	98.97	0.55	PHE 1		
<i>Serratia odorifera</i> biovar 1	0.83	0.14			
<i>Enterobacter aerogenes</i>	0.20	-.09			
527673	Low discrimination				527673
<i>Serratia odorifera</i> biovar 1	77.02	0.55	PHE 1		
<i>Enterobacter aerogenes</i>	18.12	0.33			
<i>Serratia marcescens</i>	4.86	0.29			
527773	Very good identification				527773
<i>Enterobacter aerogenes</i>	99.68	0.59	PHE 1		
<i>Serratia odorifera</i> biovar 1	0.23	0.14			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.05	-.09			
530001	Very good identification				530001
<i>Escherichia coli</i>	96.48	0.56	SOR 88		
<i>Shigella dysenteriae</i> (group A)	1.07	0.09	MAN 95		
<i>Escherichia fergusonii</i>	1.01	0.10			
530002	Very good identification				530002
<i>Escherichia coli</i>	96.30	0.56	SOR 88		
<i>Escherichia fergusonii</i>	2.03	0.16	TRE 95		
<i>Escherichia hermannii</i>	0.73	0.03			
530003	Identification to the genus				530003
<i>Escherichia coli</i>	88.77	0.82	SOR 88		
<i>Escherichia fergusonii</i>	4.84	0.51			
<i>Escherichia hermannii</i>	3.50	0.44			
530012	Identification to the genus				530012
<i>Escherichia fergusonii</i>	59.91	0.42	ADO 93		
<i>Escherichia hermannii</i>	36.54	0.34	TRE 98		
<i>Escherichia coli</i>	3.05	0.21			
530013	Identification to the genus				530013
<i>Escherichia hermannii</i>	54.18	0.75	LYS 6		
<i>Escherichia fergusonii</i>	43.96	0.77			
<i>Escherichia coli</i>	0.87	0.47			
530021	Good identification				530021
<i>Escherichia coli</i>	99.08	0.52	SOR 88		
<i>Escherichia hermannii</i>	0.92	0.02	MAN 95		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
530022	Good identification				530022
<i>Escherichia coli</i>	99.08	0.52	SOR 88		
<i>Escherichia hermannii</i>	0.92	0.02	TRE 95		
530023	Good identification				530023
<i>Escherichia coli</i>	94.90	0.79	SOR 88		
<i>Escherichia hermannii</i>	4.60	0.43			
<i>Hafnia alvei</i>	0.42	0.38			
530033	Very good identification				530033
<i>Escherichia hermannii</i>	97.29	0.74	LYS 6		
<i>Escherichia coli</i>	1.27	0.44			
<i>Escherichia fergusonii</i>	0.98	0.36			
530040	Good identification				530040
<i>Escherichia coli</i>	100.0	0.47	TRE 95		
530041	Very good identification				530041
<i>Escherichia coli</i>	99.94	0.74	MAN 95		
<i>Shigella dysenteriae (group A)</i>	0.07	0.01			
530042	Very good identification				530042
<i>Escherichia coli</i>	99.44	0.74	TRE 95		
<i>Salmonella enterica subsp. enterica</i>	0.56	0.18			
530043	Excellent identification				530043
<i>Escherichia coli</i>	99.90	1.00			
<i>Citrobacter braakii</i>	0.07	0.36			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.01	0.13			
530051	Good identification				530051
<i>Escherichia coli</i>	95.27	0.39	CEL 2		
<i>Yersinia kristensenii</i>	3.16	-.01	MAN 95		
<i>Escherichia hermannii</i>	1.57	-.07			
530052	Acceptable identification				530052
<i>Escherichia coli</i>	92.87	0.39	CEL 2		
<i>Yersinia kristensenii</i>	3.08	-.01	TRE 95		
<i>Escherichia fergusonii</i>	2.52	0.01			
530053	Low discrimination				530053
<i>Escherichia coli</i>	69.67	0.65	CEL 2		
<i>Yersinia kristensenii</i>	12.04	0.41			
<i>Escherichia hermannii</i>	6.00	0.34			
530060	Good identification				530060
<i>Escherichia coli</i>	100.0	0.44	TRE 95		
530061	Very good identification				530061
<i>Escherichia coli</i>	99.92	0.70	MAN 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.08	0.05			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
530062	Very good identification				530062
<i>Escherichia coli</i>	99.92	0.70	TRE 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.08	0.05			
530063	Excellent identification				530063
<i>Escherichia coli</i>	99.71	0.96			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.20	0.39			
<i>Citrobacter farmeri</i>	0.07	0.18			
530071	Low discrimination				530071
<i>Escherichia coli</i>	55.89	0.35	CEL 2		
<i>Citrobacter farmeri</i>	36.64	0.18	MAN 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	6.34	0.14			
530072	Low discrimination				530072
<i>Escherichia coli</i>	55.89	0.35	CEL 2		
<i>Citrobacter farmeri</i>	36.64	0.18	TRE 95		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	6.34	0.14			
530073	Low discrimination				530073
<i>Citrobacter farmeri</i>	70.73	0.59	LYS 1		
<i>Escherichia coli</i>	20.71	0.62			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	6.06	0.49			
530103	Low discrimination				530103
<i>Escherichia fergusonii</i>	44.04	0.45	ADO 93		
<i>Hafnia alvei</i>	40.20	0.57	CEL 95		
<i>Escherichia coli</i>	15.16	0.41			
530112	Good identification				530112
<i>Escherichia fergusonii</i>	98.87	0.37	ADO 93		
<i>Escherichia hermannii</i>	1.13	-0.07	TRE 98		
530113	Very good identification				530113
<i>Escherichia fergusonii</i>	96.22	0.71	ADO 93		
<i>Escherichia hermannii</i>	2.22	0.34			
<i>Hafnia alvei</i>	0.82	0.42			
530123	Low discrimination				530123
<i>Escherichia coli</i>	64.30	0.38	MAL 1		
<i>Hafnia alvei</i>	28.41	0.38	SOR 88		
<i>Escherichia hermannii</i>	3.11	0.02			
530143	Very good identification				530143
<i>Escherichia coli</i>	98.94	0.59	MAL 1		
<i>Escherichia fergusonii</i>	0.40	0.04			
<i>Hafnia alvei</i>	0.36	0.16			
530163	Very good identification				530163
<i>Escherichia coli</i>	100.0	0.55	MAL 1		
530203	Identification to the genus				530203

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	89.23	0.41	INO 1		
<i>Escherichia fergusonii</i>	4.86	0.10	SOR 88		
<i>Escherichia hermannii</i>	3.52	0.03			
530223	Good identification				530223
<i>Escherichia coli</i>	95.38	0.38	INO 1		
<i>Escherichia hermannii</i>	4.62	0.02	SOR 88		
530243	Very good identification				530243
<i>Escherichia coli</i>	99.71	0.59	INO 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.30	0.05			
530263	Good identification				530263
				VPT	
<i>Escherichia coli</i>	91.81	0.55	INO 1	1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	7.75	0.32		2	
<i>Serratia marcescens</i>	0.44	-.02		98	
530273	Low discrimination				530273
<i>Yersinia enterocolitica ssp. enterocolitica</i>	46.80	0.42	LYS 1		
<i>Serratia odorifera biovar 1</i>	36.15	0.33			
<i>Citrobacter farmeri</i>	12.88	0.18			
530402	Identification to the genus				530402
<i>Escherichia fergusonii</i>	84.21	0.39	CEL 95		
<i>Escherichia coli</i>	15.79	0.30	TRE 98		
530403	Good identification				530403
<i>Escherichia fergusonii</i>	93.14	0.74	CEL 95		
<i>Escherichia coli</i>	6.77	0.56			
<i>Escherichia hermannii</i>	0.05	0.03			
530411	Very good identification				530411
<i>Escherichia fergusonii</i>	99.91	0.59	MAN 99		
<i>Escherichia hermannii</i>	0.09	-.07			
530412	Very good identification				530412
<i>Escherichia fergusonii</i>	99.95	0.65	TRE 98		
<i>Escherichia hermannii</i>	0.05	-.07			
530413	Excellent identification				530413
<i>Escherichia fergusonii</i>	99.90	1.00			
<i>Escherichia hermannii</i>	0.09	0.34			
<i>Escherichia coli</i>	0.01	0.21			
530423	Identification to the genus				530423
<i>Escherichia coli</i>	82.13	0.52	ADO 5		
<i>Escherichia fergusonii</i>	17.11	0.33	SOR 88		
<i>Escherichia hermannii</i>	0.76	0.02			
530433	Good identification				530433
<i>Escherichia fergusonii</i>	92.50	0.59	SUC 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	7.02	0.33			
<i>Escherichia coli</i>	0.48	0.17			
530441	Good identification				530441
<i>Escherichia coli</i>	100.0	0.47	ADO 5		
530442	Good identification				530442
<i>Escherichia coli</i>	99.27	0.47	ADO 5		
<i>Escherichia fergusonii</i>	0.73	-.02	TRE 95		
530443	Very good identification				530443
<i>Escherichia coli</i>	98.14	0.74	ADO 5		
<i>Escherichia fergusonii</i>	1.86	0.33			
530453	Good identification				530453
<i>Escherichia fergusonii</i>	94.27	0.59	SOR 1		
<i>Escherichia coli</i>	5.35	0.39			
<i>Yersinia kristensenii</i>	0.18	-.01			
530461	Good identification				530461
<i>Escherichia coli</i>	100.0	0.44	ADO 5		
530462	Good identification				530462
<i>Escherichia coli</i>	100.0	0.44	ADO 5		
530463	Very good identification				530463
<i>Escherichia coli</i>	100.0	0.70	ADO 5		
530473	Low discrimination				530473
<i>Escherichia coli</i>	50.02	0.35	ADO 5		
<i>Citrobacter farmeri</i>	32.79	0.18	CEL 2		
<i>Escherichia fergusonii</i>	13.37	0.18			
530503	Very good identification				530503
<i>Escherichia fergusonii</i>	99.80	0.68	CEL 95		
<i>Escherichia coli</i>	0.14	0.15			
<i>Hafnia alvei</i>	0.07	0.16			
530511	Very good identification				530511
<i>Escherichia fergusonii</i>	100.0	0.53	MAN 99		
530512	Very good identification				530512
<i>Escherichia fergusonii</i>	100.0	0.60	TRE 98		
530513	Excellent identification				530513
<i>Escherichia fergusonii</i>	100.0	0.95			
<i>Escherichia hermannii</i>	0.00	-.07			
530533	Very good identification				530533
<i>Escherichia fergusonii</i>	99.67	0.53	SUC 1		
<i>Kluyvera ascorbata</i>	0.19	-.11			
<i>Escherichia hermannii</i>	0.14	-.09			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
530553	Very good identification				530553
<i>Escherichia fergusonii</i>	98.44	0.53	SOR 1		
<i>Citrobacter koseri</i>	1.56	0.15			
530613	Very good identification				530613
<i>Escherichia fergusonii</i>	99.82	0.59	INO 1		
<i>Escherichia hermannii</i>	0.09	-.07			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.08	0.06			
530713	Very good identification				530713
<i>Escherichia fergusonii</i>	100.0	0.53	INO 1		
531003	Identification to the genus				531003
<i>Escherichia coli</i>	89.23	0.41	PHE 1		
<i>Escherichia fergusonii</i>	4.86	0.10	SOR 88		
<i>Escherichia hermannii</i>	3.52	0.03			
531023	Good identification				531023
<i>Escherichia coli</i>	95.38	0.38	PHE 1		
<i>Escherichia hermannii</i>	4.62	0.02	SOR 88		
531043	Very good identification				531043
<i>Escherichia coli</i>	100.0	0.59	PHE 1		
531063	Very good identification				531063
<i>Escherichia coli</i>	100.0	0.55	PHE 1		
531413	Very good identification				531413
<i>Escherichia fergusonii</i>	99.91	0.59	PHE 1		
<i>Escherichia hermannii</i>	0.09	-.07			
531513	Very good identification				531513
<i>Escherichia fergusonii</i>	100.0	0.53	PHE 1		
532001	Acceptable identification				532001
<i>Escherichia coli</i>	94.71	0.44	SOR 88		
<i>Escherichia fergusonii</i>	3.37	0.08	MAN 95		
<i>Escherichia hermannii</i>	1.91	0.00			
532002	Acceptable identification				532002
<i>Escherichia coli</i>	91.56	0.44	SOR 88		
<i>Escherichia fergusonii</i>	6.59	0.14	TRE 95		
<i>Escherichia hermannii</i>	1.85	0.00			
532003	Identification to the genus				532003
<i>Escherichia coli</i>	76.68	0.70	SOR 88		
<i>Escherichia fergusonii</i>	14.23	0.49			
<i>Escherichia hermannii</i>	8.07	0.41			
532012	Identification to the genus				532012
<i>Escherichia fergusonii</i>	66.13	0.41	ADO 93		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia hermannii</i>	31.57	0.31	TRE 98		
<i>Yokenella regensburgei</i>	1.32	-.04			
532013	Identification to the genus				532013
<i>Escherichia fergusonii</i>	49.68	0.75	ADO 93		
<i>Escherichia hermannii</i>	47.92	0.72			
<i>Yokenella regensburgei</i>	2.01	0.37			
532021	Good identification				532021
<i>Escherichia coli</i>	97.58	0.40	SOR 88		
<i>Escherichia hermannii</i>	2.42	-.02	MAN 95		
532022	Good identification				532022
<i>Escherichia coli</i>	97.58	0.40	SOR 88		
<i>Escherichia hermannii</i>	2.42	-.02	TRE 95		
532023	Identification to the genus				532023
<i>Escherichia coli</i>	87.92	0.66	SOR 88		
<i>Escherichia hermannii</i>	11.35	0.39			
<i>Kluyvera ascorbata</i>	0.31	0.02			
532033	Good identification				532033
<i>Escherichia hermannii</i>	90.84	0.70	LYS 6		
<i>Kluyvera ascorbata</i>	7.50	0.43			
<i>Escherichia fergusonii</i>	1.16	0.34			
532040	Good identification				532040
<i>Escherichia coli</i>	100.0	0.35	TRE 95		
532041	Very good identification				532041
<i>Escherichia coli</i>	100.0	0.61	MAN 95		
532042	Very good identification				532042
<i>Escherichia coli</i>	100.0	0.61	TRE 95		
532043	Very good identification				532043
<i>Escherichia coli</i>	99.95	0.88			
<i>Escherichia fergusonii</i>	0.03	0.08			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.01	0.03			
532053	Identification to the genus				532053
<i>Escherichia coli</i>	65.84	0.53	CEL 2		
<i>Escherichia fergusonii</i>	15.67	0.34			
<i>Escherichia hermannii</i>	15.12	0.31			
532061	Very good identification				532061
<i>Escherichia coli</i>	100.0	0.58	MAN 95		
532062	Very good identification				532062
<i>Escherichia coli</i>	100.0	0.58	TRE 95		
532063	Very good identification				532063

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	99.57	0.84		1	
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.26	0.30		2	
<i>Serratia marcescens</i>	0.12	0.14		98	
532073	Low discrimination				532073
<i>Kluyvera ascorbata</i>	44.92	0.40	SCI 96		
<i>Escherichia coli</i>	29.24	0.49	MAL 96		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	11.40	0.39			
532103	Low discrimination				532103
<i>Escherichia fergusonii</i>	80.51	0.44	ADO 93		
<i>Hafnia alvei</i>	9.59	0.38	CEL 95		
<i>Escherichia coli</i>	8.14	0.29			
532112	Good identification				532112
<i>Escherichia fergusonii</i>	97.15	0.35	ADO 93		
<i>Kluyvera ascorbata</i>	2.85	-.04	TRE 98		
532113	Good identification				532113
<i>Escherichia fergusonii</i>	92.49	0.70	ADO 93		
<i>Kluyvera ascorbata</i>	5.48	0.37			
<i>Escherichia hermannii</i>	1.67	0.31			
532133	Very good identification				532133
<i>Kluyvera ascorbata</i>	99.14	0.72	SCI 96		
<i>Escherichia hermannii</i>	0.51	0.29			
<i>Escherichia fergusonii</i>	0.35	0.29			
532143	Good identification				532143
<i>Escherichia coli</i>	97.67	0.47	MAL 1		
<i>Escherichia fergusonii</i>	1.33	0.03			
<i>Kluyvera ascorbata</i>	1.00	-.08			
532163	Low discrimination				532163
<i>Escherichia coli</i>	57.07	0.43	MAL 1		
<i>Kluyvera ascorbata</i>	42.94	0.27			
532173	Very good identification				532173
<i>Kluyvera ascorbata</i>	99.97	0.68	SCI 96		
<i>Escherichia coli</i>	0.03	0.08			
532243	Good identification				532243
<i>Escherichia coli</i>	100.0	0.47	INO 1		
532263	Low discrimination				532263
				VPT	
<i>Escherichia coli</i>	61.49	0.43	INO 1	1	
<i>Serratia marcescens</i>	22.36	0.24		98	
<i>Serratia odorifera biovar 1</i>	9.23	0.18		50	
532273	Very good identification				532273
<i>Serratia odorifera biovar 1</i>	97.33	0.59	SCI 99		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	2.21	0.32			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Kluyvera ascorbata</i>	0.21	-.02			
532402	Acceptable identification				532402
<i>Escherichia fergusonii</i>	94.78	0.38	CEL 95		
<i>Escherichia coli</i>	5.22	0.17	TRE 98		
532403	Very good identification				532403
<i>Escherichia fergusonii</i>	97.87	0.72	CEL 95		
<i>Escherichia coli</i>	2.09	0.44			
<i>Escherichia hermannii</i>	0.04	0.00			
532411	Very good identification				532411
<i>Escherichia fergusonii</i>	100.0	0.58	MAN 99		
532412	Very good identification				532412
<i>Escherichia fergusonii</i>	100.0	0.64	TRE 98		
532413	Excellent identification				532413
<i>Escherichia fergusonii</i>	99.92	0.99			
<i>Escherichia hermannii</i>	0.07	0.31			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.00	0.17			
532423	Identification to the genus				532423
<i>Escherichia coli</i>	57.65	0.40	ADO 5		
<i>Escherichia fergusonii</i>	40.93	0.31	SOR 88		
<i>Escherichia hermannii</i>	1.43	-.02			
532433	Good identification				532433
<i>Escherichia fergusonii</i>	93.72	0.58	SUC 1		
<i>Escherichia hermannii</i>	5.57	0.29			
<i>Kluyvera ascorbata</i>	0.46	0.02			
532441	Good identification				532441
<i>Escherichia coli</i>	100.0	0.35	ADO 5		
532442	Good identification				532442
<i>Escherichia coli</i>	97.56	0.35	ADO 5		
<i>Escherichia fergusonii</i>	2.44	-.04	TRE 95		
532443	Good identification				532443
<i>Escherichia coli</i>	93.94	0.61	ADO 5		
<i>Escherichia fergusonii</i>	6.06	0.31			
532453	Very good identification				532453
<i>Escherichia fergusonii</i>	97.78	0.58	SOR 1		
<i>Escherichia coli</i>	1.63	0.27			
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.59	0.22			
532463	Very good identification				532463
<i>Escherichia coli</i>	98.47	0.58	ADO 5	VPT 1	
<i>Serratia marcescens</i>	1.53	0.11		98	
532503	Very good identification				532503

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	99.96	0.67	CEL 95		
<i>Escherichia coli</i>	0.04	0.02			
532511	Good identification				532511
<i>Escherichia fergusonii</i>	100.0	0.52	MAN 99		
532512	Very good identification				532512
<i>Escherichia fergusonii</i>	100.0	0.58	TRE 98		
532513	Very good identification				532513
<i>Escherichia fergusonii</i>	99.98	0.93			
<i>Leclercia adecarboxylata</i>	0.02	0.12			
<i>Kluyvera ascorbata</i>	0.01	-.04			
532533	Low discrimination				532533
<i>Escherichia fergusonii</i>	79.92	0.52	SUC 1		
<i>Kluyvera ascorbata</i>	17.48	0.31			
<i>Leclercia adecarboxylata</i>	2.45	0.18			
532553	Good identification				532553
<i>Escherichia fergusonii</i>	99.70	0.52	SOR 1		
<i>Kluyvera ascorbata</i>	0.30	-.08			
532613	Very good identification				532613
<i>Escherichia fergusonii</i>	99.61	0.58	INO 1		
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.40	0.19			
532673	Very good identification				532673
				VPT	
<i>Serratia odorifera biovar 1</i>	98.98	0.59	SCI 99	50	
<i>Enterobacter aerogenes</i>	0.82	0.06		98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.12	0.12		1	
532713	Good identification				532713
<i>Escherichia fergusonii</i>	100.0	0.52	INO 1		
533043	Good identification				533043
<i>Escherichia coli</i>	100.0	0.47	PHE 1		
533063	Good identification				533063
<i>Escherichia coli</i>	100.0	0.43	PHE 1		
533413	Very good identification				533413
<i>Escherichia fergusonii</i>	100.0	0.58	PHE 1		
533513	Good identification				533513
<i>Escherichia fergusonii</i>	100.0	0.52	PHE 1		
534003	Low discrimination				534003
<i>Hafnia alvei</i>	52.89	0.57	IND 1		
<i>Escherichia fergusonii</i>	22.04	0.36			
<i>Escherichia coli</i>	19.95	0.41			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
534013	Low discrimination				534013
<i>Escherichia fergusonii</i>	49.00	0.63	ADO 93		
<i>Yokenella regensburgei</i>	46.61	0.53			
<i>Escherichia hermannii</i>	2.98	0.34			
534023	Low discrimination				534023
<i>Escherichia coli</i>	65.45	0.38	SCI 1		
<i>Hafnia alvei</i>	28.92	0.38	SOR 88		
<i>Escherichia hermannii</i>	3.17	0.02			
534043	Low discrimination				534043
<i>Escherichia coli</i>	76.08	0.59	SCI 1		
<i>Citrobacter braakii</i>	15.54	0.46			
<i>Salmonella bongori</i>	6.09	0.18			
534053	Low discrimination				534053
<i>Citrobacter amalonaticus</i>	59.39	0.41	LYS 1		
<i>Citrobacter braakii</i>	32.25	0.53	URE 88		
<i>Escherichia fergusonii</i>	2.25	0.22			
534063	Low discrimination				534063
				VPT	
<i>Escherichia coli</i>	89.89	0.55	SCI 1	1	
<i>Serratia marcescens</i>	7.02	0.23		98	
<i>Citrobacter braakii</i>	2.07	0.23		1	
534073	Low discrimination				534073
<i>Citrobacter farmeri</i>	58.11	0.39	LYS 1		
<i>Serratia odorifera</i> biovar 1	14.82	0.33	SCI 10		
<i>Kluyvera ascorbata</i>	14.26	0.27			
534103	Low discrimination				534103
<i>Hafnia alvei</i>	81.40	0.57	IND 1		
<i>Escherichia fergusonii</i>	18.26	0.31			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.34	-.17			
534113	Low discrimination				534113
<i>Escherichia fergusonii</i>	88.94	0.57	ADO 93		
<i>Kluyvera ascorbata</i>	5.32	0.24			
<i>Hafnia alvei</i>	3.68	0.42			
534133	Very good identification				534133
<i>Kluyvera ascorbata</i>	99.34	0.59	ESL 99		
<i>Escherichia fergusonii</i>	0.34	0.16			
<i>Hafnia alvei</i>	0.16	0.22			
534173	Very good identification				534173
				VPT	
<i>Kluyvera ascorbata</i>	96.64	0.55	ESL 99	1	
<i>Citrobacter koseri</i>	2.88	0.30		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.32	0.12		99	
534253	Identification to the genus				534253
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 2	88.68	0.57	ORN 1	99	
<i>Serratia odorifera</i> biovar 1	10.37	0.33		50	
<i>Citrobacter amalonaticus</i>	0.61	0.00		1	
534273	Very good identification				534273
<i>Serratia odorifera</i> biovar 1	99.80	0.74	ESL 95		
<i>Serratia odorifera</i> biovar 2	0.09	0.16			
<i>Serratia marcescens</i>	0.06	0.06			
534403	Very good identification				534403
<i>Escherichia fergusonii</i>	99.46	0.60	CEL 95		
<i>Escherichia coli</i>	0.36	0.15			
<i>Hafnia alvei</i>	0.18	0.16			
534411	Good identification				534411
<i>Escherichia fergusonii</i>	100.0	0.45	MAN 99		
534412	Good identification				534412
<i>Escherichia fergusonii</i>	100.0	0.51	TRE 98		
534413	Very good identification				534413
<i>Escherichia fergusonii</i>	99.91	0.86			
<i>Yokenella regensburgei</i>	0.07	0.12			
<i>Citrobacter koseri</i>	0.02	0.07			
534433	Good identification				534433
<i>Escherichia fergusonii</i>	97.70	0.45	SUC 1		
<i>Citrobacter koseri</i>	1.46	0.05			
<i>Kluyvera ascorbata</i>	0.48	-.11			
534453	Low discrimination				534453
				VPT	
<i>Escherichia fergusonii</i>	75.19	0.45	SOR 1	1	
<i>Citrobacter koseri</i>	19.79	0.31		1	
<i>Serratia odorifera</i> biovar 2	2.69	0.18		99	
534503	Very good identification				534503
<i>Escherichia fergusonii</i>	99.07	0.54	CEL 95		
<i>Citrobacter koseri</i>	0.59	0.07			
<i>Hafnia alvei</i>	0.34	0.16			
534511	Good identification				534511
<i>Escherichia fergusonii</i>	100.0	0.39	MAN 99		
534512	Good identification				534512
<i>Escherichia fergusonii</i>	100.0	0.46	TRE 98		
534513	Very good identification				534513
<i>Escherichia fergusonii</i>	99.51	0.80			
<i>Citrobacter koseri</i>	0.49	0.31			
534533	Low discrimination				534533
<i>Escherichia fergusonii</i>	60.10	0.39	SUC 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter koseri</i>	26.05	0.30			
<i>Kluyvera ascorbata</i>	13.25	0.18			
534553	Low discrimination				534553
<i>Citrobacter koseri</i>	88.45	0.56	LYS 1		
<i>Escherichia fergusonii</i>	11.55	0.39			
534573	Very good identification				534573
				VPT	
<i>Citrobacter koseri</i>	96.98	0.55	LYS 1	1	
<i>Kluyvera ascorbata</i>	2.10	0.14		1	
<i>Enterobacter aerogenes</i>	0.55	-0.02		98	
534613	Good identification				534613
				VPT	
<i>Escherichia fergusonii</i>	96.54	0.45	INO 1	1	
<i>Serratia odorifera biovar 2</i>	3.46	0.18		99	
534653	Good identification				534653
				VPT	
<i>Serratia odorifera biovar 2</i>	91.03	0.59	ORN 1	99	
<i>Serratia odorifera biovar 1</i>	8.71	0.33		50	
<i>Escherichia fergusonii</i>	0.26	0.04		1	
534673	Very good identification				534673
<i>Serratia odorifera biovar 1</i>	99.79	0.74	ESL 95		
<i>Serratia odorifera biovar 2</i>	0.11	0.18			
<i>Enterobacter aerogenes</i>	0.06	-0.02			
534713	Good identification				534713
<i>Escherichia fergusonii</i>	100.0	0.39	INO 1		
535413	Good identification				535413
<i>Escherichia fergusonii</i>	100.0	0.45	PHE 1		
535513	Good identification				535513
<i>Escherichia fergusonii</i>	100.0	0.39	PHE 1		
536013	Low discrimination				536013
<i>Yokenella regensburgei</i>	65.27	0.59	IND 1		
<i>Escherichia fergusonii</i>	28.79	0.61			
<i>Kluyvera ascorbata</i>	4.49	0.37			
536033	Very good identification				536033
				VPT	
<i>Kluyvera ascorbata</i>	98.44	0.72	MAL 96	1	
<i>Escherichia hermannii</i>	0.50	0.29		1	
<i>Cronobacter sakazakii</i>	0.50	0.30		99	
536043	Acceptable identification				536043
				VPT	
<i>Escherichia coli</i>	94.48	0.47	SCI 1	1	
<i>Serratia marcescens</i>	3.78	0.08		98	
<i>Kluyvera ascorbata</i>	0.97	-0.08		1	
536063	Low discrimination				536063
				VPT	
<i>Serratia marcescens</i>	75.74	0.49	IND 1	98	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	12.75	0.43		1	
<i>Kluyvera ascorbata</i>	9.60	0.27		1	
536073	Low discrimination				536073
				VPT	
<i>Kluyvera ascorbata</i>	83.00	0.68	MAL 96	1	
<i>Serratia odorifera</i> biovar 1	16.56	0.59		50	
<i>Serratia marcescens</i>	0.35	0.23		98	
536113	Low discrimination				536113
<i>Kluyvera ascorbata</i>	86.89	0.65	SUC 98		
<i>Escherichia fergusonii</i>	12.51	0.56			
<i>Yokenella regensburgei</i>	0.53	0.18			
536123	Very good identification				536123
<i>Kluyvera ascorbata</i>	99.90	0.59	CEL 99		
<i>Hafnia alvei</i>	0.10	0.18			
536131	Very good identification				536131
<i>Kluyvera ascorbata</i>	100.0	0.59	MAN 99		
536132	Very good identification				536132
<i>Kluyvera ascorbata</i>	100.0	0.59	TRE 99		
536133	Excellent identification				536133
				VPT	
<i>Kluyvera ascorbata</i>	99.99	1.00		1	
<i>Cronobacter sakazakii</i>	0.01	0.17		99	
<i>Escherichia fergusonii</i>	0.00	0.15		1	
536153	Very good identification				536153
<i>Kluyvera ascorbata</i>	99.61	0.62	SUC 98		
<i>Escherichia fergusonii</i>	0.22	0.15			
<i>Citrobacter sedlakii</i>	0.18	0.04			
536163	Very good identification				536163
				VPT	
<i>Kluyvera ascorbata</i>	98.94	0.55	CEL 99	1	
<i>Serratia marcescens</i>	1.01	0.18		98	
<i>Escherichia coli</i>	0.06	0.02		1	
536171	Very good identification				536171
<i>Kluyvera ascorbata</i>	100.0	0.55	MAN 99		
536172	Very good identification				536172
<i>Kluyvera ascorbata</i>	100.0	0.55	TRE 99		
536173	Excellent identification				536173
				VPT	
<i>Kluyvera ascorbata</i>	99.99	0.96		1	
<i>Serratia odorifera</i> biovar 1	0.01	0.18		50	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.00	0.05		99	
536233	Low discrimination				536233
				VPT	
<i>Serratia odorifera</i> biovar 1	83.93	0.59	SOR 99	50	
<i>Cronobacter sakazakii</i>	9.64	0.40		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Kluyvera ascorbata</i>	6.37	0.31		1	
536253	Identification to the genus				536253
				VPT	
<i>Serratia odorifera</i> biovar 1	76.83	0.59	SUC 99	50	
<i>Serratia odorifera</i> biovar 2	23.05	0.54		99	
<i>Kluyvera ascorbata</i>	0.08	-.08		1	
536263	Identification to the genus				536263
				VPT	
<i>Serratia marcescens</i>	54.50	0.59	IND 1	98	
<i>Serratia odorifera</i> biovar 1	45.47	0.59		50	
<i>Escherichia coli</i>	0.03	0.02		1	
536271	Very good identification				536271
<i>Serratia odorifera</i> biovar 1	99.94	0.59	MAN 99		
<i>Serratia marcescens</i>	0.06	-.09			
536272	Very good identification				536272
<i>Serratia odorifera</i> biovar 1	99.94	0.59	TRE 99		
<i>Serratia marcescens</i>	0.06	-.09			
536273	Excellent identification				536273
				VPT	
<i>Serratia odorifera</i> biovar 1	99.88	1.00		50	
<i>Serratia marcescens</i>	0.06	0.33		98	
<i>Kluyvera ascorbata</i>	0.05	0.27		1	
536333	Very good identification				536333
				VPT	
<i>Kluyvera ascorbata</i>	98.07	0.59	INO 1	1	
<i>Cronobacter sakazakii</i>	1.36	0.27		99	
<i>Serratia odorifera</i> biovar 1	0.54	0.18		50	
536373	Low discrimination				536373
				VPT	
<i>Kluyvera ascorbata</i>	53.26	0.55	INO 1	1	
<i>Serratia odorifera</i> biovar 1	43.84	0.59		50	
<i>Enterobacter aerogenes</i>	2.67	0.24		98	
536403	Very good identification				536403
<i>Escherichia fergusonii</i>	99.90	0.58	CEL 95		
<i>Escherichia coli</i>	0.11	0.02			
536411	Good identification				536411
<i>Escherichia fergusonii</i>	100.0	0.43	MAN 99		
536412	Good identification				536412
<i>Escherichia fergusonii</i>	100.0	0.50	TRE 98		
536413	Very good identification				536413
<i>Escherichia fergusonii</i>	99.81	0.84			
<i>Yokenella regensburgei</i>	0.17	0.18			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.01	0.09			
536433	Low discrimination				536433
<i>Escherichia fergusonii</i>	60.33	0.43	SUC 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Kluyvera ascorbata</i>	34.68	0.31			
<i>Serratia odorifera</i> biovar 1	4.61	0.18			
536453	Low discrimination				536453
				VPT	
<i>Escherichia fergusonii</i>	88.89	0.43	SOR 1	1	
<i>Serratia odorifera</i> biovar 1	6.80	0.18		50	
<i>Serratia odorifera</i> biovar 2	2.49	0.14		99	
536463	Good identification				536463
				VPT	
<i>Serratia marcescens</i>	95.13	0.46	IND 1	98	
<i>Serratia odorifera</i> biovar 1	3.61	0.18		50	
<i>Escherichia coli</i>	1.27	0.17		1	
536473	Good identification				536473
				VPT	
<i>Serratia odorifera</i> biovar 1	93.09	0.59	INO 99	50	
<i>Kluyvera ascorbata</i>	4.71	0.27		1	
<i>Serratia marcescens</i>	1.31	0.19		98	
536503	Good identification				536503
<i>Escherichia fergusonii</i>	100.0	0.53	CEL 95		
536511	Good identification				536511
<i>Escherichia fergusonii</i>	100.0	0.38	MAN 99		
536512	Good identification				536512
<i>Escherichia fergusonii</i>	100.0	0.44	TRE 98		
536513	Very good identification				536513
<i>Escherichia fergusonii</i>	99.48	0.79			
<i>Kluyvera ascorbata</i>	0.53	0.24			
536533	Very good identification				536533
				VPT	
<i>Kluyvera ascorbata</i>	95.50	0.59	ADO 1	1	
<i>Escherichia fergusonii</i>	3.73	0.38		1	
<i>Serratia rubidaea</i>	0.69	0.18		99	
536553	Low discrimination				536553
<i>Escherichia fergusonii</i>	68.41	0.38	SOR 1		
<i>Kluyvera ascorbata</i>	23.85	0.21			
<i>Citrobacter koseri</i>	6.21	0.15			
536573	Low discrimination				536573
				VPT	
<i>Kluyvera ascorbata</i>	87.08	0.55	ADO 1	1	
<i>Enterobacter aerogenes</i>	11.24	0.33		98	
<i>Serratia odorifera</i> biovar 1	0.72	0.18		50	
536613	Low discrimination				536613
				VPT	
<i>Escherichia fergusonii</i>	89.86	0.43	INO 1	1	
<i>Serratia odorifera</i> biovar 1	6.87	0.18		50	
<i>Serratia odorifera</i> biovar 2	2.52	0.14		99	
536633	Very good identification				536633
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia odorifera</i> biovar 1	99.52	0.59	SOR 99	50	
<i>Enterobacter aerogenes</i>	0.16	-.09		98	
<i>Escherichia fergusonii</i>	0.13	0.02		1	
536653	Identification to the genus				536653
				VPT	
<i>Serratia odorifera</i> biovar 1	72.91	0.59	SUC 99	50	
<i>Serratia odorifera</i> biovar 2	26.73	0.55		99	
<i>Klebsiella pneumoniae</i> subsp. ozaenae	0.15	0.17		1	
536663	Identification to the genus				536663
<i>Serratia odorifera</i> biovar 1	55.54	0.59	CEL 99		
<i>Serratia marcescens</i>	44.38	0.55			
<i>Enterobacter aerogenes</i>	0.09	-.09			
536671	Very good identification				536671
<i>Serratia odorifera</i> biovar 1	99.84	0.59	MAN 99		
<i>Enterobacter aerogenes</i>	0.16	-.09			
536672	Very good identification				536672
<i>Serratia odorifera</i> biovar 1	99.84	0.59	TRE 99		
<i>Enterobacter aerogenes</i>	0.16	-.09			
536673	Excellent identification				536673
<i>Serratia odorifera</i> biovar 1	99.79	1.00			
<i>Enterobacter aerogenes</i>	0.16	0.33			
<i>Serratia marcescens</i>	0.04	0.29			
536713	Good identification				536713
<i>Escherichia fergusonii</i>	100.0	0.38	INO 1		
536773	Low discrimination				536773
<i>Enterobacter aerogenes</i>	68.79	0.59	IND 1		
<i>Serratia odorifera</i> biovar 1	23.09	0.59			
<i>Klebsiella oxytoca</i>	7.78	0.39			
537133	Very good identification				537133
				VPT	
<i>Kluyvera ascorbata</i>	99.54	0.59	PHE 1	1	
<i>Cronobacter sakazakii</i>	0.46	0.17		99	
537173	Very good identification				537173
<i>Kluyvera ascorbata</i>	100.0	0.55	PHE 1		
537233	Acceptable identification				537233
				VPT	
<i>Cronobacter sakazakii</i>	91.35	0.40	LYS 1	99	
<i>Serratia odorifera</i> biovar 1	8.04	0.18	IND 11	50	
<i>Kluyvera ascorbata</i>	0.61	-.11		1	
537273	Very good identification				537273
<i>Serratia odorifera</i> biovar 1	99.82	0.59	PHE 1		
<i>Cronobacter sakazakii</i>	0.12	-.01			
<i>Serratia marcescens</i>	0.06	-.09			
537413	Good identification				537413

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	100.0	0.43	PHE 1		
537513	Good identification				537513
<i>Escherichia fergusonii</i>	100.0	0.38	PHE 1		
537673	Very good identification				537673
<i>Serratia odorifera</i> biovar 1	99.84	0.59	PHE 1		
<i>Enterobacter aerogenes</i>	0.16	-.09			
540003	Low discrimination				540003
<i>Hafnia alvei</i>	69.05	0.63	ORN 98		
<i>Yersinia pseudotuberculosis</i>	28.47	0.33			
<i>Escherichia coli</i>	1.04	0.19			
540013	Low discrimination				540013
<i>Escherichia vulneris</i>	85.05	0.43	URE 1		
<i>Hafnia alvei</i>	12.77	0.48			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.41	0.26			
540023	Low discrimination				540023
<i>Hafnia alvei</i>	79.04	0.44	ORN 98		
<i>Yersinia rohdei</i>	10.89	0.15	SUC 10		
<i>Escherichia coli</i>	7.11	0.15			
540043	Low discrimination				540043
<i>Citrobacter youngae</i>	56.07	0.44	LYS 1		
<i>Escherichia coli</i>	26.42	0.36			
<i>Citrobacter freundii</i>	3.78	0.22			
540053	Low discrimination				540053
<i>Yersinia kristensenii</i>	53.62	0.37	LYS 1		
<i>Citrobacter youngae</i>	31.52	0.42	ORN 92		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.98	0.32			
540063	Low discrimination				540063
<i>Yersinia rohdei</i>	83.89	0.56	LYS 1		
<i>Citrobacter freundii</i>	7.04	0.41			
<i>Escherichia coli</i>	4.06	0.33			
540073	Low discrimination				540073
<i>Yersinia rohdei</i>	67.05	0.47	LYS 1		
<i>Citrobacter freundii</i>	13.27	0.39			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.31	0.33			
540103	Good identification				540103
<i>Hafnia alvei</i>	92.74	0.63	ORN 98		
<i>Escherichia vulneris</i>	6.24	0.18			
<i>Citrobacter werkmanii</i>	0.64	-.04			
540113	Very good identification				540113
<i>Escherichia vulneris</i>	97.42	0.59	URE 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	2.58	0.48			
540123	Acceptable identification				540123
<i>Hafnia alvei</i>	95.00	0.44	ORN 98		
<i>Escherichia vulneris</i>	5.00	-.04	SUC 10		
540133	Good identification				540133
<i>Escherichia vulneris</i>	96.73	0.37	URE 1		
<i>Hafnia alvei</i>	3.27	0.28	SUC 8		
540403	Low discrimination				540403
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.35	0.35	URE 10		
<i>Hafnia alvei</i>	14.62	0.22	CEL 92		
<i>Yersinia pseudotuberculosis</i>	6.03	-.09			
540413	Very good identification				540413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.15	0.57	URE 10		
<i>Escherichia vulneris</i>	1.85	0.02			
540433	Good identification				540433
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.45	URE 10		
540443	Acceptable identification				540443
<i>Klebsiella pneumoniae subsp. ozaenae</i>	92.60	0.41	URE 10		
<i>Escherichia coli</i>	5.26	0.10	CEL 92		
<i>Citrobacter youngae</i>	2.14	0.03			
540453	Very good identification				540453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	99.72	0.63	URE 10		
<i>Yersinia kristensenii</i>	0.28	-.04			
540473	Good identification				540473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.29	0.50	URE 10		
<i>Yersinia rohdei</i>	1.71	0.06			
540603	Good identification				540603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.37	URE 10		
540613	Very good identification				540613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.59	URE 10		
540633	Good identification				540633
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.46	URE 10		
540643	Good identification				540643
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.43	URE 10		
540653	Very good identification				540653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.13	0.64	URE 10	1	
<i>Serratia odorifera biovar 2</i>	3.87	0.28		99	
540673	Good identification				540673
				VPT	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.21	0.52	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	3.79	0.01		98	
541001	Good identification				541001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	ONP 1		
542003	Very good identification				542003
<i>Yersinia pseudotuberculosis</i>	98.43	0.59	LYS 1		
<i>Hafnia alvei</i>	1.40	0.44			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.09	0.17			
542053	Low discrimination				542053
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	89.89	0.44	URE 10		
<i>Citrobacter youngae</i>	6.23	0.16	ADO 97		
<i>Yersinia kristensenii</i>	2.04	-.04			
542103	Low discrimination				542103
<i>Hafnia alvei</i>	53.66	0.44	ORN 98		
<i>Yersinia pseudotuberculosis</i>	38.22	0.18	ESL 10		
<i>Escherichia vulneris</i>	8.12	0.05			
542113	Good identification				542113
<i>Escherichia vulneris</i>	98.70	0.47	URE 1		
<i>Hafnia alvei</i>	1.16	0.28			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.14	0.07			
542213	Good identification				542213
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	96.98	0.40	URE 10		
<i>Escherichia vulneris</i>	3.02	-.10	ADO 97		
542253	Low discrimination				542253
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	84.91	0.46	URE 10	1	
<i>Serratia odorifera</i> biovar 2	15.09	0.22	ADO 97	99	
542373	Good identification				542373
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	99.74	0.46	SCI 98		
<i>Klebsiella oxytoca</i>	0.27	-.09	ADO 90		
542403	Low discrimination				542403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	73.49	0.48	URE 10		
<i>Yersinia pseudotuberculosis</i>	26.52	0.18	CEL 92		
542413	Very good identification				542413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.88	0.69	URE 10		
<i>Escherichia vulneris</i>	0.12	-.10			
542423	Good identification				542423
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.35	URE 10		
542433	Very good identification				542433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.09	0.57	URE 10	1	
<i>Serratia rubidaea</i>	4.50	0.14		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Leclercia adecarboxylata</i>	0.41	-.05		1	
542443	Very good identification				542443
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.53	URE 10		
542452	Good identification				542452
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.40	URE 10		
542453	Very good identification				542453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.75	URE 10		
542463	Good identification				542463
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	96.90	0.41	URE 10	1	
<i>Serratia marcescens</i>	3.10	-.05	CEL 92	98	
542473	Good identification				542473
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	94.10	0.63	URE 10	1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	5.90	0.16		98	
542513	Low discrimination				542513
<i>Klebsiella pneumoniae subsp. ozaenae</i>	66.02	0.38	URE 10		
<i>Leclercia adecarboxylata</i>	15.75	0.12	MAL 3		
<i>Escherichia vulneris</i>	14.24	0.05			
542533	Low discrimination				542533
				VPT	
<i>Serratia rubidaea</i>	87.71	0.39	URE 2	99	
<i>Leclercia adecarboxylata</i>	6.78	0.18	SCI 95	1	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.66	0.26		1	
542553	Acceptable identification				542553
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.63	0.44	URE 10	1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	6.37	-.02	MAL 3	98	
542573	Acceptable identification				542573
				VPT	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	94.94	0.39	SCI 98	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	3.52	0.32	INO 95	1	
<i>Klebsiella oxytoca</i>	1.08	-.02		95	
542603	Good identification				542603
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.49	URE 10		
542612	Good identification				542612
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.36	URE 10		
542613	Very good identification				542613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.71	URE 10		
542623	Good identification				542623
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.37	URE 10		
542633	Very good identification				542633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	97.28	0.59	URE 10	1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.78	0.01		98	
<i>Serratia rubidaea</i>	0.94	0.02		99	
542643	Very good identification				542643
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.55	URE 10		
542651	Good identification				542651
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.36	URE 10		
542652	Good identification				542652
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.42	URE 10		
542653	Very good identification				542653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.09	0.77	URE 10	1	
<i>Serratia odorifera</i> biovar 2	0.67	0.24		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.24	0.01		98	
542663	Low discrimination				542663
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	76.49	0.43	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	17.51	0.07	CEL 92	98	
<i>Serratia marcescens</i>	6.00	0.05		98	
542673	Identification to the genus				542673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	50.43	0.64	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	49.18	0.42		98	
<i>Klebsiella oxytoca</i>	0.39	-.02		95	
542713	Good identification				542713
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.40	URE 10		
542773	Very good identification				542773
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	96.83	0.65	SCI 98	98	
<i>Klebsiella oxytoca</i>	2.83	0.33		95	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.23	0.33		1	
543653	Good identification				543653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.36	URE 10		
544003	Very good identification				544003
<i>Hafnia alvei</i>	98.26	0.63	ORN 98		
<i>Citrobacter werkmanii</i>	0.67	-.04			
<i>Citrobacter youngae</i>	0.66	0.12			
544013	Low discrimination				544013
<i>Hafnia alvei</i>	73.58	0.48	ORN 98		
<i>Yokenella regensburgei</i>	15.70	0.12			
<i>Escherichia vulneris</i>	4.95	0.02			
544023	Good identification				544023
<i>Hafnia alvei</i>	95.58	0.44	ORN 98		
<i>Citrobacter freundii</i>	4.42	0.12	SUC 10		
544043	Identification to the genus				544043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	80.50	0.53	LYS 1		
<i>Citrobacter freundii</i>	7.62	0.35			
<i>Citrobacter werkmanii</i>	7.48	0.15			
544053	Low discrimination				544053
<i>Citrobacter youngae</i>	76.37	0.52	LYS 1		
<i>Citrobacter braakii</i>	7.48	0.31			
<i>Citrobacter freundii</i>	6.95	0.33			
544063	Identification to the genus				544063
<i>Citrobacter freundii</i>	71.15	0.54	LYS 1		
<i>Citrobacter youngae</i>	24.68	0.42			
<i>Yersinia rohdei</i>	2.14	0.15			
544073	Low discrimination				544073
				VPT	
<i>Citrobacter freundii</i>	66.85	0.51	LYS 1	1	
<i>Citrobacter youngae</i>	24.15	0.40		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	5.83	0.21		99	
544103	Good identification				544103
<i>Hafnia alvei</i>	92.69	0.63	ORN 98		
<i>Citrobacter werkmanii</i>	7.31	0.17			
544113	Low discrimination				544113
<i>Hafnia alvei</i>	72.40	0.48	ORN 98		
<i>Escherichia vulneris</i>	27.60	0.18			
544123	Good identification				544123
<i>Hafnia alvei</i>	100.0	0.44	ORN 98		
544143	Acceptable identification				544143
<i>Citrobacter werkmanii</i>	93.35	0.37	H2S 92		
<i>Citrobacter youngae</i>	4.60	0.27	LYS 1		
<i>Hafnia alvei</i>	1.33	0.22			
544253	Very good identification				544253
				VPT	
<i>Serratia odorifera</i> biovar 2	96.98	0.57	URE 1	99	
<i>Citrobacter youngae</i>	1.82	0.25		1	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.21	0.26		1	
544373	Good identification				544373
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.22	0.39	ESL 99		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	1.78	0.15	ADO 90		
544413	Good identification				544413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.49	URE 10		
544433	Low discrimination				544433
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	65.14	0.37	URE 10	1	
<i>Serratia rubidaea</i>	34.86	0.16		99	
544453	Very good identification				544453

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	95.38	0.55	URE 10	1	
<i>Serratia odorifera</i> biovar 2	3.58	0.18		99	
<i>Citrobacter youngae</i>	1.04	0.11		1	
544473	Low discrimination				544473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	70.69	0.43	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	20.49	0.10		98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	6.55	0.11		99	
544533	Good identification				544533
				VPT	
<i>Serratia rubidaea</i>	98.79	0.41	URE 2	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.85	-.09	ESL 94	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.36	0.06		1	
544613	Acceptable identification				544613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	94.60	0.51	URE 10	1	
<i>Serratia odorifera</i> biovar 2	5.40	0.18		99	
544633	Low discrimination				544633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	83.75	0.39	URE 10	1	
<i>Serratia rubidaea</i>	9.17	0.04		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	7.08	-.05		98	
544653	Low discrimination				544653
				VPT	
<i>Serratia odorifera</i> biovar 2	75.04	0.59	URE 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	24.68	0.57		1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.28	-.05		98	
544673	Identification to the genus				544673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	79.09	0.36	ESL 99	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	17.56	0.44	MAL 93	1	
<i>Serratia odorifera</i> biovar 2	2.16	0.18		99	
544773	Very good identification				544773
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.67	0.59	ESL 99		
<i>Klebsiella oxytoca</i>	1.12	0.18			
<i>Enterobacter aerogenes</i>	0.09	-.04			
546003	Low discrimination				546003
<i>Hafnia alvei</i>	57.52	0.44	ORN 98		
<i>Yersinia pseudotuberculosis</i>	40.97	0.18	ESL 10		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.51	0.09			
546053	Low discrimination				546053
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	57.44	0.36	URE 10	1	
<i>Citrobacter youngae</i>	26.45	0.25	ADO 97	1	
<i>Serratia odorifera</i> biovar 2	9.51	0.12		99	
546103	Good identification				546103
<i>Hafnia alvei</i>	100.0	0.44	ORN 98		
546173	Very good identification				546173

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	99.06	0.54	INO 95	98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.84	0.23	ADO 90	99	
<i>Kluyvera ascorbata</i>	0.07	-.08		1	
546253	Low discrimination				546253
				VPT	
<i>Serratia odorifera</i> biovar 2	86.95	0.54	URE 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	6.56	0.16		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	6.49	0.38		1	
546263	Low discrimination				546263
<i>Serratia marcescens</i>	82.22	0.43	ORN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	17.78	0.22			
546273	Very good identification				546273
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	96.71	0.57	MAL 93		
<i>Serratia odorifera</i> biovar 1	1.51	0.29	ADO 90		
<i>Serratia ficaria</i>	0.86	0.18			
546333	Good identification				546333
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	97.85	0.39	ADO 90		
<i>Serratia rubidaea</i>	2.15	0.12	SOR 99		
546353	Good identification				546353
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.78	0.39	ADO 90	98	
<i>Serratia odorifera</i> biovar 2	1.00	0.12	SUC 99	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.23	0.07		1	
546363	Good identification				546363
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.94	0.46	ADO 90		
<i>Serratia marcescens</i>	1.07	0.12	CEL 98		
546371	Good identification				546371
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	100.0	0.39	ADO 90		
546372	Good identification				546372
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	100.0	0.39	ADO 90		
546373	Very good identification				546373
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	99.88	0.80	ADO 90		
<i>Klebsiella oxytoca</i>	0.10	0.18			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.01	0.07			
546403	Good identification				546403
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.40	URE 10		
546413	Very good identification				546413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	99.47	0.62	URE 10	1	
<i>Serratia rubidaea</i>	0.53	-.01		99	
546433	Low discrimination				546433
				VPT	
<i>Serratia rubidaea</i>	64.88	0.41	URE 2	99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	30.95	0.49	MAL 94	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	4.17	0.10		98	
546443	Good identification				546443
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.46	URE 10		
546453	Very good identification				546453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.62	0.67	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.77	0.10		98	
<i>Serratia odorifera</i> biovar 2	0.61	0.14		99	
546473	Identification to the genus				546473
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	87.27	0.51	MAL 93	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	12.17	0.55	INO 95	1	
<i>Serratia marcescens</i>	0.20	0.04		98	
546523	Good identification				546523
<i>Serratia rubidaea</i>	98.29	0.41	URE 2		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.71	-0.02	CEL 94		
546533	Good identification				546533
				VPT	
<i>Serratia rubidaea</i>	94.73	0.65	URE 2	99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	5.16	0.33		98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.09	0.18		1	
546563	Good identification				546563
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.71	0.39	INO 95		
<i>Serratia rubidaea</i>	0.58	-0.01	CEL 98		
<i>Serratia marcescens</i>	0.50	-0.01			
546573	Very good identification				546573
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	99.27	0.74	INO 95		
<i>Klebsiella oxytoca</i>	0.44	0.24			
<i>Serratia rubidaea</i>	0.19	0.24			
546603	Good identification				546603
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.42	URE 10		
546613	Very good identification				546613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	98.54	0.64	URE 10	1	
<i>Serratia odorifera</i> biovar 2	0.94	0.14		99	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.52	-0.05		98	
546633	Low discrimination				546633
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	59.31	0.36	MAL 93	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	28.35	0.51	SOR 99	1	
<i>Serratia rubidaea</i>	12.16	0.28		99	
546643	Low discrimination				546643
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	87.14	0.47	URE 10	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	5.76	0.01	CEL 92	98	
<i>Serratia odorifera</i> biovar 2	5.13	0.14		99	

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
546653	Low discrimination					546653
					VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		55.89	0.69	URE 10	1	
<i>Serratia odorifera biovar 2</i>		28.32	0.55		99	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		15.74	0.36		98	
546663	Low discrimination					546663
					VPT	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		72.34	0.42	MAL 93	98	
<i>Serratia marcescens</i>		24.79	0.40	CEL 98	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		2.76	0.35		1	
546671	Good identification					546671
					VPT	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		98.81	0.36	MAL 93	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		0.89	0.16	MAN 99	1	
<i>Klebsiella oxytoca</i>		0.30	-.17		95	
546672	Good identification					546672
					VPT	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		97.93	0.36	MAL 93	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		1.77	0.22	TRE 99	1	
<i>Klebsiella oxytoca</i>		0.30	-.17		95	
546673	Very good identification					546673
					VPT	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		98.56	0.77	MAL 93	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		0.88	0.57		1	
<i>Klebsiella oxytoca</i>		0.30	0.24		95	
546733	Low discrimination					546733
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		79.71	0.59	SOR 99		
<i>Serratia rubidaea</i>		19.27	0.53			
<i>Klebsiella oxytoca</i>		0.90	0.18			
546753	Very good identification					546753
					VPT	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		97.90	0.59	SUC 99	98	
<i>Klebsiella oxytoca</i>		1.11	0.18		95	
<i>Klebsiella pneumoniae subsp. ozaenae</i>		0.81	0.38		1	
546763	Very good identification					546763
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		99.34	0.65	CEL 98		
<i>Klebsiella oxytoca</i>		0.56	0.18			
<i>Serratia marcescens</i>		0.08	0.09			
546771	Very good identification					546771
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		98.84	0.59	MAN 99		
<i>Klebsiella oxytoca</i>		1.12	0.18			
<i>Enterobacter aerogenes</i>		0.05	-.11			
546772	Very good identification					546772
<i>Klebsiella pneumoniae subsp. pneumoniae</i>		98.84	0.59	TRE 99		
<i>Klebsiella oxytoca</i>		1.12	0.18			
<i>Enterobacter aerogenes</i>		0.05	-.11			
546773	Very good identification					546773

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.83	1.00			
<i>Klebsiella oxytoca</i>	1.12	0.59			
<i>Enterobacter aerogenes</i>	0.05	0.30			
547373	Good identification				547373
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	100.0	0.39	PHE 1		
547673	Good identification				547673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.81	0.36	PHE 1	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.89	0.16	MAL 93	1	
<i>Klebsiella oxytoca</i>	0.30	-.17		95	
547773	Very good identification				547773
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	98.84	0.59	PHE 1		
<i>Klebsiella oxytoca</i>	1.12	0.18			
<i>Enterobacter aerogenes</i>	0.05	-.11			
550003	Acceptable identification				550003
<i>Escherichia coli</i>	92.36	0.40	URE 1		
<i>Hafnia alvei</i>	5.41	0.22	SOR 88		
<i>Yersinia pseudotuberculosis</i>	2.23	-.09			
550023	Good identification				550023
<i>Escherichia coli</i>	100.0	0.37	URE 1		
550043	Very good identification				550043
<i>Escherichia coli</i>	95.96	0.58	URE 1		
<i>Citrobacter youngae</i>	3.13	0.29			
<i>Citrobacter freundii</i>	0.59	0.16			
550063	Low discrimination				550063
<i>Escherichia coli</i>	87.78	0.55	URE 1		
<i>Citrobacter freundii</i>	6.53	0.35			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.96	0.23			
551001	Good identification				551001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.46	ONP 1		
552043	Good identification				552043
<i>Escherichia coli</i>	99.32	0.46	URE 1		
<i>Citrobacter youngae</i>	0.68	0.02			
552063	Good identification				552063
<i>Escherichia coli</i>	95.70	0.42	URE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.30	0.13			
552133	Good identification				552133
<i>Leclercia adecarboxylata</i>	99.04	0.36	LYS 1		
<i>Kluyvera ascorbata</i>	0.96	-.11	ADO 93		
552433	Good identification				552433
<i>Leclercia adecarboxylata</i>	97.69	0.36	LYS 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.31	0.16	MAL 93		
552513	Very good identification				552513
<i>Leclercia adecarboxylata</i>	99.36	0.53	LYS 1		
<i>Escherichia fergusonii</i>	0.64	0.11			
552533	Very good identification				552533
				VPT	
<i>Leclercia adecarboxylata</i>	99.56	0.59	LYS 1	1	
<i>Klebsiella oxytoca</i>	0.31	-.02		95	
<i>Serratia rubidaea</i>	0.13	-.02		99	
552573	Good identification				552573
				VPT	
<i>Klebsiella oxytoca</i>	95.97	0.39	SCI 95	95	
<i>Leclercia adecarboxylata</i>	3.17	0.18	INO 98	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.87	-.02		98	
552653	Low discrimination				552653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	53.88	0.36	IND 1	1	
<i>Serratia odorifera</i> biovar 2	35.83	0.24	URE 10	99	
<i>Klebsiella oxytoca</i>	10.29	-.02		95	
552673	Good identification				552673
				VPT	
<i>Klebsiella oxytoca</i>	97.46	0.39	SCI 95	95	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.29	0.23	MAL 98	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.26	0.01		98	
552773	Very good identification				552773
<i>Klebsiella oxytoca</i>	99.65	0.74	SCI 95		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.35	0.24			
554043	Low discrimination				554043
<i>Citrobacter youngae</i>	65.55	0.38	LYS 1		
<i>Citrobacter freundii</i>	17.33	0.29			
<i>Citrobacter braakii</i>	7.22	0.19			
554063	Identification to the genus				554063
<i>Citrobacter freundii</i>	86.34	0.47	LYS 1		
<i>Citrobacter youngae</i>	10.73	0.26			
<i>Escherichia coli</i>	2.93	0.14			
554073	Identification to the genus				554073
<i>Citrobacter freundii</i>	75.46	0.45	LYS 1		
<i>Citrobacter amalonaticus</i>	11.97	0.10			
<i>Citrobacter youngae</i>	9.77	0.24			
554253	Very good identification				554253
				VPT	
<i>Serratia odorifera</i> biovar 2	99.35	0.57	URE 1	99	
<i>Citrobacter youngae</i>	0.33	0.10		1	
<i>Citrobacter amalonaticus</i>	0.32	-.07		1	
554653	Very good identification				554653
				VPT	
<i>Serratia odorifera</i> biovar 2	99.56	0.59	URE 1	99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.33	0.16		1	
<i>Klebsiella oxytoca</i>	0.11	-.17		95	
554773	Very good identification				554773
<i>Klebsiella oxytoca</i>	99.11	0.59	ESL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.89	0.18			
556253	Very good identification				556253
<i>Serratia odorifera</i> biovar 2	99.79	0.54	URE 1		
<i>Klebsiella oxytoca</i>	0.21	-.17			
556373	Good identification				556373
<i>Klebsiella oxytoca</i>	90.98	0.59	ADO 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	9.02	0.39			
556573	Very good identification				556573
<i>Klebsiella oxytoca</i>	97.73	0.65	INO 98		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2.27	0.33			
556653	Low discrimination				556653
				VPT	
<i>Serratia odorifera</i> biovar 2	83.73	0.55	URE 1	99	
<i>Klebsiella oxytoca</i>	14.14	0.24		95	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.67	0.28		1	
556673	Very good identification				556673
<i>Klebsiella oxytoca</i>	95.90	0.65	MAL 98		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	3.19	0.36			
<i>Serratia odorifera</i> biovar 1	0.82	0.33			
556733	Very good identification				556733
<i>Klebsiella oxytoca</i>	98.89	0.59	SOR 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.89	0.18			
<i>Serratia rubidaea</i>	0.22	0.12			
556753	Very good identification				556753
<i>Klebsiella oxytoca</i>	98.99	0.59	SUC 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.89	0.18			
<i>Serratia odorifera</i> biovar 2	0.12	0.14			
556763	Very good identification				556763
<i>Klebsiella oxytoca</i>	98.21	0.59	CEL 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.79	0.24			
556771	Very good identification				556771
<i>Klebsiella oxytoca</i>	99.11	0.59	MAN 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.89	0.18			
556772	Very good identification				556772
<i>Klebsiella oxytoca</i>	99.11	0.59	TRE 99		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.89	0.18			
556773	Excellent identification				556773

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella oxytoca</i>	99.11	1.00			
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.89	0.59			
<i>Enterobacter aerogenes</i>	0.00	-.11			
557773	Very good identification				557773
<i>Klebsiella oxytoca</i>	99.11	0.59	PHE 1		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.89	0.18			
560001	Low discrimination				560001
<i>Hafnia alvei</i>	87.32	0.57	MAN 99		
<i>Morganella morganii subsp. sibonii</i>	12.68	0.28			
560002	Very good identification				560002
<i>Hafnia alvei</i>	99.11	0.57	TRE 99		
<i>Salmonella enterica subsp. enterica</i>	0.89	-.02			
560003	Excellent identification				560003
<i>Hafnia alvei</i>	99.74	0.98			
<i>Shigella sonnei</i>	0.21	0.18			
<i>Escherichia coli</i>	0.03	0.19			
560011	Good identification				560011
<i>Hafnia alvei</i>	96.39	0.42	MAN 99		
<i>Yokenella regensburgei</i>	3.61	-.10			
560012	Good identification				560012
<i>Hafnia alvei</i>	96.39	0.42	TRE 99		
<i>Yokenella regensburgei</i>	3.61	-.10			
560013	Very good identification				560013
<i>Hafnia alvei</i>	95.71	0.83			
<i>Yokenella regensburgei</i>	3.59	0.31			
<i>Yersinia kristensenii</i>	0.42	0.18			
560021	Acceptable identification				560021
<i>Hafnia alvei</i>	92.30	0.38	SUC 10		
<i>Morganella morganii subsp. sibonii</i>	7.70	0.03	MAN 99		
560022	Good identification				560022
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
560023	Very good identification				560023
<i>Hafnia alvei</i>	99.61	0.79	SUC 10		
<i>Escherichia coli</i>	0.20	0.16			
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.10	0.08			
560033	Very good identification				560033
<i>Hafnia alvei</i>	97.80	0.63	SUC 10		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	1.66	0.18			
<i>Yokenella regensburgei</i>	0.33	-.10			
560043	Low discrimination				560043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	60.54	0.57	SOR 1		
<i>Escherichia coli</i>	14.56	0.37			
<i>Citrobacter braakii</i>	14.19	0.38			
560053	Low discrimination				560053
<i>Yersinia kristensenii</i>	89.72	0.59	LYS 1		
<i>Citrobacter braakii</i>	5.66	0.45			
<i>Hafnia alvei</i>	2.10	0.42			
560063	Low discrimination				560063
<i>Yersinia enterocolitica ssp. enterocolitica</i>	44.46	0.49	LYS 1		
<i>Yersinia rohdei</i>	41.64	0.47			
<i>Escherichia coli</i>	6.55	0.34			
560073	Low discrimination				560073
<i>Yersinia enterocolitica ssp. enterocolitica</i>	84.80	0.59	LYS 1		
<i>Yersinia rohdei</i>	8.82	0.37			
<i>Citrobacter farmeri</i>	2.52	0.15			
560101	Very good identification				560101
<i>Hafnia alvei</i>	100.0	0.57	MAN 99		
560102	Very good identification				560102
<i>Hafnia alvei</i>	100.0	0.57	TRE 99		
560103	Excellent identification				560103
<i>Hafnia alvei</i>	100.0	0.98			
560111	Good identification				560111
<i>Hafnia alvei</i>	100.0	0.42	MAN 99		
560112	Good identification				560112
<i>Hafnia alvei</i>	100.0	0.42	TRE 99		
560113	Very good identification				560113
<i>Hafnia alvei</i>	99.13	0.83			
<i>Escherichia vulneris</i>	0.77	0.18			
<i>Yokenella regensburgei</i>	0.04	-.10			
560121	Good identification				560121
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
560122	Good identification				560122
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
560123	Very good identification				560123
<i>Hafnia alvei</i>	100.0	0.79	SUC 10		
560133	Very good identification				560133
<i>Hafnia alvei</i>	99.40	0.63	SUC 10		
<i>Escherichia vulneris</i>	0.61	-.04			
560143	Very good identification				560143

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	98.98	0.57	SOR 1		
<i>Citrobacter sedlakii</i>	0.60	-.11			
<i>Salmonella enterica subsp. diarizonae</i>	0.42	-.17			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
560163	Low discrimination				560163
<i>Hafnia alvei</i>	83.91	0.38	SUC 10		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	8.31	0.08	SOR 1		
<i>Yersinia rohdei</i>	7.78	0.06			
560203	Very good identification				560203
<i>Hafnia alvei</i>	100.0	0.57	INO 1		
560213	Low discrimination				560213
<i>Hafnia alvei</i>	89.79	0.42	INO 1		
<i>Yersinia kristensenii</i>	6.84	0.02			
<i>Yokenella regensburgei</i>	3.37	-.10			
560223	Good identification				560223
<i>Hafnia alvei</i>	95.93	0.38	INO 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.07	0.00	SUC 10		
560253	Acceptable identification				560253
<i>Yersinia kristensenii</i>	94.43	0.43	LYS 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.23	0.25			
<i>Citrobacter braakii</i>	0.34	0.04			
560263	Low discrimination				560263
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	73.96	0.42	LYS 1	2	
<i>Serratia marcescens</i>	24.41	0.23		98	
<i>Yersinia rohdei</i>	1.63	0.06		1	
560273	Good identification				560273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	97.62	0.51	LYS 1		
<i>Yersinia kristensenii</i>	0.94	0.02			
<i>Serratia odorifera</i> biovar 1	0.88	0.03			
560303	Very good identification				560303
<i>Hafnia alvei</i>	100.0	0.57	INO 1		
560313	Good identification				560313
<i>Hafnia alvei</i>	100.0	0.42	INO 1		
560323	Good identification				560323
<i>Hafnia alvei</i>	100.0	0.38	INO 1		
560403	Very good identification				560403
<i>Hafnia alvei</i>	99.45	0.57	ADO 1		
<i>Escherichia fergusonii</i>	0.55	-.02			
560413	Low discrimination				560413
<i>Hafnia alvei</i>	53.74	0.42	ADO 1		
<i>Escherichia fergusonii</i>	32.24	0.24			
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	12.00	0.26			
560423	Good identification				560423

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	100.0	0.38	ADO 1		
560503	Very good identification				560503
<i>Hafnia alvei</i>	100.0	0.57	ADO 1		
560513	Low discrimination				560513
<i>Hafnia alvei</i>	75.58	0.42	ADO 1		
<i>Escherichia fergusonii</i>	24.42	0.19			
560523	Good identification				560523
<i>Hafnia alvei</i>	100.0	0.38	ADO 1		
561001	Good identification				561001
<i>Morganella morganii subsp. sibonii</i>	99.48	0.51	ONP 1		
<i>Hafnia alvei</i>	0.52	0.16			
561003	Very good identification				561003
<i>Hafnia alvei</i>	98.09	0.57	PHE 1		
<i>Morganella morganii subsp. sibonii</i>	1.91	0.10			
561013	Good identification				561013
<i>Hafnia alvei</i>	96.39	0.42	PHE 1		
<i>Yokenella regensburgei</i>	3.61	-.10			
561023	Good identification				561023
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
561103	Very good identification				561103
<i>Hafnia alvei</i>	100.0	0.57	PHE 1		
561113	Good identification				561113
<i>Hafnia alvei</i>	100.0	0.42	PHE 1		
561123	Good identification				561123
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
562001	Good identification				562001
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
562002	Good identification				562002
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
562003	Very good identification				562003
<i>Hafnia alvei</i>	98.38	0.79	ESL 10		
<i>Yersinia pseudotuberculosis</i>	1.43	0.18			
<i>Yokenella regensburgei</i>	0.12	-.04			
562013	Low discrimination				562013
<i>Hafnia alvei</i>	59.03	0.63	ESL 10		
<i>Yokenella regensburgei</i>	40.43	0.37			
<i>Escherichia fergusonii</i>	0.21	0.00			

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
562023	Very good identification					562023
					VPT	
<i>Hafnia alvei</i>		98.76	0.59	ESL 10	85	
<i>Serratia marcescens</i>		0.80	-.01	SUC 10	98	
<i>Escherichia coli</i>		0.44	0.03		1	
562033	Low discrimination					562033
<i>Hafnia alvei</i>		89.82	0.43	ESL 10		
<i>Yokenella regensburgei</i>		5.59	-.04	SUC 10		
<i>Yersinia enterocolitica ssp. enterocolitica</i>		4.58	0.08			
562043	Low discrimination					562043
<i>Hafnia alvei</i>		55.49	0.38	ESL 10		
<i>Escherichia coli</i>		30.04	0.25	SOR 1		
<i>Yersinia enterocolitica ssp. enterocolitica</i>		9.55	0.13			
562063	Low discrimination					562063
					VPT	
<i>Serratia marcescens</i>		69.62	0.40	SCI 98	98	
<i>Yersinia enterocolitica ssp. enterocolitica</i>		25.90	0.39		2	
<i>Escherichia coli</i>		2.86	0.21		1	
562073	Acceptable identification					562073
					VPT	
<i>Yersinia enterocolitica ssp. enterocolitica</i>		94.89	0.49	LYS 1	2	
<i>Serratia marcescens</i>		4.48	0.14		98	
<i>Enterobacter cloacae subsp. cloacae</i>		0.64	0.00		99	
562101	Good identification					562101
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		
562102	Good identification					562102
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		
562103	Very good identification					562103
<i>Hafnia alvei</i>		100.0	0.79	ESL 10		
562113	Very good identification					562113
<i>Hafnia alvei</i>		97.62	0.63	ESL 10		
<i>Escherichia vulneris</i>		1.71	0.05			
<i>Yokenella regensburgei</i>		0.68	-.04			
562123	Very good identification					562123
<i>Hafnia alvei</i>		100.0	0.59	ESL 10		
562133	Low discrimination					562133
<i>Hafnia alvei</i>		82.66	0.43	ESL 10		
<i>Kluyvera ascorbata</i>		17.34	0.09	SUC 10		
562143	Good identification					562143
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		
562203	Good identification					562203
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
562263	Acceptable identification				562263
				VPT	
<i>Serratia marcescens</i>	94.95	0.50	SCI 98	98	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	5.05	0.32		2	
562273	Low discrimination				562273
				VPT	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	54.20	0.42	LYS 1	2	
<i>Serratia odorifera</i> biovar 1	27.91	0.29		50	
<i>Serratia marcescens</i>	17.89	0.23		98	
562303	Good identification				562303
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
562403	Low discrimination				562403
<i>Hafnia alvei</i>	85.76	0.38	ESL 10		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	10.58	0.17	ADO 1		
<i>Escherichia fergusonii</i>	3.66	-0.04			
562413	Low discrimination				562413
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	56.12	0.38	ORN 3		
<i>Escherichia fergusonii</i>	32.11	0.23	URE 10		
<i>Hafnia alvei</i>	6.98	0.22			
562453	Good identification				562453
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.44	ORN 3		
562463	Good identification				562463
				VPT	
<i>Serratia marcescens</i>	99.03	0.36	SCI 98	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.97	0.10		1	
562503	Good identification				562503
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
562613	Good identification				562613
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.40	ORN 3		
562653	Good identification				562653
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	100.0	0.46	ORN 3		
562663	Good identification				562663
				VPT	
<i>Serratia marcescens</i>	99.60	0.46	SCI 98	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.40	0.11		1	
562773	Low discrimination				562773
<i>Enterobacter aerogenes</i>	84.79	0.39	URE 2		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	14.78	0.24	SCI 95		
<i>Klebsiella oxytoca</i>	0.43	-0.09			
563003	Good identification				563003
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
563103	Good identification				563103

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
564001	Very good identification				564001
<i>Hafnia alvei</i>	100.0	0.57	MAN 99		
564002	Very good identification				564002
<i>Hafnia alvei</i>	100.0	0.57	TRE 99		
564003	Excellent identification				564003
<i>Hafnia alvei</i>	99.92	0.98			
<i>Yokenella regensburgei</i>	0.08	0.12			
<i>Citrobacter braakii</i>	0.01	0.07			
564011	Low discrimination				564011
<i>Hafnia alvei</i>	69.88	0.42	MAN 99		
<i>Yokenella regensburgei</i>	30.12	0.12			
564012	Low discrimination				564012
<i>Hafnia alvei</i>	69.88	0.42	TRE 99		
<i>Yokenella regensburgei</i>	30.12	0.12			
564013	Low discrimination				564013
<i>Hafnia alvei</i>	69.81	0.83			
<i>Yokenella regensburgei</i>	30.09	0.53			
<i>Citrobacter braakii</i>	0.06	0.14			
564021	Good identification				564021
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
564022	Good identification				564022
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
564023	Very good identification				564023
<i>Hafnia alvei</i>	99.77	0.79	SUC 10		
<i>Serratia marcescens</i>	0.23	0.07			
564033	Good identification				564033
				VPT	
<i>Hafnia alvei</i>	92.17	0.63	SUC 10	85	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	4.22	0.23		99	
<i>Yokenella regensburgei</i>	3.61	0.12		1	
564043	Low discrimination				564043
<i>Hafnia alvei</i>	49.06	0.57	SOR 1		
<i>Citrobacter braakii</i>	34.50	0.48			
<i>Salmonella bongori</i>	10.86	0.18			
564053	Low discrimination				564053
<i>Citrobacter braakii</i>	49.90	0.55	LYS 1		
<i>Citrobacter amalonaticus</i>	34.56	0.34			
<i>Hafnia alvei</i>	6.17	0.42			
564063	Acceptable identification				564063

VPT

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia marcescens</i>	91.84	0.48	ESL 95	98	
<i>Hafnia alvei</i>	4.05	0.38		85	
<i>Citrobacter braakii</i>	1.93	0.25		1	
564073	Low discrimination				564073
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	81.01	0.49	LYS 1	99	
<i>Serratia marcescens</i>	6.35	0.22		98	
<i>Citrobacter braakii</i>	5.15	0.31		1	
564101	Very good identification				564101
<i>Hafnia alvei</i>	100.0	0.57	MAN 99		
564102	Very good identification				564102
<i>Hafnia alvei</i>	100.0	0.57	TRE 99		
564103	Excellent identification				564103
<i>Hafnia alvei</i>	100.0	0.98			
564111	Good identification				564111
<i>Hafnia alvei</i>	100.0	0.42	MAN 99		
564112	Good identification				564112
<i>Hafnia alvei</i>	100.0	0.42	TRE 99		
564113	Very good identification				564113
<i>Hafnia alvei</i>	99.35	0.83			
<i>Yokenella regensburgei</i>	0.43	0.12			
<i>Citrobacter sedlakii</i>	0.17	0.04			
564121	Good identification				564121
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
564122	Good identification				564122
<i>Hafnia alvei</i>	100.0	0.38	SUC 10		
564123	Very good identification				564123
<i>Hafnia alvei</i>	100.0	0.79	SUC 10		
564133	Low discrimination				564133
				VPT	
<i>Hafnia alvei</i>	87.48	0.63	SUC 10	85	
<i>Enterobacter cloacae subsp. cloacae</i>	12.03	0.33		99	
<i>Kluyvera ascorbata</i>	0.49	-.04		1	
564143	Low discrimination				564143
<i>Hafnia alvei</i>	65.71	0.57	SOR 1		
<i>Salmonella enterica subsp. arizonae</i>	15.48	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	13.53	0.18			
564153	Low discrimination				564153
				VPT	
<i>Citrobacter sedlakii</i>	89.03	0.45	LYS 1	1	
<i>Hafnia alvei</i>	5.35	0.42		85	
<i>Enterobacter cloacae subsp. cloacae</i>	4.76	0.28		99	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
564163	Low discrimination				564163
<i>Hafnia alvei</i>	44.26	0.38	SUC 10		
<i>Serratia marcescens</i>	31.02	0.17	SOR 1		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	20.40	0.18			
564173	Very good identification				564173
				VPT	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	98.82	0.59	LYS 1	99	
<i>Citrobacter sedlakii</i>	0.58	0.04		1	
<i>Hafnia alvei</i>	0.38	0.22		85	
564203	Very good identification				564203
<i>Hafnia alvei</i>	100.0	0.57	INO 1		
564213	Low discrimination				564213
<i>Hafnia alvei</i>	69.88	0.42	INO 1		
<i>Yokenella regensburgei</i>	30.12	0.12			
564223	Low discrimination				564223
<i>Hafnia alvei</i>	59.29	0.38	INO 1		
<i>Serratia marcescens</i>	40.71	0.17	SUC 10		
564263	Very good identification				564263
				VPT	
<i>Serratia marcescens</i>	99.77	0.58	ESL 95	98	
<i>Serratia odorifera</i> biovar 1	0.17	0.03		50	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.06	0.00		2	
564273	Low discrimination				564273
<i>Serratia odorifera</i> biovar 1	63.83	0.44	URE 5		
<i>Serratia marcescens</i>	20.25	0.32	ESL 95		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	15.20	0.34			
564303	Very good identification				564303
<i>Hafnia alvei</i>	100.0	0.57	INO 1		
564313	Good identification				564313
<i>Hafnia alvei</i>	100.0	0.42	INO 1		
564323	Good identification				564323
<i>Hafnia alvei</i>	100.0	0.38	INO 1		
564373	Acceptable identification				564373
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	93.43	0.43	LYS 1		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	2.17	-.02			
<i>Enterobacter aerogenes</i>	1.79	-.04			
564403	Very good identification				564403
<i>Hafnia alvei</i>	100.0	0.57	ADO 1		
564413	Low discrimination				564413
<i>Hafnia alvei</i>	60.62	0.42	ADO 1		
<i>Yokenella regensburgei</i>	26.13	0.12			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia fergusonii</i>	7.45	0.10			
564423	Low discrimination				564423
<i>Hafnia alvei</i>	86.76	0.38	ADO 1		
<i>Serratia marcescens</i>	13.24	0.04	SUC 10		
564463	Good identification				564463
<i>Serratia marcescens</i>	99.66	0.45	ESL 95		
<i>Enterobacter cloacae subsp. cloacae</i>	0.34	-.02			
564473	Low discrimination				564473
<i>Enterobacter cloacae subsp. cloacae</i>	83.81	0.39	LYS 1		
<i>Serratia marcescens</i>	13.14	0.18			
<i>Serratia odorifera biovar 1</i>	1.88	0.03			
564503	Very good identification				564503
<i>Hafnia alvei</i>	100.0	0.57	ADO 1		
564513	Acceptable identification				564513
<i>Hafnia alvei</i>	91.81	0.42	ADO 1		
<i>Escherichia fergusonii</i>	6.07	0.04			
<i>Citrobacter koseri</i>	2.12	-.07			
564523	Good identification				564523
<i>Hafnia alvei</i>	100.0	0.38	ADO 1		
564573	Acceptable identification				564573
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	93.86	0.49	LYS 1	99	
<i>Citrobacter koseri</i>	3.14	0.17		1	
<i>Enterobacter aerogenes</i>	2.46	0.04		98	
564663	Very good identification				564663
<i>Serratia marcescens</i>	99.75	0.55	ESL 95		
<i>Serratia odorifera biovar 1</i>	0.25	0.03			
564673	Low discrimination				564673
<i>Serratia odorifera biovar 1</i>	74.34	0.44	URE 5		
<i>Serratia marcescens</i>	15.73	0.28	ESL 95		
<i>Enterobacter cloacae subsp. cloacae</i>	5.90	0.24			
565003	Very good identification				565003
<i>Hafnia alvei</i>	100.0	0.57	PHE 1		
565013	Low discrimination				565013
<i>Hafnia alvei</i>	69.88	0.42	PHE 1		
<i>Yokenella regensburgei</i>	30.12	0.12			
565023	Good identification				565023
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
565103	Very good identification				565103
<i>Hafnia alvei</i>	100.0	0.57	PHE 1		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
565113	Good identification					565113
<i>Hafnia alvei</i>		100.0	0.42	PHE 1		
565123	Good identification					565123
<i>Hafnia alvei</i>		100.0	0.38	PHE 1		
566001	Good identification					566001
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		
566002	Good identification					566002
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		
566003	Very good identification					566003
					VPT	
<i>Hafnia alvei</i>		98.57	0.79	ESL 10	85	
<i>Yokenella regensburgei</i>		1.38	0.18		1	
<i>Serratia marcescens</i>		0.04	-.08		98	
566013	Low discrimination					566013
<i>Yokenella regensburgei</i>		88.74	0.59	URE 1		
<i>Hafnia alvei</i>		11.27	0.63			
566023	Low discrimination					566023
<i>Hafnia alvei</i>		71.67	0.59	ESL 10		
<i>Serratia marcescens</i>		28.33	0.34	SUC 10		
566033	Low discrimination					566033
<i>Hafnia alvei</i>		43.11	0.43	ESL 10		
<i>Yokenella regensburgei</i>		30.87	0.18	SUC 10		
<i>Kluyvera ascorbata</i>		9.04	0.09			
566063	Very good identification					566063
<i>Serratia marcescens</i>		99.96	0.75			
<i>Hafnia alvei</i>		0.03	0.18			
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>		0.02	0.00			
566073	Low discrimination					566073
<i>Serratia marcescens</i>		71.16	0.48	CEL 5		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>		20.48	0.42			
<i>Serratia odorifera</i> biovar 1		6.80	0.29			
566101	Good identification					566101
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		
566102	Good identification					566102
<i>Hafnia alvei</i>		100.0	0.38	ESL 10		
566103	Very good identification					566103
<i>Hafnia alvei</i>		100.0	0.79	ESL 10		
566113	Good identification					566113
<i>Hafnia alvei</i>		91.40	0.63	ESL 10		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Yokenella regensburgei</i>	7.27	0.18			
<i>Kluyvera ascorbata</i>	1.04	0.02			
566123	Very good identification				566123
				VPT	
<i>Hafnia alvei</i>	97.92	0.59	ESL 10	85	
<i>Serratia marcescens</i>	1.20	0.03	SUC 10	98	
<i>Kluyvera ascorbata</i>	0.88	-0.04		1	
566133	Low discrimination				566133
				VPT	
<i>Kluyvera ascorbata</i>	76.44	0.37	IND 92	1	
<i>Hafnia alvei</i>	15.18	0.43	URE 1	85	
<i>Enterobacter cloacae subsp. cloacae</i>	8.05	0.25		99	
566143	Low discrimination				566143
				VPT	
<i>Hafnia alvei</i>	80.95	0.38	ESL 10	85	
<i>Serratia marcescens</i>	10.89	0.03	SOR 1	98	
<i>Citrobacter sedlakii</i>	4.42	-0.11		1	
566163	Good identification				566163
<i>Serratia marcescens</i>	97.26	0.44	MAL 3		
<i>Enterobacter cloacae subsp. cloacae</i>	1.44	0.10			
<i>Hafnia alvei</i>	0.81	0.18			
566173	Low discrimination				566173
				VPT	
<i>Enterobacter cloacae subsp. cloacae</i>	69.35	0.51	LYS 1	99	
<i>Kluyvera ascorbata</i>	23.10	0.34		1	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	3.46	0.13		98	
566203	Low discrimination				566203
<i>Hafnia alvei</i>	88.36	0.38	ESL 10		
<i>Serratia marcescens</i>	11.64	0.02	INO 1		
566223	Good identification				566223
<i>Serratia marcescens</i>	99.16	0.43	SOR 99		
<i>Hafnia alvei</i>	0.85	0.18			
566243	Good identification				566243
<i>Serratia marcescens</i>	100.0	0.43	SUC 99		
566261	Good identification				566261
<i>Serratia marcescens</i>	100.0	0.43	MAN 99		
566262	Good identification				566262
<i>Serratia marcescens</i>	100.0	0.43	TRE 99		
566263	Very good identification				566263
<i>Serratia marcescens</i>	99.83	0.85			
<i>Serratia odorifera biovar 1</i>	0.17	0.29			
566273	Identification to the genus				566273
<i>Serratia odorifera biovar 1</i>	75.12	0.70	URE 5		
<i>Serratia marcescens</i>	23.83	0.58			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.49	0.16			
566303	Good identification				566303
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
566363	Very good identification				566363
<i>Serratia marcescens</i>	98.87	0.53	MAL 3		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.94	0.05			
<i>Enterobacter aerogenes</i>	0.19	-.11			
566373	Low discrimination				566373
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	54.70	0.39	ORN 1		
<i>Enterobacter aerogenes</i>	22.35	0.30	ADO 90		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	10.18	0.36			
566403	Acceptable identification				566403
<i>Hafnia alvei</i>	94.98	0.38	ESL 10		
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	5.02	0.09	ADO 1		
566453	Low discrimination				566453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	83.71	0.36	ORN 3	1	
<i>Serratia marcescens</i>	11.31	0.04	URE 10	98	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	4.98	0.01		99	
566463	Very good identification				566463
<i>Serratia marcescens</i>	100.0	0.71			
566473	Low discrimination				566473
<i>Serratia marcescens</i>	70.54	0.45	CEL 5		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	10.15	0.32			
<i>Serratia odorifera</i> biovar 1	10.11	0.29			
566503	Good identification				566503
<i>Hafnia alvei</i>	100.0	0.38	ESL 10		
566563	Good identification				566563
<i>Serratia marcescens</i>	95.25	0.40	MAL 3		
<i>Enterobacter aerogenes</i>	2.12	-.02			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	1.92	-.02			
566573	Low discrimination				566573
<i>Enterobacter aerogenes</i>	55.18	0.39	URE 2		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	24.80	0.33	INO 95		
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	18.41	0.42			
566623	Good identification				566623
<i>Serratia marcescens</i>	100.0	0.40	SOR 99		
566643	Good identification				566643
				VPT	
<i>Serratia marcescens</i>	98.64	0.40	SUC 99	98	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1.36	0.16		1	
566661	Good identification				566661

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Serratia marcescens</i>	100.0	0.40	MAN 99		
566662	Good identification				566662
<i>Serratia marcescens</i>	100.0	0.40	TRE 99		
566663	Very good identification				566663
<i>Serratia marcescens</i>	99.70	0.81			
<i>Serratia odorifera</i> biovar 1	0.25	0.29			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.03	0.01			
566673	Low discrimination				566673
<i>Serratia odorifera</i> biovar 1	73.26	0.70	URE 5		
<i>Serratia marcescens</i>	15.50	0.55			
<i>Enterobacter aerogenes</i>	6.68	0.39			
566763	Low discrimination				566763
<i>Serratia marcescens</i>	78.82	0.50	MAL 3		
<i>Enterobacter aerogenes</i>	11.10	0.24			
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	10.08	0.24			
566773	Low discrimination				566773
<i>Enterobacter aerogenes</i>	68.15	0.65	URE 2		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	30.64	0.59			
<i>Serratia odorifera</i> biovar 1	0.40	0.29			
567003	Good identification				567003
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
567103	Good identification				567103
<i>Hafnia alvei</i>	100.0	0.38	PHE 1		
567263	Good identification				567263
<i>Serratia marcescens</i>	100.0	0.43	PHE 1		
567663	Good identification				567663
<i>Serratia marcescens</i>	100.0	0.40	PHE 1		
570003	Low discrimination				570003
<i>Hafnia alvei</i>	70.79	0.57	IND 1		
<i>Escherichia coli</i>	26.70	0.41			
<i>Escherichia fergusonii</i>	1.46	0.10			
570023	Low discrimination				570023
<i>Escherichia coli</i>	65.19	0.38	URE 1		
<i>Hafnia alvei</i>	28.80	0.38	SOR 88		
<i>Escherichia hermannii</i>	3.16	0.02			
570043	Good identification				570043
<i>Escherichia coli</i>	92.77	0.59	URE 1		
<i>Citrobacter braakii</i>	3.87	0.32			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	1.92	0.23			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
570053	Low discrimination				570053
<i>Yersinia kristensenii</i>	81.15	0.51	LYS 1		
<i>Citrobacter braakii</i>	5.88	0.38			
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	4.32	0.33			
570063	Low discrimination				570063
<i>Escherichia coli</i>	60.47	0.55	URE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	35.73	0.49			
<i>Citrobacter farmeri</i>	3.18	0.15			
570073	Low discrimination				570073
<i>Citrobacter farmeri</i>	74.01	0.56	LYS 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	25.20	0.59			
<i>Escherichia coli</i>	0.29	0.21			
570103	Very good identification				570103
<i>Hafnia alvei</i>	98.91	0.57	IND 1		
<i>Escherichia fergusonii</i>	1.09	0.04			
570123	Good identification				570123
<i>Hafnia alvei</i>	100.0	0.38	IND 1		
570153	Good identification				570153
<i>Citrobacter sedlakii</i>	98.76	0.45	LYS 1		
<i>Yersinia kristensenii</i>	1.10	0.10			
<i>Citrobacter koseri</i>	0.14	-0.7			
570253	Identification to the genus				570253
<i>Yersinia kristensenii</i>	88.56	0.36	LYS 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	11.44	0.25			
570263	Good identification				570263
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	96.16	0.42	LYS 1		
<i>Escherichia coli</i>	3.84	0.14			
570273	Acceptable identification				570273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	92.01	0.51	LYS 1		
<i>Citrobacter farmeri</i>	6.37	0.15			
<i>Serratia odorifera</i> biovar 1	1.25	0.06			
570413	Very good identification				570413
<i>Escherichia fergusonii</i>	99.91	0.59	URE 1		
<i>Escherichia hermannii</i>	0.09	-0.7			
570513	Very good identification				570513
<i>Escherichia fergusonii</i>	99.86	0.53	URE 1		
<i>Citrobacter koseri</i>	0.15	-0.7			
571000	Good identification				571000
<i>Morganella morganii</i> subsp. <i>morganii</i>	98.87	0.39	ONP 10		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.13	0.10	LYS 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
571001	Good identification				571001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	99.12	0.51	ONP 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.88	-.02			
572003	Low discrimination				572003
<i>Hafnia alvei</i>	47.72	0.38	IND 1		
<i>Escherichia coli</i>	40.50	0.29	ESL 10		
<i>Escherichia fergusonii</i>	7.52	0.08			
572043	Good identification				572043
<i>Escherichia coli</i>	97.31	0.47	URE 1		
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	2.69	0.13			
572063	Low discrimination				572063
				VPT	
<i>Escherichia coli</i>	55.28	0.43	URE 1	1	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	43.54	0.39		2	
<i>Serratia marcescens</i>	1.18	-.01		98	
572073	Acceptable identification				572073
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	90.02	0.49	LYS 1		
<i>Citrobacter farmeri</i>	8.01	0.15			
<i>Kluyvera ascorbata</i>	1.19	-.02			
572103	Acceptable identification				572103
<i>Hafnia alvei</i>	92.18	0.38	IND 1		
<i>Escherichia fergusonii</i>	7.82	0.03	ESL 10		
572273	Low discrimination				572273
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	56.42	0.42	LYS 1		
<i>Serratia odorifera</i> biovar 1	43.58	0.33			
572413	Very good identification				572413
<i>Escherichia fergusonii</i>	100.0	0.58	URE 1		
572513	Good identification				572513
<i>Escherichia fergusonii</i>	98.45	0.52	URE 1		
<i>Leclercia adecarboxylata</i>	1.56	0.12			
574003	Very good identification				574003
<i>Hafnia alvei</i>	99.58	0.57	IND 1		
<i>Escherichia fergusonii</i>	0.42	-.05			
574013	Low discrimination				574013
<i>Hafnia alvei</i>	35.23	0.42	IND 1		
<i>Citrobacter amalonaticus</i>	31.24	0.18			
<i>Escherichia fergusonii</i>	15.96	0.22			
574023	Good identification				574023
<i>Hafnia alvei</i>	100.0	0.38	IND 1		
574043	Low discrimination				574043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	63.18	0.42	LYS 1		
<i>Citrobacter amalonaticus</i>	28.55	0.18			
<i>Escherichia coli</i>	5.10	0.18			
574053	Good identification				574053
<i>Citrobacter amalonaticus</i>	94.38	0.59	LYS 1		
<i>Citrobacter braakii</i>	4.28	0.48			
<i>Citrobacter sedlakii</i>	0.88	0.18			
574073	Identification to the genus				574073
<i>Citrobacter farmeri</i>	48.39	0.37	LYS 1		
<i>Citrobacter amalonaticus</i>	44.86	0.34	SCI 10		
<i>Citrobacter braakii</i>	2.40	0.25			
574103	Very good identification				574103
<i>Hafnia alvei</i>	100.0	0.57	IND 1		
574113	Low discrimination				574113
<i>Hafnia alvei</i>	45.26	0.42	IND 1		
<i>Citrobacter sedlakii</i>	37.11	0.18			
<i>Escherichia fergusonii</i>	11.04	0.16			
574123	Good identification				574123
<i>Hafnia alvei</i>	100.0	0.38	IND 1		
574153	Very good identification				574153
<i>Citrobacter sedlakii</i>	96.20	0.59	LYS 1		
<i>Citrobacter koseri</i>	2.70	0.34			
<i>Citrobacter amalonaticus</i>	1.05	0.18			
574273	Good identification				574273
<i>Serratia odorifera biovar 1</i>	97.97	0.47	URE 5		
<i>Yersinia enterocolitica ssp. enterocolitica</i>	0.74	0.10	ESL 95		
<i>Citrobacter farmeri</i>	0.56	-.04			
574413	Good identification				574413
<i>Escherichia fergusonii</i>	97.64	0.45	URE 1		
<i>Citrobacter koseri</i>	2.36	0.10			
574513	Low discrimination				574513
<i>Escherichia fergusonii</i>	58.71	0.39	URE 1		
<i>Citrobacter koseri</i>	41.29	0.34			
574553	Very good identification				574553
<i>Citrobacter koseri</i>	97.67	0.59	LYS 1		
<i>Citrobacter sedlakii</i>	2.24	0.18			
<i>Escherichia fergusonii</i>	0.09	-.02			
574573	Very good identification				574573
				VPT	
<i>Citrobacter koseri</i>	99.62	0.58	LYS 1	1	
<i>Enterobacter cloacae subsp. cloacae</i>	0.30	0.08		99	
<i>Klebsiella oxytoca</i>	0.08	-.17		95	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
574673	Good identification				574673
<i>Serratia odorifera</i> biovar 1	99.77	0.47	URE 5		
<i>Klebsiella oxytoca</i>	0.23	-.17	ESL 95		
576003	Good identification				576003
<i>Hafnia alvei</i>	100.0	0.38	IND 1		
576053	Good identification				576053
<i>Citrobacter amalonaticus</i>	97.22	0.38	LYS 1		
<i>Citrobacter sedlakii</i>	1.88	0.04	ESL 9		
<i>Citrobacter braakii</i>	0.45	0.07			
576103	Good identification				576103
<i>Hafnia alvei</i>	100.0	0.38	IND 1		
576133	Very good identification				576133
<i>Kluyvera ascorbata</i>	100.0	0.59	URE 1		
576153	Acceptable identification				576153
<i>Citrobacter sedlakii</i>	93.94	0.45	LYS 1		
<i>Kluyvera ascorbata</i>	5.44	0.21			
<i>Citrobacter amalonaticus</i>	0.50	-.03			
576173	Very good identification				576173
				VPT	
<i>Kluyvera ascorbata</i>	99.33	0.55	URE 1	1	
<i>Citrobacter sedlakii</i>	0.35	0.04		1	
<i>Enterobacter cloacae</i> subsp. <i>cloacae</i>	0.26	0.10		99	
576263	Identification to the genus				576263
<i>Serratia marcescens</i>	80.08	0.43	IND 1		
<i>Serratia odorifera</i> biovar 1	19.92	0.33			
576273	Very good identification				576273
				VPT	
<i>Serratia odorifera</i> biovar 1	99.76	0.74	URE 5	50	
<i>Serratia marcescens</i>	0.21	0.17		98	
<i>Yersinia enterocolitica</i> ssp. <i>enterocolitica</i>	0.01	0.00		2	
576413	Good identification				576413
<i>Escherichia fergusonii</i>	100.0	0.43	URE 1		
576513	Good identification				576513
<i>Escherichia fergusonii</i>	99.17	0.38	URE 1		
<i>Citrobacter koseri</i>	0.83	-.07			
576663	Identification to the genus				576663
<i>Serratia marcescens</i>	72.59	0.40	IND 1		
<i>Serratia odorifera</i> biovar 1	27.09	0.33			
<i>Klebsiella oxytoca</i>	0.32	-.17			
576673	Very good identification				576673
<i>Serratia odorifera</i> biovar 1	98.59	0.74	URE 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella oxytoca</i>	1.17	0.24			
<i>Serratia marcescens</i>	0.14	0.14			
576773	Very good identification				576773
<i>Klebsiella oxytoca</i>	95.56	0.59	ORN 1		
<i>Enterobacter aerogenes</i>	1.92	0.24			
<i>Serratia odorifera</i> biovar 1	1.66	0.33			
600002	Identification to the genus				600002
<i>Salmonella enterica</i> subsp. <i>enterica</i>	76.05	0.39	ORN 99		
<i>Salmonella</i> serovar <i>typhi</i>	20.30	0.18	SOR 90		
<i>Shigella flexneri</i> (group B)	2.42	0.12			
600003	Very good identification				600003
<i>Salmonella</i> serovar <i>typhi</i>	98.76	0.59	SOR 99		
<i>Salmonella</i> serovar <i>enteritidis</i>	0.44	0.16			
<i>Shigella boydii</i> (group C)	0.34	0.18			
600041	Very good identification				600041
<i>Salmonella</i> serovar <i>typhi</i>	99.78	0.59	MAN 99		
<i>Shigella dysenteriae</i> (group A)	0.11	0.10			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.09	0.02			
600042	Identification to the genus				600042
<i>Salmonella</i> serovar <i>typhi</i>	74.49	0.59	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	25.38	0.59			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.06	0.02			
600043	Excellent identification				600043
<i>Salmonella</i> serovar <i>typhi</i>	99.88	1.00			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.09	0.43			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.01	0.24			
600053	Very good identification				600053
<i>Salmonella</i> serovar <i>typhi</i>	98.35	0.59	CEL 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.97	0.24			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.44	0.16			
600063	Very good identification				600063
<i>Salmonella</i> serovar <i>typhi</i>	99.22	0.59	SUC 1		
<i>Citrobacter freundii</i>	0.27	0.29			
<i>Escherichia coli</i>	0.21	0.23			
600143	Very good identification				600143
<i>Salmonella</i> serovar <i>typhi</i>	99.07	0.59	MAL 1		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.69	0.18			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.15	0.02			
600243	Very good identification				600243
<i>Salmonella</i> serovar <i>typhi</i>	95.61	0.59	INO 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	4.39	0.37			
600443	Very good identification				600443

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar typhi</i>	99.84	0.59	ADO 1		
<i>Salmonella serovar enteritidis</i>	0.09	0.02			
<i>Salmonella enterica subsp. houtenae</i>	0.05	-0.02			
601043	Very good identification				601043
<i>Salmonella serovar typhi</i>	99.91	0.59	PHE 1		
<i>Salmonella serovar enteritidis</i>	0.09	0.02			
602043	Very good identification				602043
<i>Salmonella serovar typhi</i>	99.48	0.59	ESL 1		
<i>Salmonella serovar enteritidis</i>	0.45	0.16			
<i>Escherichia coli</i>	0.08	0.14			
602413	Good identification				602413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.36	H2S 1		
602453	Good identification				602453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	H2S 1		
602613	Good identification				602613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.37	H2S 1		
602653	Good identification				602653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.43	H2S 1		
604003	Identification to the genus				604003
<i>Salmonella serovar enteritidis</i>	83.35	0.43	ORN 97		
<i>Salmonella serovar typhi</i>	9.88	0.18	SOR 95		
<i>Salmonella enterica subsp. houtenae</i>	4.79	0.18			
604042	Identification to the genus				604042
<i>Salmonella enterica subsp. enterica</i>	77.84	0.49	ORN 99		
<i>Salmonella serovar enteritidis</i>	11.21	0.28			
<i>Salmonella serovar typhi</i>	6.93	0.18			
604043	Identification to the genus				604043
<i>Salmonella serovar enteritidis</i>	50.40	0.69	ORN 97		
<i>Salmonella serovar typhi</i>	31.13	0.59			
<i>Salmonella enterica subsp. houtenae</i>	15.09	0.59			
604053	Identification to the genus				604053
<i>Salmonella enterica subsp. houtenae</i>	82.51	0.59	ORN 99		
<i>Salmonella serovar enteritidis</i>	14.51	0.43			
<i>Salmonella serovar typhi</i>	1.72	0.18			
604073	Low discrimination				604073
<i>Citrobacter freundii</i>	55.34	0.39	ONP 88		
<i>Salmonella enterica subsp. houtenae</i>	31.67	0.18	LYS 1		
<i>Citrobacter youngae</i>	7.42	0.19			
604143	Identification to the genus				604143

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>salamae</i>	85.45	0.59	ORN 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	9.27	0.37			
<i>Salmonella</i> serovar <i>enteritidis</i>	2.02	0.28			
604203	Good identification				604203
<i>Salmonella</i> serovar <i>enteritidis</i>	100.0	0.37	ORN 97		
604243	Very good identification				604243
<i>Salmonella</i> serovar <i>enteritidis</i>	98.00	0.63	ORN 97		
<i>Salmonella</i> serovar <i>typhi</i>	1.14	0.18			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.55	0.18			
604253	Identification to the genus				604253
				VPT	
<i>Salmonella</i> serovar <i>enteritidis</i>	87.69	0.37	ORN 97	1	
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	9.36	0.18	CEL 5	1	
<i>Serratia odorifera</i> biovar 2	2.52	0.16		99	
606043	Low discrimination				606043
<i>Salmonella</i> serovar <i>enteritidis</i>	79.25	0.43	ORN 97		
<i>Salmonella</i> serovar <i>typhi</i>	9.39	0.18	ESL 5		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	5.98	0.17			
606143	Good identification				606143
<i>Salmonella enterica</i> subsp. <i>salamae</i>	98.69	0.43	ORN 99		
<i>Salmonella</i> serovar <i>enteritidis</i>	0.70	0.02			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.61	-.04			
606243	Good identification				606243
<i>Salmonella</i> serovar <i>enteritidis</i>	99.27	0.37	ORN 97		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.73	-.09	ESL 5		
606653	Low discrimination				606653
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	81.62	0.35	H2S 1	1	
<i>Serratia odorifera</i> biovar 2	18.38	0.14		99	
610000	Very good identification				610000
<i>Edwardsiella tarda</i>	99.98	0.59	ORN 99		
<i>Shigella dysenteriae</i> (group A)	0.02	-.04			
610043	Very good identification				610043
<i>Salmonella</i> serovar <i>typhi</i>	96.23	0.59	IND 1		
<i>Escherichia coli</i>	3.47	0.48			
<i>Shigella flexneri</i> (group B)	0.10	0.10			
610063	Low discrimination				610063
<i>Escherichia coli</i>	67.78	0.45	H2S 1		
<i>Salmonella</i> serovar <i>typhi</i>	28.45	0.18			
<i>Citrobacter freundii</i>	3.78	0.22			
620000	Good identification				620000
<i>Edwardsiella tarda</i>	93.10	0.59	IND 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	6.91	0.46			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
620002	Very good identification				620002
<i>Salmonella enterica subsp. enterica</i>	99.67	0.80	SOR 90		
<i>Edwardsiella tarda</i>	0.28	0.18			
<i>Salmonella serovar enteritidis</i>	0.04	0.06			
620003	Low discrimination				620003
<i>Salmonella serovar enteritidis</i>	54.70	0.47	SCI 95		
<i>Hafnia alvei</i>	19.55	0.59	SOR 95		
<i>Salmonella enterica subsp. enterica</i>	14.28	0.39			
620012	Good identification				620012
<i>Salmonella enterica subsp. enterica</i>	100.0	0.39	CEL 1		
620022	Good identification				620022
<i>Salmonella enterica subsp. enterica</i>	100.0	0.39	SUC 1		
620023	Low discrimination				620023
<i>Hafnia alvei</i>	72.76	0.39	H2S 1		
<i>Salmonella serovar enteritidis</i>	18.51	0.06	SUC 10		
<i>Salmonella enterica subsp. enterica</i>	4.83	-.02			
620040	Very good identification				620040
<i>Salmonella enterica subsp. enterica</i>	98.44	0.65	MAN 98		
<i>Edwardsiella tarda</i>	1.49	0.18			
<i>Salmonella serovar enteritidis</i>	0.04	-.09			
620042	Excellent identification				620042
<i>Salmonella enterica subsp. enterica</i>	99.84	1.00			
<i>Salmonella serovar enteritidis</i>	0.08	0.33			
<i>Salmonella enterica subsp. houtenae</i>	0.03	0.24			
620043	Low discrimination				620043
<i>Salmonella serovar enteritidis</i>	49.26	0.74	SCI 95		
<i>Salmonella serovar typhi</i>	17.88	0.59			
<i>Salmonella enterica subsp. houtenae</i>	17.51	0.65			
620052	Very good identification				620052
<i>Salmonella enterica subsp. enterica</i>	96.77	0.59	CEL 1		
<i>Salmonella enterica subsp. houtenae</i>	2.81	0.24			
<i>Salmonella serovar enteritidis</i>	0.42	0.06			
620053	Identification to the genus				620053
<i>Salmonella enterica subsp. houtenae</i>	85.01	0.65	SCI 98		
<i>Salmonella serovar enteritidis</i>	12.59	0.47			
<i>Salmonella serovar typhi</i>	0.88	0.18			
620062	Very good identification				620062
<i>Salmonella enterica subsp. enterica</i>	99.92	0.59	SUC 1		
<i>Salmonella serovar enteritidis</i>	0.08	-.09			
620102	Good identification				620102

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>enterica</i>	98.64	0.39	MAL 1		
<i>Hafnia alvei</i>	1.36	0.18	SOR 90		
620103	Low discrimination				620103
<i>Hafnia alvei</i>	83.32	0.59	H2S 1		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	11.25	0.18			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	2.47	0.02			
620113	Good identification				620113
<i>Hafnia alvei</i>	100.0	0.43	H2S 1		
620123	Good identification				620123
<i>Hafnia alvei</i>	100.0	0.39	H2S 1		
620142	Very good identification				620142
<i>Salmonella enterica</i> subsp. <i>enterica</i>	97.48	0.59	MAL 1		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	2.00	0.18			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.44	0.02			
620143	Identification to the genus				620143
<i>Salmonella enterica</i> subsp. <i>salamae</i>	76.03	0.59	SCI 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	16.67	0.43			
<i>Salmonella</i> serovar <i>enteritidis</i>	3.06	0.33			
620202	Good identification				620202
<i>Salmonella enterica</i> subsp. <i>enterica</i>	97.96	0.39	INO 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	2.04	0.01	SOR 90		
620203	Good identification				620203
<i>Salmonella</i> serovar <i>enteritidis</i>	98.85	0.42	SCI 95		
<i>Hafnia alvei</i>	0.66	0.18	SOR 95		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.48	-.02			
620242	Very good identification				620242
<i>Salmonella enterica</i> subsp. <i>enterica</i>	95.79	0.59	INO 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	4.21	0.27			
620243	Very good identification				620243
<i>Salmonella</i> serovar <i>enteritidis</i>	98.01	0.68	SCI 95		
<i>Salmonella</i> serovar <i>typhi</i>	0.67	0.18			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.65	0.24			
620253	Identification to the genus				620253
<i>Salmonella</i> serovar <i>enteritidis</i>	88.76	0.42	SCI 95		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	11.24	0.24	CEL 5		
620402	Good identification				620402
<i>Salmonella enterica</i> subsp. <i>enterica</i>	100.0	0.39	ADO 1		
620442	Very good identification				620442
<i>Salmonella enterica</i> subsp. <i>enterica</i>	99.77	0.59	ADO 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.15	-.02			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar enteritidis</i>	0.08	-.09			
620443	Low discrimination				620443
<i>Salmonella enterica subsp. houtenae</i>	52.50	0.39	SCI 98		
<i>Salmonella serovar enteritidis</i>	28.35	0.33	ADO 5		
<i>Salmonella serovar typhi</i>	10.29	0.18			
620453	Good identification				620453
<i>Salmonella enterica subsp. houtenae</i>	97.24	0.39	SCI 98		
<i>Salmonella serovar enteritidis</i>	2.76	0.06	ADO 5		
621001	Low discrimination				621001
<i>Morganella morganii subsp. sibonii</i>	72.69	0.36	H2S 6		
<i>Proteus mirabilis</i>	27.31	0.19	URE 97		
621002	Good identification				621002
<i>Salmonella enterica subsp. enterica</i>	100.0	0.39	PHE 1		
621042	Very good identification				621042
<i>Salmonella enterica subsp. enterica</i>	99.92	0.59	PHE 1		
<i>Salmonella serovar enteritidis</i>	0.08	-.09			
622002	Good identification				622002
<i>Salmonella enterica subsp. enterica</i>	100.0	0.39	ESL 1		
622042	Very good identification				622042
<i>Salmonella enterica subsp. enterica</i>	99.57	0.59	ESL 1		
<i>Salmonella serovar enteritidis</i>	0.43	0.06			
622043	Low discrimination				622043
<i>Salmonella serovar enteritidis</i>	80.36	0.47	ESL 5		
<i>Salmonella serovar typhi</i>	5.60	0.18	SCI 95		
<i>Salmonella enterica subsp. houtenae</i>	5.48	0.24			
622103	Low discrimination				622103
<i>Hafnia alvei</i>	82.34	0.39	H2S 1		
<i>Salmonella enterica subsp. salamae</i>	17.66	0.02	ESL 10		
622143	Good identification				622143
<i>Salmonella enterica subsp. salamae</i>	97.61	0.43	SCI 99		
<i>Salmonella enterica subsp. diarizonae</i>	1.23	0.02			
<i>Salmonella serovar enteritidis</i>	1.17	0.06			
622243	Good identification				622243
<i>Salmonella serovar enteritidis</i>	99.57	0.42	ESL 5		
<i>Salmonella enterica subsp. salamae</i>	0.43	-.09	SCI 95		
624000	Low discrimination				624000
<i>Salmonella enterica subsp. enterica</i>	70.44	0.36	SOR 90		
<i>Edwardsiella tarda</i>	28.78	0.18	MAN 98		
<i>Salmonella serovar enteritidis</i>	0.78	-.09			
624002	Very good identification				624002

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>enterica</i>	97.33	0.71	SOR 90		
<i>Salmonella</i> serovar <i>enteritidis</i>	2.17	0.33			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.38	0.18			
624003	Identification to the genus				624003
<i>Salmonella</i> serovar <i>enteritidis</i>	80.93	0.74	SOR 95		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	14.24	0.59			
<i>Salmonella bongori</i>	1.74	0.34			
624013	Identification to the genus				624013
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	75.37	0.59	SOR 99		
<i>Salmonella</i> serovar <i>enteritidis</i>	22.55	0.47			
<i>Hafnia alvei</i>	1.42	0.43			
624040	Good identification				624040
<i>Salmonella enterica</i> subsp. <i>enterica</i>	93.40	0.55	MAN 98		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	4.03	0.24			
<i>Salmonella</i> serovar <i>enteritidis</i>	2.18	0.18			
624041	Identification to the genus				624041
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	60.80	0.65	MAN 98		
<i>Salmonella</i> serovar <i>enteritidis</i>	32.83	0.59			
<i>Salmonella bongori</i>	3.68	0.34			
624042	Good identification				624042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	90.99	0.90			
<i>Salmonella</i> serovar <i>enteritidis</i>	4.28	0.59			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	3.92	0.59			
624043	Identification to the genus				624043
<i>Salmonella</i> serovar <i>enteritidis</i>	47.42	1.00			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	43.47	1.00			
<i>Salmonella bongori</i>	5.32	0.75			
624051	Very good identification				624051
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	97.14	0.65	MAN 98		
<i>Salmonella</i> serovar <i>enteritidis</i>	2.76	0.33			
<i>Salmonella bongori</i>	0.06	-.07			
624052	Identification to the genus				624052
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	77.30	0.59	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	18.11	0.49			
<i>Salmonella</i> serovar <i>enteritidis</i>	4.44	0.33			
624053	Good identification				624053
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	94.36	1.00			
<i>Salmonella</i> serovar <i>enteritidis</i>	5.42	0.74			
<i>Salmonella bongori</i>	0.12	0.34			
624062	Acceptable identification				624062
<i>Salmonella enterica</i> subsp. <i>enterica</i>	90.87	0.49	SUC 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella</i> serovar enteritidis	4.27	0.18			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	3.92	0.18			
624063	Low discrimination				624063
<i>Salmonella</i> serovar enteritidis	46.70	0.59	SUC 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	42.80	0.59			
<i>Salmonella bongori</i>	5.24	0.34			
624073	Good identification				624073
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	94.16	0.59	SUC 1		
<i>Salmonella</i> serovar enteritidis	5.41	0.33			
<i>Citrobacter braakii</i>	0.21	0.18			
624103	Low discrimination				624103
<i>Salmonella enterica</i> subsp. <i>salamae</i>	80.27	0.59	SOR 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	8.71	0.37			
<i>Hafnia alvei</i>	6.01	0.59			
624113	Low discrimination				624113
<i>Hafnia alvei</i>	39.32	0.43	H2S 1		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	30.08	0.18			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	21.04	0.18			
624141	Identification to the genus				624141
<i>Salmonella enterica</i> subsp. <i>salamae</i>	87.28	0.59	MAN 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	9.47	0.37			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	1.26	0.18			
624142	Identification to the genus				624142
<i>Salmonella enterica</i> subsp. <i>salamae</i>	76.78	0.59	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	12.58	0.49			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	8.33	0.37			
624143	Identification to the genus				624143
<i>Salmonella enterica</i> subsp. <i>salamae</i>	87.83	1.00			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	9.53	0.78			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	1.27	0.59			
624153	Identification to the genus				624153
<i>Salmonella enterica</i> subsp. <i>salamae</i>	53.66	0.59	CEL 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	37.54	0.59			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	5.82	0.37			
624163	Identification to the genus				624163
<i>Salmonella enterica</i> subsp. <i>salamae</i>	62.68	0.59	SUC 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	35.44	0.52			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	0.90	0.18			
624203	Very good identification				624203
<i>Salmonella</i> serovar enteritidis	99.47	0.68	SOR 95		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.33	0.18			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.13	0.06			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
624213	Acceptable identification				624213
<i>Salmonella</i> serovar <i>enteritidis</i>	94.10	0.42	CEL 5		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	5.90	0.18	SOR 95		
624241	Very good identification				624241
<i>Salmonella</i> serovar <i>enteritidis</i>	95.82	0.53	MAN 99		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	3.33	0.24			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.65	0.06			
624242	Identification to the genus				624242
<i>Salmonella</i> serovar <i>enteritidis</i>	70.18	0.53	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	27.99	0.49			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	1.21	0.18			
624243	Very good identification				624243
<i>Salmonella</i> serovar <i>enteritidis</i>	97.44	0.95			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	1.68	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.66	0.47			
624253	Identification to the genus				624253
<i>Salmonella</i> serovar <i>enteritidis</i>	75.28	0.68	CEL 5		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	24.59	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.10	0.06			
624263	Very good identification				624263
<i>Salmonella</i> serovar <i>enteritidis</i>	97.07	0.53	SUC 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	1.67	0.18			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.65	0.06			
624343	Good identification				624343
<i>Salmonella enterica</i> subsp. <i>salamae</i>	90.58	0.74	INO 5		
<i>Salmonella</i> serovar <i>enteritidis</i>	7.15	0.53			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	1.89	0.37			
624441	Identification to the genus				624441
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	89.09	0.39	ADO 5		
<i>Salmonella</i> serovar <i>enteritidis</i>	9.23	0.18	MAN 98		
<i>Salmonella bongori</i>	1.04	-.07			
624442	Identification to the genus				624442
<i>Salmonella enterica</i> subsp. <i>enterica</i>	78.11	0.49	ADO 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	17.55	0.33			
<i>Salmonella</i> serovar <i>enteritidis</i>	3.67	0.18			
624443	Identification to the genus				624443
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	80.03	0.74	ADO 5		
<i>Salmonella</i> serovar <i>enteritidis</i>	16.76	0.59			
<i>Salmonella bongori</i>	1.88	0.34			
624451	Good identification				624451
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	99.46	0.39	ADO 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella serovar enteritidis</i>	0.54	-.09	MAN 98		
624453	Very good identification				624453
<i>Salmonella enterica subsp. houtenae</i>	98.87	0.74	ADO 5		
<i>Salmonella serovar enteritidis</i>	1.09	0.33			
<i>Salmonella bongori</i>	0.02	-.07			
624543	Identification to the genus				624543
<i>Salmonella enterica subsp. salamae</i>	85.59	0.59	ADO 1		
<i>Salmonella enterica subsp. diarizonae</i>	9.29	0.37			
<i>Salmonella enterica subsp. houtenae</i>	3.15	0.33			
624643	Good identification				624643
<i>Salmonella serovar enteritidis</i>	91.04	0.53	ADO 1		
<i>Salmonella enterica subsp. houtenae</i>	8.16	0.33			
<i>Salmonella enterica subsp. salamae</i>	0.61	0.06			
625042	Acceptable identification				625042
<i>Salmonella enterica subsp. enterica</i>	91.02	0.49	PHE 1		
<i>Salmonella serovar enteritidis</i>	4.28	0.18			
<i>Salmonella enterica subsp. houtenae</i>	3.92	0.18			
625043	Identification to the genus				625043
<i>Salmonella serovar enteritidis</i>	47.43	0.59	PHE 1		
<i>Salmonella enterica subsp. houtenae</i>	43.47	0.59			
<i>Salmonella bongori</i>	5.32	0.34			
625053	Good identification				625053
<i>Salmonella enterica subsp. houtenae</i>	94.39	0.59	PHE 1		
<i>Salmonella serovar enteritidis</i>	5.42	0.33			
<i>Salmonella bongori</i>	0.12	-.07			
625143	Identification to the genus				625143
<i>Salmonella enterica subsp. salamae</i>	87.83	0.59	PHE 1		
<i>Salmonella enterica subsp. diarizonae</i>	9.53	0.37			
<i>Salmonella enterica subsp. arizonae</i>	1.27	0.18			
625243	Very good identification				625243
<i>Salmonella serovar enteritidis</i>	97.46	0.53	PHE 1		
<i>Salmonella enterica subsp. houtenae</i>	1.68	0.18			
<i>Salmonella enterica subsp. salamae</i>	0.66	0.06			
626003	Low discrimination				626003
<i>Salmonella serovar enteritidis</i>	89.13	0.47	ESL 5		
<i>Salmonella enterica subsp. salamae</i>	3.96	0.17	SOR 95		
<i>Hafnia alvei</i>	3.54	0.39			
626042	Identification to the genus				626042
<i>Salmonella enterica subsp. enterica</i>	74.07	0.49	ESL 1		
<i>Salmonella serovar enteritidis</i>	18.15	0.33			
<i>Salmonella enterica subsp. salamae</i>	4.20	0.17			
626043	Identification to the genus				626043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella</i> serovar enteritidis	69.90	0.74	ESL 5		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	16.16	0.58			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	12.30	0.59			
626053	Identification to the genus				626053
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	76.12	0.59	ESL 1		
<i>Salmonella</i> serovar enteritidis	22.78	0.47			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	1.01	0.17			
626103	Acceptable identification				626103
<i>Salmonella enterica</i> subsp. <i>salamae</i>	93.87	0.43	SOR 99		
<i>Hafnia alvei</i>	4.42	0.39			
<i>Salmonella</i> serovar enteritidis	1.13	0.06			
626141	Good identification				626141
<i>Salmonella enterica</i> subsp. <i>salamae</i>	99.16	0.43	MAN 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.62	-.04			
<i>Salmonella</i> serovar enteritidis	0.23	-.09			
626142	Good identification				626142
<i>Salmonella enterica</i> subsp. <i>salamae</i>	98.24	0.43	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.92	0.08			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.61	-.04			
626143	Very good identification				626143
<i>Salmonella enterica</i> subsp. <i>salamae</i>	99.03	0.85			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.62	0.37			
<i>Salmonella</i> serovar enteritidis	0.23	0.33			
626153	Acceptable identification				626153
<i>Salmonella enterica</i> subsp. <i>salamae</i>	94.50	0.43	CEL 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	3.78	0.18			
<i>Salmonella</i> serovar enteritidis	1.13	0.06			
626163	Good identification				626163
<i>Salmonella enterica</i> subsp. <i>salamae</i>	96.51	0.43	SUC 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	3.12	0.11			
<i>Salmonella</i> serovar enteritidis	0.22	-.09			
626203	Good identification				626203
<i>Salmonella</i> serovar enteritidis	99.57	0.42	ESL 5		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.43	-.09	SOR 95		
626243	Very good identification				626243
<i>Salmonella</i> serovar enteritidis	97.43	0.68	ESL 5		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	2.20	0.32			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.32	0.18			
626253	Acceptable identification				626253
<i>Salmonella</i> serovar enteritidis	93.72	0.42	ESL 5		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	5.88	0.18	CEL 5		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>salamae</i>	0.41	-.09			
626343	Very good identification				626343
<i>Salmonella enterica</i> subsp. <i>salamae</i>	97.59	0.58	INO 5		
<i>Salmonella</i> serovar <i>enteritidis</i>	2.30	0.27			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.12	-.04			
626543	Good identification				626543
<i>Salmonella enterica</i> subsp. <i>salamae</i>	98.95	0.43	ADO 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.62	-.04			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.23	-.09			
627143	Good identification				627143
<i>Salmonella enterica</i> subsp. <i>salamae</i>	99.16	0.43	PHE 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.62	-.04			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.23	-.09			
630000	Excellent identification				630000
<i>Edwardsiella tarda</i>	100.0	1.00			
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.00	0.05			
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.00	-.08			
630001	Very good identification				630001
<i>Edwardsiella tarda</i>	99.86	0.59	TRE 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.12	0.13			
<i>Escherichia coli</i>	0.03	0.05			
630002	Very good identification				630002
<i>Edwardsiella tarda</i>	96.43	0.59	MAN 1		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	3.54	0.39			
<i>Escherichia coli</i>	0.03	0.05			
630010	Very good identification				630010
<i>Edwardsiella tarda</i>	100.0	0.59	CEL 1		
630020	Very good identification				630020
<i>Edwardsiella tarda</i>	100.0	0.59	SUC 1		
630040	Very good identification				630040
<i>Edwardsiella tarda</i>	99.33	0.59	SOR 1		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.67	0.24			
630042	Very good identification				630042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	96.39	0.59	IND 1		
<i>Edwardsiella tarda</i>	2.95	0.18			
<i>Escherichia coli</i>	0.58	0.23			
630043	Low discrimination				630043
<i>Escherichia coli</i>	40.33	0.49	H2S 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	28.70	0.33			
<i>Salmonella</i> serovar <i>typhi</i>	10.42	0.18			
630063	Good identification				630063

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	98.93	0.46	H2S 1		
<i>Salmonella</i> serovar enteritidis	1.07	-.09			
630100	Very good identification				630100
<i>Edwardsiella tarda</i>	100.0	0.59	MAL 1		
630200	Very good identification				630200
<i>Edwardsiella tarda</i>	100.0	0.59	INO 1		
630400	Very good identification				630400
<i>Edwardsiella tarda</i>	100.0	0.59	ADO 1		
630413	Good identification				630413
<i>Escherichia fergusonii</i>	100.0	0.45	H2S 1		
630513	Good identification				630513
<i>Escherichia fergusonii</i>	100.0	0.39	H2S 1		
631000	Very good identification				631000
<i>Edwardsiella tarda</i>	99.35	0.59	PHE 1		
<i>Morganella morganii</i> subsp. <i>morganii</i>	0.65	0.18			
631001	Low discrimination				631001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	60.56	0.36	H2S 6		
<i>Edwardsiella tarda</i>	39.44	0.18	URE 97		
632000	Very good identification				632000
<i>Edwardsiella tarda</i>	100.0	0.59	ESL 1		
632043	Low discrimination				632043
<i>Escherichia coli</i>	86.97	0.37	H2S 1		
<i>Salmonella</i> serovar enteritidis	13.03	0.06			
632413	Good identification				632413
<i>Escherichia fergusonii</i>	100.0	0.43	H2S 1		
632513	Good identification				632513
<i>Escherichia fergusonii</i>	100.0	0.38	H2S 1		
634000	Very good identification				634000
<i>Edwardsiella tarda</i>	99.98	0.59	SCI 1		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	0.03	-.05			
634042	Acceptable identification				634042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	90.75	0.49	IND 1		
<i>Salmonella</i> serovar enteritidis	4.27	0.18			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	3.91	0.18			
634043	Low discrimination				634043
<i>Salmonella</i> serovar enteritidis	45.59	0.59	IND 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	41.78	0.59			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.35	0.39			
634053	Good identification				634053
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	93.01	0.59	IND 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	5.34	0.33			
<i>Citrobacter braakii</i>	1.33	0.35			
634143	Identification to the genus				634143
<i>Salmonella enterica</i> subsp. <i>salamae</i>	89.02	0.65	IND 2		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	9.66	0.43			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	0.64	0.18			
634243	Very good identification				634243
<i>Salmonella</i> serovar <i>enteritidis</i>	96.81	0.53	IND 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	1.67	0.18			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	1.32	0.13			
634343	Acceptable identification				634343
<i>Salmonella enterica</i> subsp. <i>salamae</i>	94.35	0.39	IND 2		
<i>Salmonella</i> serovar <i>enteritidis</i>	3.68	0.12	INO 5		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	1.97	0.02			
636143	Good identification				636143
<i>Salmonella enterica</i> subsp. <i>salamae</i>	99.27	0.50	IND 2		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	0.62	0.02			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.11	-.09			
640001	Good identification				640001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	100.0	0.39	H2S 6		
640043	Very good identification				640043
<i>Salmonella</i> serovar <i>typhi</i>	99.46	0.59	URE 1		
<i>Citrobacter youngae</i>	0.41	0.30			
<i>Salmonella</i> serovar <i>enteritidis</i>	0.09	0.02			
641001	Very good identification				641001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	97.77	0.62	H2S 6		
<i>Proteus mirabilis</i>	1.00	0.12			
<i>Proteus vulgaris</i>	0.64	0.20			
641020	Identification to the genus				641020
<i>Proteus vulgaris</i>	50.32	0.59	LYS 1		
<i>Proteus penneri</i>	49.61	0.50			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.07	-.03			
641021	Low discrimination				641021
<i>Proteus penneri</i>	68.23	0.51	LYS 1		
<i>Proteus vulgaris</i>	24.27	0.51			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	7.30	0.38			
643020	Very good identification				643020
<i>Proteus vulgaris</i>	99.01	0.59	LYS 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus penneri</i>	0.99	0.09			
643021	Good identification				643021
<i>Proteus vulgaris</i>	96.95	0.51	LYS 1		
<i>Proteus penneri</i>	2.75	0.10			
<i>Morganella morganii subsp. sibonii</i>	0.29	-.03			
644063	Identification to the genus				644063
<i>Citrobacter freundii</i>	73.27	0.39	ONP 88		
<i>Citrobacter youngae</i>	26.73	0.27	LYS 1		
644073	Identification to the genus				644073
<i>Citrobacter freundii</i>	72.47	0.37	ONP 88		
<i>Citrobacter youngae</i>	27.53	0.26	LYS 1		
645020	Acceptable identification				645020
<i>Proteus vulgaris</i>	94.66	0.43	LYS 1		
<i>Proteus penneri</i>	5.34	0.09			
645021	Identification to the genus				645021
<i>Proteus vulgaris</i>	78.89	0.36	LYS 1		
<i>Proteus penneri</i>	12.70	0.10			
<i>Proteus mirabilis</i>	7.06	0.02			
647020	Good identification				647020
<i>Proteus vulgaris</i>	100.0	0.43	LYS 1		
647021	Good identification				647021
<i>Proteus vulgaris</i>	100.0	0.36	LYS 1		
650001	Good identification				650001
<i>Morganella morganii subsp. sibonii</i>	100.0	0.39	H2S 6		
651001	Very good identification				651001
<i>Morganella morganii subsp. sibonii</i>	99.35	0.62	H2S 6		
<i>Proteus vulgaris</i>	0.65	0.20			
651020	Very good identification				651020
<i>Proteus vulgaris</i>	98.89	0.59	LYS 1		
<i>Proteus penneri</i>	0.99	0.09			
<i>Morganella morganii subsp. sibonii</i>	0.13	-.03			
651021	Low discrimination				651021
<i>Proteus vulgaris</i>	75.24	0.51	LYS 1		
<i>Morganella morganii subsp. sibonii</i>	22.63	0.38			
<i>Proteus penneri</i>	2.14	0.10			
653020	Very good identification				653020
<i>Proteus vulgaris</i>	100.0	0.59	LYS 1		
653021	Good identification				653021
<i>Proteus vulgaris</i>	99.70	0.51	LYS 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.30	-.03			
655020	Good identification				655020
<i>Proteus vulgaris</i>	100.0	0.43	LYS 1		
655021	Good identification				655021
<i>Proteus vulgaris</i>	98.31	0.36	LYS 1		
<i>Morganella morganii</i> subsp. <i>sibonii</i>	1.69	-.03			
657020	Good identification				657020
<i>Proteus vulgaris</i>	100.0	0.43	LYS 1		
657021	Good identification				657021
<i>Proteus vulgaris</i>	100.0	0.36	LYS 1		
660001	Low discrimination				660001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	85.63	0.44	H2S 6		
<i>Proteus mirabilis</i>	13.22	0.19	PHE 93		
<i>Hafnia alvei</i>	1.15	0.18			
660002	Good identification				660002
<i>Salmonella enterica</i> subsp. <i>enterica</i>	98.64	0.39	URE 1		
<i>Hafnia alvei</i>	1.36	0.18	SOR 90		
660003	Very good identification				660003
<i>Hafnia alvei</i>	95.50	0.59	H2S 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	2.70	0.06			
<i>Morganella morganii</i> subsp. <i>sibonii</i>	0.72	0.03			
660013	Good identification				660013
<i>Hafnia alvei</i>	97.84	0.43	H2S 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	2.16	-.11			
660023	Good identification				660023
<i>Hafnia alvei</i>	100.0	0.39	H2S 1		
660042	Very good identification				660042
<i>Salmonella enterica</i> subsp. <i>enterica</i>	99.86	0.59	URE 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	0.08	-.09			
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	0.06	-.11			
660103	Very good identification				660103
<i>Hafnia alvei</i>	100.0	0.59	H2S 1		
660113	Good identification				660113
<i>Hafnia alvei</i>	100.0	0.43	H2S 1		
660123	Good identification				660123
<i>Hafnia alvei</i>	100.0	0.39	H2S 1		
661001	Low discrimination				661001
<i>Morganella morganii</i> subsp. <i>sibonii</i>	63.72	0.67	H2S 6		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus mirabilis</i>	36.29	0.53			
661021	Low discrimination				661021
<i>Proteus mirabilis</i>	59.49	0.38	LYS 1		
<i>Morganella morganii subsp. sibonii</i>	37.79	0.43			
<i>Proteus penneri</i>	2.01	0.10			
662003	Good identification				662003
<i>Hafnia alvei</i>	100.0	0.39	H2S 1		
662103	Good identification				662103
<i>Hafnia alvei</i>	100.0	0.39	H2S 1		
664003	Low discrimination				664003
<i>Hafnia alvei</i>	57.26	0.59	H2S 1		
<i>Salmonella serovar enteritidis</i>	30.75	0.33			
<i>Salmonella enterica subsp. houtenae</i>	10.93	0.24			
664023	Good identification				664023
<i>Hafnia alvei</i>	95.35	0.39	H2S 1		
<i>Salmonella serovar enteritidis</i>	4.65	-.09	SUC 10		
664042	Identification to the genus				664042
<i>Salmonella enterica subsp. enterica</i>	87.51	0.49	URE 1		
<i>Salmonella enterica subsp. houtenae</i>	7.62	0.24			
<i>Salmonella serovar enteritidis</i>	4.12	0.18			
664043	Identification to the genus				664043
<i>Salmonella enterica subsp. houtenae</i>	60.65	0.65	URE 2		
<i>Salmonella serovar enteritidis</i>	32.75	0.59			
<i>Salmonella bongori</i>	3.68	0.34			
664053	Very good identification				664053
<i>Salmonella enterica subsp. houtenae</i>	96.29	0.65	URE 2		
<i>Salmonella serovar enteritidis</i>	2.74	0.33			
<i>Citrobacter braakii</i>	0.85	0.37			
664103	Low discrimination				664103
<i>Hafnia alvei</i>	86.57	0.59	H2S 1		
<i>Salmonella enterica subsp. salamae</i>	11.69	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	1.27	-.04			
664113	Good identification				664113
<i>Hafnia alvei</i>	100.0	0.43	H2S 1		
664123	Good identification				664123
<i>Hafnia alvei</i>	100.0	0.39	H2S 1		
664143	Identification to the genus				664143
<i>Salmonella enterica subsp. salamae</i>	87.22	0.59	URE 1		
<i>Salmonella enterica subsp. diarizonae</i>	9.46	0.37			
<i>Salmonella enterica subsp. arizonae</i>	1.26	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
664243	Very good identification				664243
<i>Salmonella serovar enteritidis</i>	95.82	0.53	URE 1		
<i>Salmonella enterica subsp. houtenae</i>	3.33	0.24			
<i>Salmonella enterica subsp. salamae</i>	0.65	0.06			
664443	Identification to the genus				664443
<i>Salmonella enterica subsp. houtenae</i>	89.09	0.39	URE 2		
<i>Salmonella serovar enteritidis</i>	9.23	0.18	ADO 5		
<i>Salmonella bongori</i>	1.04	-.07			
664453	Good identification				664453
<i>Salmonella enterica subsp. houtenae</i>	99.46	0.39	URE 2		
<i>Salmonella serovar enteritidis</i>	0.54	-.09	ADO 5		
665001	Very good identification				665001
<i>Proteus mirabilis</i>	99.05	0.59	LYS 1		
<i>Morganella morganii subsp. sibonii</i>	0.95	0.26			
665021	Good identification				665021
<i>Proteus mirabilis</i>	99.66	0.43	LYS 1		
<i>Morganella morganii subsp. sibonii</i>	0.34	0.02			
666003	Low discrimination				666003
<i>Hafnia alvei</i>	79.72	0.39	H2S 1		
<i>Salmonella serovar enteritidis</i>	20.28	0.06	ESL 10		
666103	Low discrimination				666103
<i>Hafnia alvei</i>	82.34	0.39	H2S 1		
<i>Salmonella enterica subsp. salamae</i>	17.66	0.02	ESL 10		
666143	Good identification				666143
<i>Salmonella enterica subsp. salamae</i>	99.16	0.43	URE 1		
<i>Salmonella enterica subsp. diarizonae</i>	0.62	-.04			
<i>Salmonella serovar enteritidis</i>	0.23	-.09			
670000	Very good identification				670000
<i>Edwardsiella tarda</i>	99.14	0.59	URE 1		
<i>Morganella morganii subsp. morganii</i>	0.82	0.20			
<i>Morganella morganii subsp. sibonii</i>	0.04	0.03			
670001	Low discrimination				670001
<i>Morganella morganii subsp. sibonii</i>	78.89	0.44	H2S 6		
<i>Edwardsiella tarda</i>	21.11	0.18	PHE 93		
671000	Acceptable identification				671000
<i>Morganella morganii subsp. morganii</i>	91.21	0.47	LYS 1		
<i>Edwardsiella tarda</i>	5.86	0.18			
<i>Morganella morganii subsp. sibonii</i>	2.94	0.26			
671001	Very good identification				671001
<i>Morganella morganii subsp. sibonii</i>	98.54	0.67	H2S 6		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Proteus mirabilis</i>	1.15	0.19			
<i>Morganella morganii subsp. morganii</i>	0.31	0.05			
671021	Good identification				671021
<i>Morganella morganii subsp. sibonii</i>	95.15	0.43	H2S 6		
<i>Proteus mirabilis</i>	3.06	0.03	SUC 6		
<i>Proteus vulgaris</i>	1.80	0.10			
700013	Good identification				700013
<i>Escherichia vulneris</i>	99.72	0.43	H2S 1		
<i>Yokenella regensburgei</i>	0.28	-.10			
700043	Good identification				700043
<i>Salmonella serovar typhi</i>	91.52	0.59	ONP 1		
<i>Salmonella bongori</i>	5.43	0.34			
<i>Citrobacter youngae</i>	1.53	0.42			
700053	Low discrimination				700053
<i>Citrobacter youngae</i>	46.26	0.41	LYS 1		
<i>Salmonella serovar typhi</i>	34.24	0.18			
<i>Citrobacter freundii</i>	6.57	0.26			
700063	Low discrimination				700063
<i>Citrobacter freundii</i>	46.30	0.47	LYS 1		
<i>Salmonella serovar typhi</i>	23.43	0.18			
<i>Escherichia coli</i>	14.56	0.33			
700073	Identification to the genus				700073
<i>Citrobacter freundii</i>	78.85	0.44	LYS 1		
<i>Citrobacter youngae</i>	18.24	0.29			
<i>Yersinia rohdei</i>	2.91	0.08			
700113	Very good identification				700113
<i>Escherichia vulneris</i>	100.0	0.59	H2S 1		
700133	Good identification				700133
<i>Escherichia vulneris</i>	100.0	0.37	H2S 1		
700413	Low discrimination				700413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	82.84	0.36	H2S 1		
<i>Escherichia vulneris</i>	17.16	0.02			
700453	Good identification				700453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	H2S 1		
700613	Good identification				700613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.37	H2S 1		
700653	Low discrimination				700653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	69.28	0.43	H2S 1	VPT 1	
<i>Serratia odorifera biovar 2</i>	30.72	0.28		99	
702113	Good identification				702113

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia vulneris</i>	100.0	0.47	H2S 1		
702413	Good identification				702413
<i>Klebsiella pneumoniae subsp. ozaenae</i>	98.72	0.48	H2S 1		
<i>Escherichia vulneris</i>	1.28	-.10			
702433	Low discrimination				702433
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	79.53	0.36	H2S 1	1	
<i>Serratia rubidaea</i>	20.47	0.08		99	
702453	Very good identification				702453
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.54	H2S 1		
702473	Good identification				702473
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.41	H2S 1		
702613	Good identification				702613
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.50	H2S 1		
702633	Acceptable identification				702633
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	95.00	0.37	H2S 1	1	
<i>Serratia rubidaea</i>	5.00	-.04		99	
702653	Good identification				702653
				VPT	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	93.12	0.55	H2S 1	1	
<i>Serratia odorifera biovar 2</i>	6.88	0.24		99	
702673	Good identification				702673
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.43	H2S 1		
704043	Low discrimination				704043
<i>Salmonella bongori</i>	81.06	0.59	ORN 99		
<i>Salmonella enterica subsp. arizonae</i>	4.54	0.33			
<i>Citrobacter youngae</i>	4.14	0.52			
704053	Low discrimination				704053
<i>Citrobacter youngae</i>	55.41	0.50	LYS 1		
<i>Salmonella bongori</i>	13.40	0.18			
<i>Citrobacter freundii</i>	11.06	0.38			
704063	Low discrimination				704063
<i>Citrobacter freundii</i>	75.83	0.59	LYS 1		
<i>Citrobacter youngae</i>	11.98	0.40			
<i>Salmonella bongori</i>	8.92	0.18			
704073	Identification to the genus				704073
<i>Citrobacter freundii</i>	85.42	0.57	LYS 1		
<i>Citrobacter youngae</i>	14.06	0.38			
<i>Citrobacter braakii</i>	0.53	0.09			
704143	Identification to the genus				704143

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	48.26	0.59	ORN 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	42.17	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	5.96	0.43			
704253	Very good identification				704253
				VPT	
<i>Serratia odorifera</i> biovar 2	97.77	0.57	H2S 1	99	
<i>Citrobacter youngae</i>	1.53	0.24		1	
<i>Salmonella</i> serovar <i>enteritidis</i>	0.70	0.02		1	
704653	Very good identification				704653
				VPT	
<i>Serratia odorifera</i> biovar 2	97.10	0.59	H2S 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	2.90	0.35		1	
706253	Very good identification				706253
				VPT	
<i>Serratia odorifera</i> biovar 2	99.33	0.54	H2S 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	0.67	0.17		1	
706413	Good identification				706413
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	97.20	0.40	H2S 1	1	
<i>Serratia rubidaea</i>	2.80	-.07		99	
706453	Acceptable identification				706453
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	93.56	0.46	H2S 1	1	
<i>Serratia odorifera</i> biovar 2	6.44	0.14		99	
706533	Very good identification				706533
<i>Serratia rubidaea</i>	100.0	0.59	H2S 1		
706613	Acceptable identification				706613
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	90.53	0.42	H2S 1	1	
<i>Serratia odorifera</i> biovar 2	9.47	0.14		99	
706653	Low discrimination				706653
				VPT	
<i>Serratia odorifera</i> biovar 2	84.79	0.55	H2S 1	99	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	15.21	0.48		1	
706673	Low discrimination				706673
				VPT	
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	40.30	0.35	H2S 1	1	
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	26.28	0.10		98	
<i>Serratia odorifera</i> biovar 1	16.50	0.14		50	
706733	Good identification				706733
<i>Serratia rubidaea</i>	99.37	0.47	H2S 1		
<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	0.44	-.09			
<i>Enterobacter aerogenes</i>	0.19	-.17			
710003	Good identification				710003
<i>Escherichia coli</i>	100.0	0.40	H2S 1		
710023	Good identification				710023
<i>Escherichia coli</i>	100.0	0.37	H2S 1		
710043	Low discrimination				710043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Escherichia coli</i>	87.64	0.58	H2S 1		
<i>Salmonella serovar typhi</i>	8.18	0.18			
<i>Citrobacter youngae</i>	2.38	0.27			
710063	Low discrimination				710063
<i>Escherichia coli</i>	87.18	0.55	H2S 1		
<i>Citrobacter freundii</i>	11.87	0.40			
<i>Citrobacter youngae</i>	0.95	0.15			
710073	Low discrimination				710073
<i>Citrobacter freundii</i>	78.52	0.38	LYS 1		
<i>Escherichia coli</i>	14.98	0.20			
<i>Citrobacter youngae</i>	6.51	0.13			
712043	Good identification				712043
<i>Escherichia coli</i>	100.0	0.46	H2S 1		
712063	Good identification				712063
<i>Escherichia coli</i>	100.0	0.42	H2S 1		
714063	Acceptable identification				714063
<i>Citrobacter freundii</i>	93.01	0.53	LYS 1		
<i>Citrobacter youngae</i>	5.27	0.24			
<i>Escherichia coli</i>	1.73	0.14			
714073	Acceptable identification				714073
<i>Citrobacter freundii</i>	93.88	0.50	LYS 1		
<i>Citrobacter youngae</i>	5.54	0.23			
<i>Citrobacter braakii</i>	0.58	0.03			
714253	Very good identification				714253
				VPT	
<i>Serratia odorifera biovar 2</i>	99.73	0.57	H2S 1	99	
<i>Citrobacter youngae</i>	0.28	0.08		1	
714653	Very good identification				714653
<i>Serratia odorifera biovar 2</i>	100.0	0.59	H2S 1		
716253	Very good identification				716253
<i>Serratia odorifera biovar 2</i>	100.0	0.54	H2S 1		
716653	Very good identification				716653
				VPT	
<i>Serratia odorifera biovar 2</i>	99.82	0.55	H2S 1	99	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.18	0.07		1	
716773	Good identification				716773
<i>Klebsiella oxytoca</i>	99.39	0.39	H2S 1		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.42	-.09	URE 90		
<i>Enterobacter aerogenes</i>	0.18	-.17			
720002	Good identification				720002
<i>Salmonella enterica subsp. enterica</i>	97.36	0.39	ONP 1		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella bongori</i>	1.54	-.07	SOR 90		
<i>Hafnia alvei</i>	1.10	0.16			
720023	Low discrimination				720023
<i>Hafnia alvei</i>	75.53	0.38	H2S 1		
<i>Escherichia coli</i>	14.87	0.16	SUC 10		
<i>Salmonella bongori</i>	9.61	-.07			
720042	Identification to the genus				720042
<i>Salmonella enterica subsp. enterica</i>	84.63	0.59	ONP 1		
<i>Salmonella bongori</i>	14.74	0.34			
<i>Salmonella enterica subsp. diarizonae</i>	0.23	-.02			
720043	Very good identification				720043
<i>Salmonella bongori</i>	95.86	0.75	SCI 94		
<i>Salmonella enterica subsp. diarizonae</i>	1.50	0.39			
<i>Salmonella serovar enteritidis</i>	0.92	0.39			
720103	Low discrimination				720103
<i>Hafnia alvei</i>	59.00	0.57	H2S 1		
<i>Salmonella enterica subsp. diarizonae</i>	24.55	0.24			
<i>Salmonella enterica subsp. arizonae</i>	13.90	0.18			
720113	Low discrimination				720113
<i>Hafnia alvei</i>	53.88	0.42	H2S 1		
<i>Escherichia vulneris</i>	41.51	0.18			
<i>Yokenella regensburgei</i>	2.02	-.10			
720123	Low discrimination				720123
<i>Hafnia alvei</i>	83.54	0.38	H2S 1		
<i>Salmonella enterica subsp. diarizonae</i>	16.46	-.02	SUC 10		
720143	Identification to the genus				720143
<i>Salmonella enterica subsp. diarizonae</i>	59.85	0.65	SCI 98		
<i>Salmonella enterica subsp. arizonae</i>	33.90	0.59			
<i>Salmonella enterica subsp. salamae</i>	4.19	0.43			
720163	Identification to the genus				720163
<i>Salmonella enterica subsp. diarizonae</i>	88.60	0.39	SCI 98		
<i>Salmonella enterica subsp. arizonae</i>	9.63	0.18	SUC 5		
<i>Salmonella enterica subsp. salamae</i>	1.19	0.02			
722003	Low discrimination				722003
<i>Hafnia alvei</i>	75.65	0.38	H2S 1		
<i>Salmonella bongori</i>	9.62	-.07	ESL 10		
<i>Yokenella regensburgei</i>	9.14	-.04			
722013	Good identification				722013
<i>Yokenella regensburgei</i>	97.62	0.37	H2S 1		
<i>Hafnia alvei</i>	1.44	0.22	SCI 92		
<i>Escherichia fergusonii</i>	0.50	0.00			
722103	Acceptable identification				722103

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Hafnia alvei</i>	92.25	0.38	H2S 1		
<i>Salmonella enterica</i> subsp. <i>salamae</i>	4.27	-.13	ESL 10		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	3.49	-.17			
724003	Low discrimination				724003
<i>Salmonella bongori</i>	81.49	0.59	SOR 99		
<i>Salmonella</i> serovar <i>enteritidis</i>	4.93	0.39			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	4.57	0.33			
724013	Acceptable identification				724013
<i>Yokenella regensburgei</i>	92.36	0.53	H2S 1		
<i>Salmonella bongori</i>	2.72	0.18			
<i>Hafnia alvei</i>	2.16	0.42			
724041	Identification to the genus				724041
<i>Salmonella bongori</i>	88.14	0.59	MAN 99		
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	4.94	0.33			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	4.32	0.33			
724042	Low discrimination				724042
<i>Salmonella bongori</i>	79.92	0.59	TRE 99		
<i>Salmonella enterica</i> subsp. <i>enterica</i>	9.76	0.49			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	4.48	0.33			
724043	Identification to the genus				724043
<i>Salmonella bongori</i>	88.56	1.00			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	4.96	0.74			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	4.34	0.74			
724053	Low discrimination				724053
<i>Salmonella bongori</i>	56.41	0.59	CEL 1		
<i>Salmonella enterica</i> subsp. <i>houtenae</i>	29.41	0.59			
<i>Citrobacter braakii</i>	4.17	0.56			
724063	Identification to the genus				724063
<i>Salmonella bongori</i>	74.32	0.59	SUC 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	18.96	0.47			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	4.16	0.33			
724103	Identification to the genus				724103
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	48.77	0.59	SOR 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	42.62	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.03	0.43			
724141	Identification to the genus				724141
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	49.83	0.59	MAN 99		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	43.54	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.16	0.43			
724142	Identification to the genus				724142
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	49.80	0.59	TRE 99		

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	43.52	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.15	0.43			
724143	Identification to the genus				724143
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	49.82	1.00			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	43.54	1.00			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.16	0.85			
724153	Identification to the genus				724153
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	49.67	0.59	CEL 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	43.41	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.14	0.43			
724163	Identification to the genus				724163
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	80.07	0.74	SUC 5		
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	17.59	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	2.17	0.43			
724243	Low discrimination				724243
<i>Salmonella bongori</i>	56.63	0.59	INO 1		
<i>Salmonella</i> serovar <i>enteritidis</i>	35.05	0.60			
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	3.17	0.33			
724343	Identification to the genus				724343
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	39.48	0.59	INO 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	34.50	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	25.42	0.58			
724443	Identification to the genus				724443
<i>Salmonella bongori</i>	86.86	0.59	ADO 1		
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	4.87	0.33			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	4.25	0.33			
724543	Identification to the genus				724543
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	49.82	0.59	ADO 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	43.54	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.16	0.43			
725043	Identification to the genus				725043
<i>Salmonella bongori</i>	88.56	0.59	PHE 1		
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	4.96	0.33			
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	4.34	0.33			
725143	Identification to the genus				725143
<i>Salmonella enterica</i> subsp. <i>arizonae</i>	49.83	0.59	PHE 1		
<i>Salmonella enterica</i> subsp. <i>diarizonae</i>	43.54	0.59			
<i>Salmonella enterica</i> subsp. <i>salamae</i>	6.16	0.43			
726013	Very good identification				726013
<i>Yokenella regensburgei</i>	99.87	0.59	H2S 1		
<i>Hafnia alvei</i>	0.13	0.22			
726043	Low discrimination				726043

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Salmonella bongori</i>	77.32	0.59	ESL 1		
<i>Salmonella enterica subsp. salamae</i>	9.35	0.43			
<i>Salmonella serovar enteritidis</i>	4.68	0.39			
726063	Low discrimination				726063
				VPT	
<i>Serratia marcescens</i>	89.23	0.49	H2S 1	98	
<i>Salmonella bongori</i>	7.22	0.18		1	
<i>Salmonella enterica subsp. diarizonae</i>	1.84	0.06		1	
726133	Good identification				726133
				VPT	
<i>Kluyvera ascorbata</i>	99.57	0.37	H2S 1	1	
<i>Cronobacter sakazakii</i>	0.43	-.06	IND 92	99	
726143	Identification to the genus				726143
<i>Salmonella enterica subsp. salamae</i>	53.40	0.69			
<i>Salmonella enterica subsp. arizonae</i>	24.74	0.59			
<i>Salmonella enterica subsp. diarizonae</i>	21.62	0.59			
726263	Very good identification				726263
				VPT	
<i>Serratia marcescens</i>	99.36	0.59	H2S 1	98	
<i>Serratia odorifera biovar 1</i>	0.56	0.14		50	
<i>Salmonella serovar enteritidis</i>	0.09	-.08		1	
726273	Good identification				726273
<i>Serratia odorifera biovar 1</i>	90.96	0.55	H2S 1		
<i>Serratia marcescens</i>	8.61	0.33			
<i>Enterobacter aerogenes</i>	0.44	-.02			
726343	Identification to the genus				726343
<i>Salmonella enterica subsp. salamae</i>	85.52	0.43	INO 5		
<i>Salmonella enterica subsp. arizonae</i>	7.60	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	6.64	0.18			
726463	Good identification				726463
<i>Serratia marcescens</i>	100.0	0.46	H2S 1		
726663	Very good identification				726663
<i>Serratia marcescens</i>	98.97	0.55	H2S 1		
<i>Serratia odorifera biovar 1</i>	0.83	0.14			
<i>Enterobacter aerogenes</i>	0.20	-.09			
726673	Low discrimination				726673
<i>Serratia odorifera biovar 1</i>	77.02	0.55	H2S 1		
<i>Enterobacter aerogenes</i>	18.12	0.33			
<i>Serratia marcescens</i>	4.86	0.29			
726773	Very good identification				726773
<i>Enterobacter aerogenes</i>	99.68	0.59	H2S 1		
<i>Serratia odorifera biovar 1</i>	0.23	0.14			
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.05	-.09			
730000	Very good identification				730000

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Edwardsiella tarda</i>	100.0	0.59	ONP 1		
730003	Low discrimination				730003
<i>Escherichia coli</i>	86.34	0.41	H2S 1		
<i>Escherichia fergusonii</i>	4.70	0.10	SOR 88		
<i>Escherichia hermannii</i>	3.41	0.03			
730023	Good identification				730023
<i>Escherichia coli</i>	95.38	0.38	H2S 1		
<i>Escherichia hermannii</i>	4.62	0.02	SOR 88		
730043	Low discrimination				730043
<i>Escherichia coli</i>	63.36	0.59	H2S 1		
<i>Salmonella bongori</i>	32.04	0.34			
<i>Citrobacter braakii</i>	3.00	0.33			
730053	Low discrimination				730053
<i>Citrobacter braakii</i>	75.72	0.40	LYS 1		
<i>Escherichia coli</i>	16.09	0.24			
<i>Salmonella bongori</i>	4.03	-.07			
730063	Very good identification				730063
<i>Escherichia coli</i>	98.72	0.55	H2S 1		
<i>Salmonella bongori</i>	0.76	-.07			
<i>Citrobacter braakii</i>	0.53	0.10			
730413	Very good identification				730413
<i>Escherichia fergusonii</i>	99.91	0.59	H2S 1		
<i>Escherichia hermannii</i>	0.09	-.07			
730513	Very good identification				730513
<i>Escherichia fergusonii</i>	100.0	0.53	H2S 1		
732043	Good identification				732043
<i>Escherichia coli</i>	98.00	0.47	H2S 1		
<i>Salmonella bongori</i>	2.00	-.07			
732063	Good identification				732063
<i>Escherichia coli</i>	100.0	0.43	H2S 1		
732413	Very good identification				732413
<i>Escherichia fergusonii</i>	100.0	0.58	H2S 1		
732513	Good identification				732513
<i>Escherichia fergusonii</i>	100.0	0.52	H2S 1		
734043	Identification to the genus				734043
<i>Salmonella bongori</i>	82.97	0.59	IND 1		
<i>Salmonella enterica subsp. diarizonae</i>	8.21	0.39			
<i>Salmonella enterica subsp. arizonae</i>	4.65	0.33			
734053	Low discrimination				734053

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter braakii</i>	61.42	0.49	LYS 1		
<i>Salmonella bongori</i>	17.06	0.18			
<i>Salmonella enterica subsp. houtenae</i>	8.89	0.18			
734143	Identification to the genus				734143
<i>Salmonella enterica subsp. diarizonae</i>	58.37	0.65	IND 2		
<i>Salmonella enterica subsp. arizonae</i>	33.06	0.59			
<i>Salmonella enterica subsp. salamae</i>	8.25	0.50			
734163	Identification to the genus				734163
<i>Salmonella enterica subsp. diarizonae</i>	88.04	0.39	IND 2		
<i>Salmonella enterica subsp. arizonae</i>	9.57	0.18	SUC 5		
<i>Salmonella enterica subsp. salamae</i>	2.39	0.09			
734413	Good identification				734413
<i>Escherichia fergusonii</i>	100.0	0.45	H2S 1		
734513	Good identification				734513
<i>Escherichia fergusonii</i>	100.0	0.39	H2S 1		
736133	Very good identification				736133
<i>Kluyvera ascorbata</i>	100.0	0.59	H2S 1		
736173	Very good identification				736173
<i>Kluyvera ascorbata</i>	100.0	0.55	H2S 1		
736273	Very good identification				736273
<i>Serratia odorifera biovar 1</i>	99.94	0.59	H2S 1		
<i>Serratia marcescens</i>	0.06	-.09			
736413	Good identification				736413
<i>Escherichia fergusonii</i>	100.0	0.43	H2S 1		
736513	Good identification				736513
<i>Escherichia fergusonii</i>	100.0	0.38	H2S 1		
736673	Very good identification				736673
<i>Serratia odorifera biovar 1</i>	99.84	0.59	H2S 1		
<i>Enterobacter aerogenes</i>	0.16	-.09			
740043	Low discrimination				740043
<i>Citrobacter youngae</i>	66.81	0.50	LYS 1		
<i>Salmonella serovar typhi</i>	18.18	0.18			
<i>Citrobacter werkmanii</i>	9.51	0.15			
740053	Acceptable identification				740053
<i>Citrobacter youngae</i>	91.40	0.48	LYS 1		
<i>Citrobacter freundii</i>	4.58	0.24			
<i>Citrobacter braakii</i>	3.18	0.18			
740063	Identification to the genus				740063

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter freundii</i>	58.39	0.44	LYS 1		
<i>Citrobacter youngae</i>	36.73	0.38			
<i>Yersinia rohdei</i>	4.88	0.15			
740073	Identification to the genus				740073
<i>Citrobacter freundii</i>	59.15	0.42	LYS 1		
<i>Citrobacter youngae</i>	38.75	0.36			
<i>Yersinia rohdei</i>	2.10	0.06			
740143	Good identification				740143
<i>Citrobacter werkmanii</i>	96.35	0.37	LYS 1		
<i>Citrobacter youngae</i>	3.10	0.23	SCI 92		
<i>Salmonella enterica subsp. diarizonae</i>	0.28	-.17			
742653	Good identification				742653
<i>Klebsiella pneumoniae subsp. ozaenae</i>	100.0	0.36	H2S 1		
744043	Low discrimination				744043
<i>Citrobacter youngae</i>	56.66	0.59	LYS 1		
<i>Citrobacter werkmanii</i>	32.60	0.37			
<i>Salmonella bongori</i>	5.04	0.18			
744053	Identification to the genus				744053
<i>Citrobacter youngae</i>	89.75	0.57	LYS 1		
<i>Citrobacter freundii</i>	6.33	0.36			
<i>Citrobacter braakii</i>	3.29	0.28			
744063	Identification to the genus				744063
<i>Citrobacter freundii</i>	68.61	0.57	LYS 1		
<i>Citrobacter youngae</i>	30.72	0.47			
<i>Citrobacter werkmanii</i>	0.67	-.04			
744073	Identification to the genus				744073
<i>Citrobacter freundii</i>	67.98	0.55	LYS 1		
<i>Citrobacter youngae</i>	31.69	0.45			
<i>Citrobacter braakii</i>	0.33	0.05			
744103	Good identification				744103
<i>Citrobacter werkmanii</i>	98.90	0.39	LYS 1		
<i>Hafnia alvei</i>	1.10	0.22	SOR 90		
744143	Very good identification				744143
<i>Citrobacter werkmanii</i>	96.39	0.59	LYS 1		
<i>Salmonella enterica subsp. arizonae</i>	1.38	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	1.20	0.18			
746373	Good identification				746373
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	100.0	0.39	H2S 1		
746673	Good identification				746673
				VPT	
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	98.81	0.36	H2S 1	98	
<i>Klebsiella pneumoniae subsp. ozaenae</i>	0.89	0.16	MAL 93	1	

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Klebsiella oxytoca</i>	0.30	-.17		95	
746773	Very good identification				746773
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	98.84	0.59	H2S 1		
<i>Klebsiella oxytoca</i>	1.12	0.18			
<i>Enterobacter aerogenes</i>	0.05	-.11			
750063	Low discrimination				750063
<i>Citrobacter freundii</i>	75.77	0.38	LYS 1		
<i>Citrobacter youngae</i>	17.08	0.22			
<i>Escherichia coli</i>	7.15	0.14			
750073	Identification to the genus				750073
<i>Citrobacter freundii</i>	80.99	0.36	LYS 1		
<i>Citrobacter youngae</i>	19.01	0.20			
754043	Identification to the genus				754043
<i>Citrobacter youngae</i>	78.19	0.43	LYS 1		
<i>Citrobacter freundii</i>	16.02	0.32			
<i>Citrobacter braakii</i>	3.22	0.16			
754053	Low discrimination				754053
<i>Citrobacter youngae</i>	69.27	0.42	LYS 1		
<i>Citrobacter freundii</i>	13.63	0.30			
<i>Citrobacter amalonaticus</i>	10.02	0.08			
754063	Identification to the genus				754063
<i>Citrobacter freundii</i>	86.18	0.50	LYS 1		
<i>Citrobacter youngae</i>	13.82	0.32			
754073	Identification to the genus				754073
<i>Citrobacter freundii</i>	85.69	0.48	LYS 1		
<i>Citrobacter youngae</i>	14.31	0.30			
756773	Very good identification				756773
<i>Klebsiella oxytoca</i>	99.11	0.59	H2S 1		
<i>Klebsiella pneumoniae subsp. pneumoniae</i>	0.89	0.18			
760003	Very good identification				760003
<i>Hafnia alvei</i>	98.61	0.57	H2S 1		
<i>Salmonella bongori</i>	1.39	-.07			
760013	Good identification				760013
<i>Hafnia alvei</i>	96.39	0.42	H2S 1		
<i>Yokenella regensburgei</i>	3.61	-.10			
760023	Good identification				760023
<i>Hafnia alvei</i>	100.0	0.38	H2S 1		
760053	Low discrimination				760053
<i>Citrobacter braakii</i>	73.83	0.42	LYS 1		
<i>Yersinia kristensenii</i>	17.01	0.18			

Code Taxon	ID score	T index	tests against	Differentiation tests	Code
<i>Citrobacter youngae</i>	4.95	0.17			
760103	Very good identification				760103
<i>Hafnia alvei</i>	99.58	0.57	H2S 1		
<i>Salmonella enterica subsp. diarizonae</i>	0.42	-.17			
760113	Good identification				760113
<i>Hafnia alvei</i>	100.0	0.42	H2S 1		
760123	Good identification				760123
<i>Hafnia alvei</i>	100.0	0.38	H2S 1		
762003	Good identification				762003
<i>Hafnia alvei</i>	100.0	0.38	H2S 1		
762103	Good identification				762103
<i>Hafnia alvei</i>	100.0	0.38	H2S 1		
764003	Low discrimination				764003
<i>Hafnia alvei</i>	79.18	0.57	H2S 1		
<i>Salmonella bongori</i>	17.53	0.18			
<i>Salmonella serovar enteritidis</i>	1.06	-.02			
764013	Low discrimination				764013
<i>Hafnia alvei</i>	67.21	0.42	H2S 1		
<i>Yokenella regensburgei</i>	28.97	0.12			
<i>Citrobacter braakii</i>	3.82	0.10			
764023	Good identification				764023
<i>Hafnia alvei</i>	100.0	0.38	H2S 1		
764043	Identification to the genus				764043
<i>Salmonella bongori</i>	86.13	0.59	URE 1		
<i>Salmonella enterica subsp. arizonae</i>	4.83	0.33			
<i>Salmonella enterica subsp. diarizonae</i>	4.22	0.33			
764053	Low discrimination				764053
<i>Citrobacter braakii</i>	62.07	0.51	LYS 1		
<i>Salmonella enterica subsp. houtenae</i>	14.59	0.24			
<i>Salmonella bongori</i>	13.85	0.18			
764103	Low discrimination				764103
<i>Hafnia alvei</i>	67.15	0.57	H2S 1		
<i>Salmonella enterica subsp. arizonae</i>	15.82	0.18			
<i>Salmonella enterica subsp. diarizonae</i>	13.83	0.18			
764113	Good identification				764113
<i>Hafnia alvei</i>	100.0	0.42	H2S 1		
764123	Acceptable identification				764123
<i>Hafnia alvei</i>	91.11	0.38	H2S 1		
<i>Salmonella enterica subsp. diarizonae</i>	8.89	-.09	SUC 10		

Code Taxon		ID score	T index	tests against	Differentiation tests	Code
764143	Identification to the genus					764143
<i>Salmonella enterica subsp. arizonae</i>		49.63	0.59	URE 1		
<i>Salmonella enterica subsp. diarizonae</i>		43.37	0.59			
<i>Salmonella enterica subsp. salamae</i>		6.13	0.43			
766003	Good identification					766003
<i>Hafnia alvei</i>		100.0	0.38	H2S 1		
766103	Good identification					766103
<i>Hafnia alvei</i>		95.58	0.38	H2S 1		
<i>Salmonella enterica subsp. salamae</i>		4.42	-.13	ESL 10		
766263	Good identification					766263
<i>Serratia marcescens</i>		100.0	0.43	H2S 1		
766663	Good identification					766663
<i>Serratia marcescens</i>		100.0	0.40	H2S 1		
770053	Low discrimination					770053
<i>Citrobacter braakii</i>		79.93	0.35	LYS 1		
<i>Yersinia kristensenii</i>		16.02	0.10			
<i>Citrobacter amalonaticus</i>		4.04	-.09			
774043	Low discrimination					774043
<i>Citrobacter braakii</i>		46.44	0.39	LYS 1		
<i>Salmonella bongori</i>		42.72	0.18			
<i>Salmonella enterica subsp. diarizonae</i>		4.23	-.02			

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