

Aerobic bacteria in holy water from Catholic churches in Slovenia

Aerobne bakterije v blagoslovljeni vodi iz katoliških cerkva v Sloveniji

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Abstract: Holy water plays an important role in various religions. It is used for baptisms, to bless people, places and objects. In Catholic churches, it is usually offered in the holy water fountains at the entrance of the church. But it is also considered a source of potential pathogens, such as *Pseudomonas aeruginosa*, *Acinetobacter baumannii* and enterobacteria. To estimate the potential risk, we studied the composition and antimicrobial resistance of bacteria in holy water from fountains and reservoirs of ten selected Catholic churches in Ljubljana, Slovenia. Bacterial contamination of holy water from fountains was moderate (10^2 - 10^5 CFU ml⁻¹), but one to two orders of magnitude higher than in reservoirs, probably due to frequent immersion of fingers in the water. Some genera/species occurred only in fountains (*Acinetobacter beijerinckii*, *A. haemolyticus*, *Brevundimonas aurantiaca*, *B. mediterranea*, *Delftia*, *Kocuria*, *Sphingobacterium*, *Staphylococcus warneri*), while few fecal indicator bacteria were isolated. Isolated bacteria have relatively low pathogenic potential, some of them are skin commensals. Bacterial strains isolated in this study were susceptible to antibiotics. While according to our results, the potential of holy water for spreading bacterial infections is modest, to further limit the risks, water should be changed regularly, the fountains cleaned thoroughly, and the water should not be brought in contact with the eyes, ingested or aerosolized and inhaled.

Keywords: antibiotic resistance, bacteria, fountains, holy water, NaCl, Roman Catholic churches, pathogens

Izvešček: Blagoslovljena voda ima pomembno vlogo v različnih religijah. Uporablja se pri svetem krstu, za blagoslov ljudi, krajev in predmetov. V katoliških cerkvah se običajno nahaja v kropilnikih ob vhodu v cerkev. Lahko pa predstavlja tudi vir oportunističnih patogenov, kot so *Pseudomonas aeruginosa*, *Acinetobacter baumannii* in enterobakterije. Da bi bolje razumeli to tveganje, smo proučili sestavo in protimikrobno odpornost bakterij v blagoslovljeni vodi kropilnikov in rezervoarjev desetih izbranih katoliških cerkva v Ljubljani (Slovenija). Bakterijska kontaminacija blagoslovljene vode iz krstilnikov je bila zmerna (10^2 - 10^5 CFU ml⁻¹), a za red velikosti do dva višja kot v rezervoarjih, verjetno zaradi pogostega pomakanja prstov vernikov v vodo kropilnika ob vstopu in izstopu iz cerkve. Nekateri bakterijski rodovi/vrste so se pojavili le v kropilnikih (*Acinetobacter beijerinckii*, *A. haemolyticus*, *Brevundimonas aurantiaca*, *B. mediterranea*, *Delftia*, *Kocuria*, *Sphingobacterium*, *Staphylococcus warneri*), izoliranih

pa je bilo le nekaj fekalnih indikatorskih bakterij. Izolirane bakterije imajo razmeroma nizek patogeni potencial, nekatere med njimi so kožni komenzali. Bakterijski sevi v tej študiji so bili občutljivi proti antibiotikom. Čeprav je potencial blagoslovljene vode za širjenje bakterijskih okužb glede na naše rezultate majhen, lahko tveganja dodatno zmanjšamo z redno menjavo vode, s temeljitim čiščenjem kropilnikov in s preprečevanjem vnosa vode v oči, njenega zaužitja ter aerosolizacije in vdihavanja.

Ključne besede: bakterije, blagoslovljena voda, kropilniki, NaCl, odpornost proti antibiotikom, patogeni, rimskokatoliške cerkve

Introduction

Water is considered a sign of cleanliness and purification and has been used in many ancient and modern religious traditions (Oestigaard 2017). Holy water is water that has been blessed by a priest or comes from a well or spring considered sacred. In the Roman Catholic tradition, holy water is used as a sacrament for baptisms, to bless people, places, and objects, or to protect against evil and danger (Kirschner et al. 2012). It is commonly used to wash away sins (Flemming 2011). The Roman Catholic Church recommends adding an unregulated amount of blessed salt (sodium chloride) to the water during the blessing, which also results in varying salt concentrations of the holy water (Kirschner et al. 2012). Holy water is usually made only once a year at Easter, when tap water is blessed and then stored in metal reservoirs (tanks) located in the church. Holy water is offered in the holy water fonts at the entrance of the church (or sometimes at a separate location, the baptistery). Smaller vessels, called stoups, are usually placed on the walls of church entrances for people to bless themselves with as they enter the church. They may be larger or smaller and made of stone, marble, glass, metal, or porcelain. When the faithful enter and leave the church, they dip the fingers of their right hand into the holy water and make the sign of the cross on their forehead, lips and chest. Holy water can also be used to bless food, objects, places, or people by sprinkling them (Jurado et al. 2002, Kirschner et al. 2012).

However, it is well known that water is both a reservoir and source of pathogens that can lead to transmission of infectious diseases (Denham et al. 2013). Holy water has also been identified as a potential source of microbial and viral infections,

including COVID-19 (Gajurel and Deresinski 2021). As early as the late 19th century, bacteriologist L. Vincenzi found large numbers of microbes - staphylococci, streptococci, coli bacilli, Klebs-Loeffler bacillus (*Corynebacterium diphtheriae*), and other bacteria - in samples of holy water from a church in Sassari, Italy (Leffmann 1898). In a study from 1998, coliforms, staphylococci, yeasts, and molds were cultured from holy water from County Clare, Ireland (Payne, 2001). An examination of holy water fonts from churches in Seville, Spain, revealed heavy contamination with bacterial pathogens. The number of coliforms in the fonts exceeded 10^3 per 100 ml of water. The presence of potential pathogens was demonstrated by the identification of *Acinetobacter*, *Aeromonas*, *Haemophilus*, *Neisseria*, *Salmonella*, and *Staphylococcus* species. The most common genera in holy water were *Pseudomonas* and *Bacillus*, followed by *Staphylococcus*, *Sphingobacterium*, and *Delftia*. However, species diversity varied greatly from one church to another. According to the authors, the presence of the genera *Staphylococcus*, *Streptococcus*, *Acinetobacter*, *Pseudomonas*, and several others in holy water was associated with hand contamination and human skin transmission (Jurado et al. 2002). Contamination of holy water fonts has also been reported in Vienna, Austria. All holy water samples from churches and hospital chapels had extremely high concentrations of heterotrophic plate counts, up to 10^7 colony-forming units (CFU) ml⁻¹; while fecal indicators such as enterococci and *E. coli*, as well as *Pseudomonas aeruginosa* and *Staphylococcus aureus*, were found only in the most frequently visited churches (Kirschner et al. 2012). A similar study was conducted in the Villingen-Schwenningen area, Germany. Colony

counts revealed an average aerobic microbial load of $5.85 \pm 3.98 \times 10^3$ CFU ml⁻¹. Urban churches had significantly higher bacterial contamination levels than rural churches, likely due to a higher number of visitors. The majority of the bacteria identified were typical human skin commensals, mainly belonging to the genus *Staphylococcus*. Fifty percent of the identified species were classified as potential pathogens: *Staphylococcus* (*S. aureus*, *S. epidermidis*, *S. homini*, *S. pettenkoferi*, *S. pasteurii*), *Bacillus cereus*, *Actinomyces oris*, *Acinetobacter johnsonii*, and *Enterobacter hormaechei* (König et al. 2017).

Water that comes from Christian shrines and churches around the world is often used by hospital patients. Holy water is often administered by sprinkling, but can also be ingested, dripped into the eyes, or used to bathe affected body parts. There have been some reports of hospital patients experiencing serious complications after contact with holy water during hospital treatment. A case of hospital-acquired infection by *Acinetobacter baumannii* in a patient with burns after contact with holy water (sprinkling) has been described (Rees and Allen 1996). Based on the analysis of the holy water used (from Lourdes, Walsingham, and River Jordan), the majority of organisms isolated from the holy water samples were Gram-negative bacilli, including opportunistic pathogens such as *Pseudomonas aeruginosa*, *Escherichia coli*, *Enterobacter* spp., and *Stenotrophomonas maltophilia* (Rees and Allen 1996). A case has also been reported in which an adult male contracted *Pseudomonas aeruginosa* pneumonia while recovering from several injuries. His aunt was observed sprinkling holy water on the patient, and this water was confirmed as a source of the pathogen (Greaves and Porter 1992). Similarly, an 11-year-old boy with recurrent epilepsy requiring mechanical ventilation was found to have recurrent multidrug-resistant *Acinetobacter baumannii* pneumonia. The patient's mother had regularly sprinkled him with holy water over several months. Microbiological examination of this holy water detected the multidrug-resistant *Acinetobacter baumannii* strain previously isolated from the patient (Michel et al. 2013).

Because holy water may pose a risk for infection with pathogenic microorganisms through inoculation by hands, in this study we investigated

the quantity and diversity of the cultivable bacterial community from holy water fountains and reservoirs located in some of the most visited Roman Catholic churches of Ljubljana, Slovenia. The bacterial isolates were identified and their resistance to selected antibiotics was analyzed to assess the potential health risk.

Materials and methods

Sampling and water analyses

The sampling of holy water was carried out in ten churches in different parts of Ljubljana and the city area. In order to preserve anonymity, the names of the churches are not listed, but are labelled here with two-letter codes. Sampling took place three times at three-week intervals (the first sampling on March 11 and 12, 2019, the second on April 1 and 2, 2019, and the third on April 23 and 24, 2019). The third (final) sampling took place after Easter holiday, when churches are the most crowded. Samples were collected in sterile containers in the morning hours, before, during, or after morning Mass from the same fountains at the entrance and from the holy water reservoirs. We also collected a sample from tap water in church DC. Within two hours of collection, samples were inoculated onto culture media and incubated. The remaining water samples were stored at 4 °C until chemical analysis. During the final sampling, the temperature and pH of the holy water in the wells and reservoirs were measured. The water activity of the water samples from the first sampling was measured using the AquaLab 3TE instrument (Meter, Germany) according to manufacturer's instructions. Sodium concentration of selected water samples from the first sampling was measured using a Varian AA240 atomic absorption spectrophotometer.

Bacterial isolation and identification

Within two hours of collection, 10 µl and 100 µl of the collected water samples were inoculated onto blood agar (BA, Fluka) and onto UriSelect

4 agar (URI, Bio-Rad) and incubated aerobically at 37 °C. After three days of incubation, colonies were counted, and all morphologically different colonies were selected and isolated in pure culture on Brain Heart Infusion (BHI) agar plates (Biolife). DNA was extracted from the isolated pure cultures using PrepMan Ultra reagent (Applied Biosystems) according to the manufacturer's instructions. The 16S rRNA gene was amplified using primers 27f- CM (5'- AGAGTTTGATCMTGGCTCAG -3') (Frank et al. 2008) and 1492R (5'- GGTTACCTTGTTACGACTT -3') (Turner et al. 1999). The 16S rDNA gene amplicons were sequenced by Microsynth AG (Switzerland) using Sanger sequencing. The resulting sequences were analyzed using MUSCLE software (Edgar, 2004) implemented in the MEGA7 package (Kumar et al., 2016) and compared against the GenBank database (16S ribosomal RNA (Bacteria and Archaea) database) using BLASTN software (available at: <https://blast.ncbi.nlm.nih.gov/Blast.cgi>). All isolated strains from this study were deposited in the Ex Culture Collection of the Infrastructural Centre Mycosmo (MRIC UL) at the Department of Biology, Biotechnical Faculty, University of Ljubljana, Slovenia.

Antibiotic susceptibility testing

For antimicrobial susceptibility testing, the isolated bacterial strains were cultured on LB agar plates (Biolife) with 8 different commonly used antibiotics (Sigma) and incubated at 37 °C. The results were observed after 3 days. The following antibiotics and concentrations were used: Ampicillin (AMP) 100 mg/l; Chloramphenicol (CHL) 25 mg/l; Cefotaxime (CTX) 2 mg/l; Colistin (COL) 3.5 mg/l; Enrofloxacin (ENR) 0.5 mg/l; Erythromycin (ERY) 15 mg/l; Imipenem (IPM) 4 mg/l; Kanamycin (KAN) 50 mg/l; Tetracycline

(TET) 10 mg/l. Wild-type *Escherichia coli* strains EXBL-4239 A5 and EXBL-4240 A6 isolated from poultry with known resistance profiles were used as positive controls (recovered from Ex Culture Collection of the Infrastructural Centre Mycosmo (MRIC UL), University of Ljubljana).

Community analyses using machine learning

To analyze the obtained data and discover the connections between them, machine learning methods were used. All data analyses were performed using the R statistical programming language and environment and Microsoft Excel 2016. The hierarchical clustering method was used to determine the similarity between samples, using the function "hclust()" from the package stats v3.6.1 (Müllner 2013). The R package randomForest was used to find how well the presence of individual bacterial species predicts the various characteristics of the sample (e.g. material of vessels) using a random forests approach. We calculated 10001 trees for each condition studied and determined from the calculated models the bacterial species whose presence best predicted each characteristic of the sample (Tang et al. 2014).

Results

The holy water is located in the churches in holy water fonts and containers, which can be made of different materials. The fonts in the studied churches were made of stone, porcelain, glass or metal, while the reservoirs in all the studied churches were made of metal - stainless steel (Fig. 1).



Figure 1: Examples of holy water fountains made of different materials in the studied churches (top left metal, top right stone, bottom left glass, and bottom right porcelain).

Slika 1: Primeri kropilnikov za blagoslovljeno vodo iz različnih materialov v proučevanih cerkvah (zgoraj levo kovinski, zgoraj desno kamnit, spodaj levo steklen in spodaj desno porcelanast).

Physico-chemical parameters of holy water samples

The values of selected physicochemical parameters such as temperature, pH, water activity

(a_w), and sodium mass concentration in the holy water were measured (Tab. 1). These parameters were monitored with the aim of determining their influence on the growth of the cultivable aerobic bacterial community in fountains and reservoirs.

Table 1: Results of measurements of temperature, pH, water activity (a_w) and sodium (Na^+) mass concentration in holy water from various churches in Ljubljana and its surroundings.**Tabela 1:** Rezultati merjenja temperature, pH, vodne aktivnosti (a_w) in masne koncentracije natrija (Na^+) v blagoslovljeni vodi, vzorčeni v različnih cerkvah v Ljubljani in okolici.

Church	Sampling site	Material of container	Water T [°C]	Water pH	Water activity a_w	Na^+ [mg/l]
FC	Font	Glass	18	7.30	0.998	11.53
	Reservoir	Metal	21	7.84	0.997	8.56
SC	Font	Porcelain	18	7.76	0.998	-
	Reservoir	Metal	19	7.83	0.998	-
UC	Font	Glass	18	7.49	0.999	-
	Reservoir	Metal	17	7.79	0.999	5.72
VC	Font	Glass	19	7.49	0.998	-
	Reservoir	Metal	18	7.93	0.998	-
TC	Font	Stone	15	7.99	0.979	14958.00
	Reservoir	-	-	-	-	-
RC	Font	Metal	20	7.45	0.998	-
	Reservoir	Metal	17	7.81	0.998	-
BC	Font	Glass	17	7.67	0.998	-
	Reservoir	Metal	-	7.74	0.998	-
SI	Font	Stone	20	7.70	0.997	-
	Reservoir	Metal	18	7.79	0.997	4.72
KC	Font	Stone	18	7.38	0.997	-
	Reservoir	Metal	17	7.80	-	-
DC	Font	Glass	16	7.68	0.995	2044.80
	Reservoir	Metal	16	7.83	0.991	4109.00
Tap water (W)		-	17	7.26	0.999	6.17

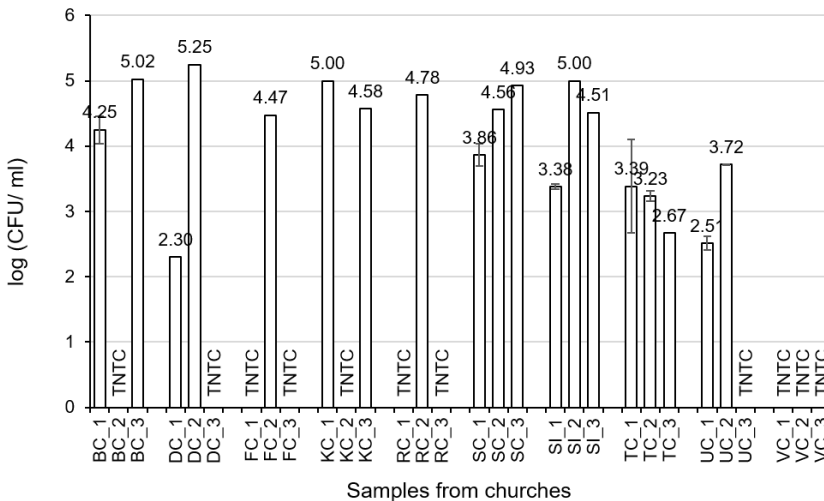
The temperature of the holy water was measured during the last, third sampling on April 23 and 24, 2019, it ranged from 15 °C to 21 °C. The pH of holy water samples from all three samplings was measured, and the average pH ranged from 7.30 to 7.99. In all sampled churches, the average pH of the holy water in the reservoir was slightly higher than in the font. The pH of the tap water (W) was 7.26. The water activity (a_w) of the samples from the first sampling was also determined and ranged from 0.979 to 0.999, with the lowest a_w value in the font of the church TC (0.979) and

in the reservoir (0.991) and font (0.995) of the church DC. We also measured the sodium mass concentration of the selected samples. Holy water from the font of the church TC had the highest measured mass concentration of sodium (14.96 g/l), followed by holy water from the reservoir (4.11 g/l) and from the font (2.04 g/l) of the church DC. Sodium concentration in most samples of holy water from churches was 0.005-0.012 g/l, which is in the range of Na^+ concentration in tap water (Tab. 1).

Load of cultivable aerobic bacteria in holy water samples

The number of cultivable aerobic bacteria in holy water samples was determined by the plate

count method on blood agar after incubation at 37 °C. The colony counts of the samples from fonts (Fig. 2) spanned four orders of magnitude ($10^2 - 10^5$ colony-forming units (CFU) ml^{-1}).



For one third of the samples no value could be determined because of confluent overgrowth (too numerous to count – TNTC). The colony counts of samples from reservoirs spanned three orders of magnitude ($10^1 - 10^3$ CFU ml^{-1} ; Fig. 3). Comparing CFU numbers between samples from the font and the reservoir for a single church, the CFU count in

the font was higher than in the reservoir in almost all cases. In some cases, it was not possible to obtain samples of holy water from reservoirs (BC, KC, RC, and especially TC; Fig. 3). There were also considerable differences in the number of CFUs in each church between samplings.

Figure 2: Aerobic colony counts (CFU ml^{-1}) in holy water samples from fonts in ten churches in different parts of Ljubljana and the city area. Values represent mean counts. TNTC – confluent overgrowth.

Slika 2: Štetje aerobnih kolonijaskih enot (CFU ml^{-1}) v vzorcih blagoslovljene vode iz kropilnikov desetih cerkva v različnih predelih Ljubljane in njeni okolici. Vrednosti predstavljajo povprečja vzorčenj. TNTC – konfluentna rast.

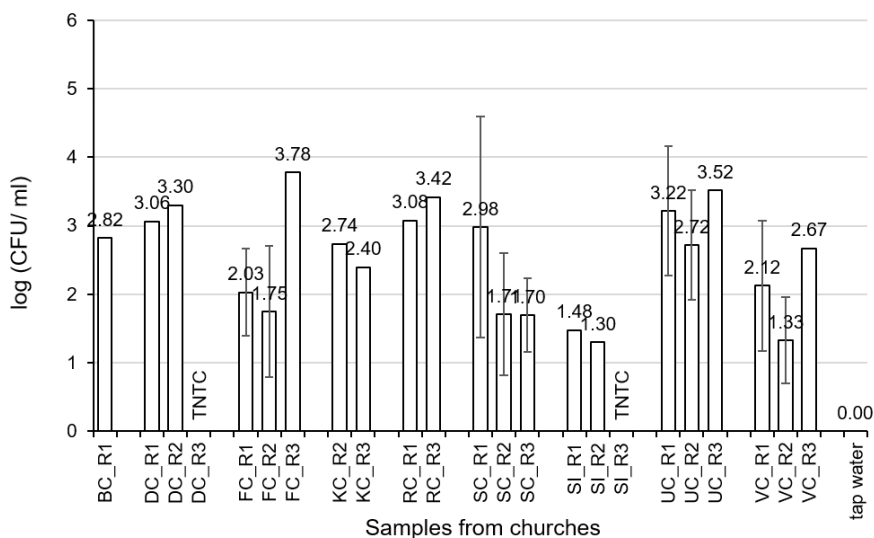


Figure 3: Aerobic colony counts (CFU ml⁻¹) in tap water and holy water samples from reservoirs in nine churches in different parts of Ljubljana and the city area. Values represent mean counts. TNTC – confluent growth.

Slika 3: Štetje aerobnih kolonijjskih enot (CFU ml⁻¹) v pitni vodi in v vzorcih blagoslovljene vode iz rezervoarjev devetih cerkva v različnih predelih Ljubljane in njeni okolici. Vrednosti predstavljajo povprečja vzorčenj. TNTC – konfluentna rast.

Bacterial identification

From 56 samples, one of which was tap water, 585 bacterial strains were isolated and identified. The results of the identification of the bacterial strains are given in the supplementary material (S1). Identification was performed by searching for homologous sequences of the 16S rRNA gene for our isolates in the GenBank database. Most of the identified strains were classified into the classes *Gammaproteobacteria* and *Actinomycetes*. The cultivable aerobic bacterial community differs from church to church, as not all taxa are present in all churches (Fig. 4). In addition, different bacterial

taxa are present in the font and reservoir of each church. The highest number of species (21 and 22) was found in the holy water of the church RC from the font and reservoir (Fig. 4). Otherwise, the studied churches differed in the number of species isolated from the fonts compared to the reservoirs. In the four studied churches, the number of different species was similar in fonts and reservoirs (DC, RC, UC, VC), in FC the species diversity in the holy water from the reservoir was higher (22) than in the font (14), and in four churches (BC, KC, SC and SI) the number of species in the water samples from the fonts was higher.

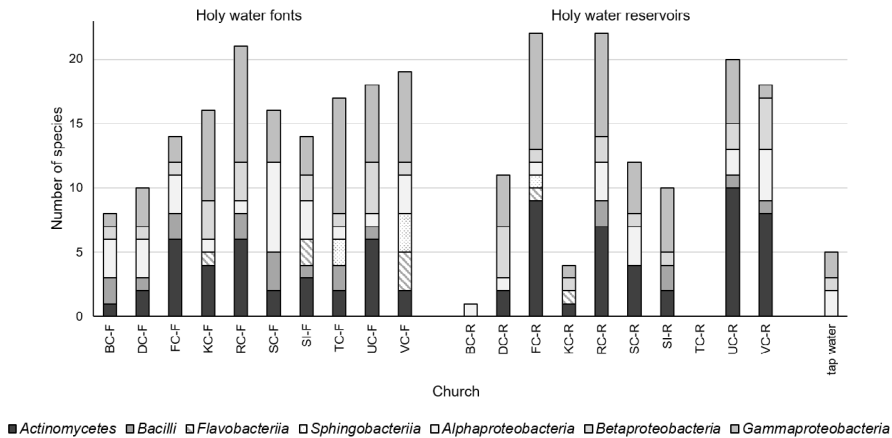


Figure 4: The number of identified species of cultivable aerobic bacteria isolated from the holy water fonts and reservoirs of the studied churches, grouped by classes.

Slika 4: Prikaz števila identificiranih vrst kultivabilnih aerobnih bakterij, izoliranih iz blagoslovljene vode kropilnikov in rezervarjev vzorčenih cerkva, združenih v razrede.

Bacterial isolates were assigned to 52 genera. Genera whose species appeared in at least two samples were compared for their occurrence in holy water fonts and reservoirs (Fig. 5). Some genera occurred only in fonts (*Delftia*, *Kocuria*,

Spingobacterium, *Staphylococcus*), and only species of two genera (*Acinetobacter*; *Pseudomonas*) were found in all three sample groups. These two genera were also the most represented.

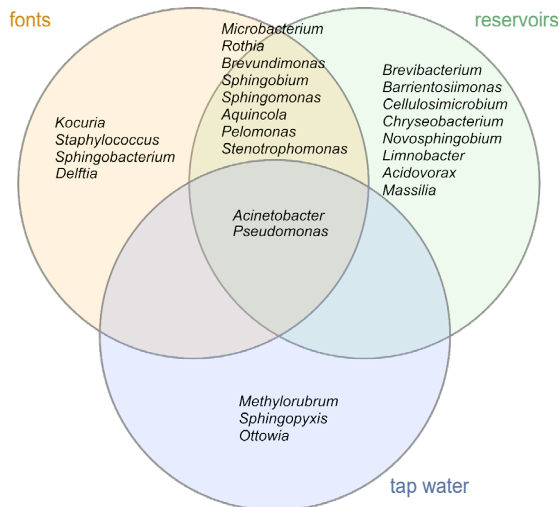


Figure 5: Venn diagram (Heberle et al. 2015) of the occurrence of the identified bacterial genera in samples of holy water from fonts and reservoirs and from tap water.

Slika 5: Vennov diagram (Heberle s sod. 2015) prisotnosti identificiranih bakterijskih rodov v vzorcih blagoslovljene vode kropilnikov in rezervarjev ter pitne vode.

Bacterial community analysis using machine learning

Machine learning methods were used to analyze the data obtained (bacterial species at different sampling sites) and to investigate the presence of bacterial species as a function of sampling site. We were interested in whether the presence of any of the species could be associated with the type of sample (font, reservoir). Certain bacterial species (*Acinetobacter beijerinckii*,

Acinetobacter haemolyticus, *Brevundimonas aurantiaca*, *Brevundimonas mediterranea*, *Staphylococcus warneri*) were present only in holy water fonts (Fig. 6). Similarly, some species were more abundant in fonts than in reservoirs (*Acinetobacter johnsonii*, *Aquincola tertiaricarbonis*, *Rothia amarae*, *Sphingobium hydrophobicum*). The opposite phenomenon was observed for *Microbacterium maritropicum*, which was more abundant in holy water reservoirs (in seven of nine sampled reservoirs) than in fonts (in three of ten sampled fonts).

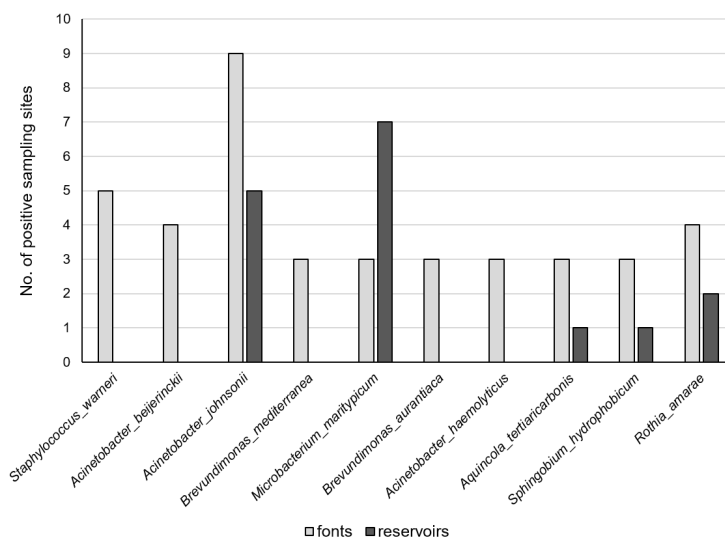


Figure 6: Occurrence of selected bacterial species depending on the container with holy water.
Slika 6: Pojavnost izbranih bakterijskih vrst v odvisnosti od posode z blagoslovljeno vodo.

The hierarchical clustering method was used to investigate the similarity between sampling sites (fonts and reservoirs) based on the matrix of the presence of different bacterial species. The more similar the bacterial communities of the sampling

sites, the closer they are in the clustering tree (Fig. 7). Some reservoirs (churches DC, KC and BC) cluster together with tap water. In most cases, there is no grouping by church (font and reservoir of each church).

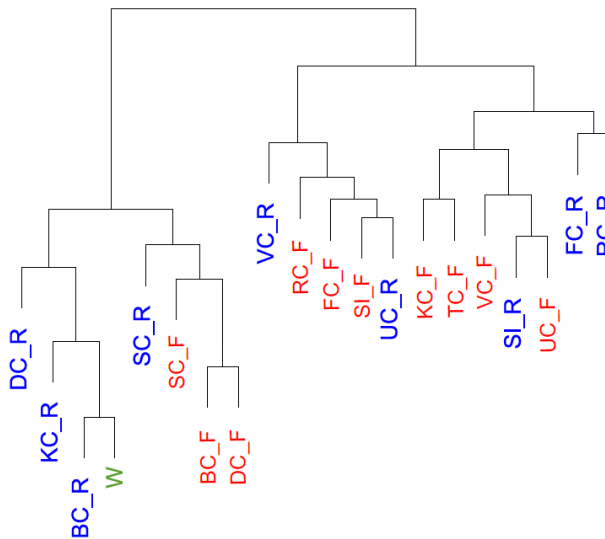


Figure 7: Display of hierarchical clustering of sample sites into groups based on the bacterial species occurrence matrix. Color marks: blue - reservoirs, red - fountains, green - tap water (W).

Slika 7: Prikaz hierarhičnega združevanja vzorčnih mest v skupine na osnovi matrice pojavljanja bakterijskih vrst. Barvne oznake: modra - rezervarji, rdeča – kropilniki, zelena - vodovodna voda (W).

A connection between the container material and the occurrence of bacterial species was also tested (not shown). *Acinetobacter beijerinckii*, *Brevundimonas mediterranea*, *Brevundimonas aurantiaca*, *Kocuria uropygioeca*, and *Sphingobacterium multivorum* were isolated only from nonmetallic fonts. However, no association was found between a single bacterial species and a metal vessel, nor with other materials (glass, stone, porcelain).

Resistance of bacterial isolates to selected antibiotics

The effects of nine antibiotics on 83 selected bacterial strains isolated from the holy water fonts and reservoirs was investigated, namely ampicillin (AMP, 100 mg/l), tetracycline (TET, 12.5 mg/l), imipenem (IPM, 4 mg/l), erythromycin (ERY, 15 mg/l), chloramphenicol (CHL, 25 mg/l), kanamycin (KAN, 50 mg/l), cefotaxime (CTX, 2 mg/l), enrofloxacin (ENR, 0.5 mg/l) and colistin (COL, 3.5 mg/l). Results are shown in the supplemental material (S2). Most strains were sensitive to tetracycline (12.5 mg/l) and chloramphenicol (25 mg/l) (Fig. 8), and more than half of the strains were resistant to colistin (3.5 mg/l) and cefotaxime (2 mg/l).

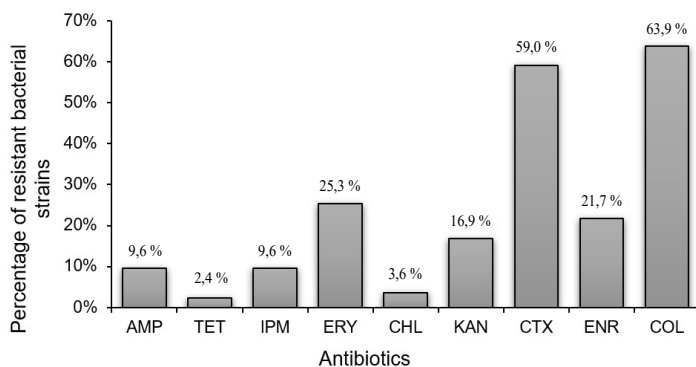


Figure 8: Summary of results for antimicrobial susceptibility for the 83 isolates tested, presented are percentages of isolates that are resistant. Ampicillin (AMP) 100 mg/l; chloramphenicol (CHL) 25 mg/l; cefotaxime (CTX) 2 mg/l; colistin (COL) 3.5 mg/l; enrofloxacin (ENR) 0.5 mg/l; erythromycin (ERY) 15 mg/l; imipenem (IPM) 4 mg/l; kanamycin (KAN) 50 mg/l; tetracycline (TET) 10 mg/l.

Slika 8: Povzetek rezultatov občutljivosti proti antibiotikom za 83 testiranih izolatov, predstavljen je odstotek izolatov, ki so odporni. Ampicilin (AMP) 100 mg/l; kloramfenikol (CHL) 25 mg/l; cefotaksim (CTX) 2 mg/l; kolistin (COL) 3.5 mg/l; enrofloksacin (ENR) 0.5 mg/l; eritromicin (ERY) 15 mg/l; imipenem (IPM) 4 mg/l; kanamicin (KAN) 50 mg/l; tetraciklin (TET) 10 mg/l.

Resistance profiles for individual species of the same genus are similar. Among bacterial species potentially pathogenic to humans and vertebrates, *Pseudomonas aeruginosa* (resistant to 7 antibiotics tested at selected concentrations) and *Stenotrophomonas maltophilia* (resistant to 4 antibiotics tested) were the most resistant to studied antibiotics.

Discussion

In Slovenia, 57.8% of the population declared themselves Roman Catholic, according to the last census in 2002 (Črnič et al. 2013). As in other Christian religions, for Catholics, holy water is water that has been blessed by a priest and is used for baptism and to bless people, churches, homes, and objects of devotion (Jurado et al. 2002, Kirschner et al. 2012). Some studies have presented holy water as a potential source of infection with pathogenic organisms (Rees and Allen 1996, Greaves and Porter 1992, Michel et al. 2013, Gajurel and Deresinski 2021). Due to COVID-19 concern, many churches emptied their holy water fonts and, in some churches, a non-contact holy water dispenser was installed (Pullella 2020; Drogo 2022). In this study, we investigated the

microbiological quality of holy water in the fonts and reservoirs of ten selected Roman Catholic churches in Ljubljana and its surroundings, focusing on bacteria. In order to assess the potential health risk of the bacterial strains isolated from the holy water, they were identified and their resistance to selected antibiotics was analyzed.

The aerobic bacterial load of the holy water was determined by the plate count method. In most of the churches studied, the number of CFU ml⁻¹ was higher in the holy water from fonts (10² - 10⁵ CFU ml⁻¹; Fig. 2) than in the reservoirs (10¹ - 10³ CFU ml⁻¹; Fig. 3), which is to be expected since the church visitors have direct daily contact with the holy water from the fonts. The bacterial load varied among the different churches and also among the sampling of a single church. This relatively moderate bacterial contamination of holy water from fonts is consistent with previous studies from churches in Vienna, Austria (Kirschner et al. 2012) and in the Villingen-Schwenningen area, Germany (König et al. 2017), where similar cultivation conditions (rich medium, incubation at 37 °C) were used. In Vienna, all holy water samples from the investigated churches and hospital chapels had high concentrations of heterotrophic microbial counts at 37 °C, up to 3 × 10⁷ CFU ml⁻¹, higher than in our study, while in Villingen-Schwenningen

(Germany) the colony count showed an average aerobic microbial load of $5.85 \pm 3.98 \times 10^3$ CFU ml⁻¹. In a study of holy water fonts from churches in Seville, Spain, total aerobic bacteria and coliforms in certain churches were ‘too numerous to count’ (Jurado et al. 2002). Bacterial load is certainly influenced by the number of visitors and the frequency of cleaning and replacement of water from fonts (König et al. 2017, Jurado et al. 2002). This type of data would help us understand the differences between the bacterial load of the sampled churches in Ljubljana, but these data were not available. Nevertheless, our results confirm that the frequent immersion of fingers in holy water fonts is probably the main reason for the higher bacterial load in the fonts compared to the reservoirs. In this way, microbes – and also nutrients for their growth – are transferred from the skin to the holy water (Kirschner et al. 2012).

The Roman Catholic Church recommends adding blessed salt (NaCl) to the water during the blessing (Kirschner et al. 2012). Salt was found only in holy water samples from two churches and its concentration was low, ranging from 0.2 to 1.5% NaCl (m/v) (Tab.1). In most churches, the sodium concentration was of the same order of magnitude as the concentration in tap water. In a study from Spain, the viability of selected bacterial species was measured as a function of different NaCl concentrations. At NaCl concentrations of 20% or more, both pathogenic and nonpathogenic bacteria lysed (Jurado et al. 2002). This process, called plasmolysis, occurs due to water efflux leading to a decrease in cytoplasmic volume. This can lead to retraction of cell walls, detachment and wrinkling of the plasmalemma, and disruption of protein assemblies that extend across the cell wall (Wood 2011). In a study by Hrenovic and Ivankovic (2009) testing the survival of *E. coli* and *Acinetobacter junii* at different NaCl concentrations, complete death of *E. coli* was achieved after 72 hours at concentrations of 20% NaCl. Thus, to prevent contamination of the holy water, larger amounts of NaCl would have to be added than was detected in our samples because only then would the growth of most microorganisms be completely inhibited. However, high NaCl concentrations can damage the fonts, so the use of NaCl should be carefully balanced with protection of cultural

heritage (Jurado et al. 2002). An alternative is to change the holy water daily and to clean the holy water fonts regularly.

From 56 samples of holy water, 585 bacterial isolates were obtained and identified based on the homologous sequences of the 16S rRNA gene in the GenBank database. The aerobic cultivable community of the holy water consisted mainly of bacterial species from the classes *Gammaproteobacteria* and *Actinomycetes* (Fig. 4). The bacterial community differed between churches as well as between the font and the reservoir of each church. Some genera were present only in the holy water from fonts (*Delftia*, *Kocuria*, *Sphingobacterium*, *Staphylococcus*), and only species of two genera (*Acinetobacter*, *Pseudomonas*) were found in the holy water from fonts, reservoirs, and tap water (Fig. 5). It is likely that some of the identified bacteria in holy water fonts originated from the skin of church visitors. In the microbiota of human hands studied by amplicon sequencing, species from the phyla *Pseudomonadota*, *Actinomycetota*, and *Bacillota* were found, accounting for 94% of all identified bacterial species, with the most abundant genera *Cutibacterium* (31.6% of all sequences; *Actinomycetota*), *Streptococcus* (17.2%; *Bacillota*), *Staphylococcus* (8.3%; *Bacillota*), *Corynebacterium* (4.3%; *Actinomycetota*), and *Lactobacillus* (3.1%; *Bacillota*) (Egert and Simmering 2016, Byrd et al. 2018, Carmona-Cruz et al. 2022). In agreement with previous studies (Rees and Allen 1996, Jurado et al. 2002, Kirschner et al. 2012, König et al. 2017), we also detected bacteria of probable fecal origin, i.e., enterococci and enterobacteria, albeit in very low abundance. The representative of fecal indicator bacteria, *Enterococcus* sp., was found in only one sample of holy water from the reservoir, while *Citrobacter freundii* and *Enterobacter cloacae* were detected in two samples from fonts.

Using machine learning methods, we aimed to investigate the occurrence of bacterial species as a function of sampling location (font or reservoir). Some bacterial species occurred only in holy water from fonts (*Acinetobacter beijerinckii*, *Acinetobacter haemolyticus*, *Brevundimonas aurantiaca*, *Brevundimonas mediterranea*, *Staphylococcus warneri*), while others, such as *Microbacterium maritopicum*, were more abundant

in holy water reservoirs (Fig. 6). These bacteria have relatively low pathogenic potential, and some of them are considered to be skin commensals. The genus *Acinetobacter* (*Pseudomonadota*) is generally found in aqueous environments, with the majority of species being non-pathogenic. The most common species causing infections is *A. baumannii*, followed by species also found on human skin, such as *A. calcoaceticus* and *A. lwoffii*, which has also been isolated from our holy water samples. These are largely opportunistic pathogens that cause infections, especially in immunocompromised patients. Other species, including *A. haemolyticus*, *A. johnsonii*, *A. junii*, *A. nosocomialis*, *A. pittii*, *A. schindleri*, and *A. ursingii*, have occasionally been reported as pathogens (Wong et al. 2017). *Brevundimonas* spp. (*Pseudomonadota*) are a genus of non-fermenting Gram-negative bacteria and, particularly *Brevundimonas diminuta* and *Brevundimonas vesicularis*, are considered to be of minor clinical importance (Ryan and Pembroke 2018). *Microbacterium* species (*Actinomycetota*), non-spore-forming, Gram-positive rods, have also rarely been associated with human disease. However, increasing amount of literature shows that *Microbacterium* species are opportunistic human pathogens, causing, for example, infective endocarditis associated with *Microbacterium maritypicum* bacteremia (Yeung et al. 2020). But *Staphylococcus warneri*, a coagulase-negative staphylococcus (CNS) commonly found in the microbiota of human and animal epithelia and mucosa, is considered an opportunistic pathogen that causes serious infections in humans and animals (Liu et al. 2020).

The hierarchical clustering was used to determine the similarity between sampling sites (fonts and reservoirs) based on the matrix of occurrence of different bacterial species. Some of the reservoirs were clustered together with the tap water, indicating that an important part of bacterial community in these reservoirs originated from the tap water (Fig. 7). However, this is not true for all sampled churches. Perhaps unexpectedly, we also did not observe clustering of samples from the reservoirs and fonts from the same church. Since the fonts in the sampled churches were made of stone, porcelain, glass, and metal, we tested whether there was a relationship between the font material

and the presence of bacterial species. Although certain bacterial species were isolated only from non-metallic fonts, unfortunately no correlation was found between the material of the vessel (metal, stone, glass, porcelain) and the presence of certain bacterial species. The choice of the material of the vessel containing the holy water affects the growth of microorganisms through the smoothness of its surface. Rougher surfaces provide a better substrate for microbial attachment and biofilm formation. Microorganisms adhere more quickly to hydrophobic and nonpolar materials (plastic) than to hydrophilic materials (glass or metal) (Donlan 2002). To reduce contamination of the holy water, it would be better to use fonts made of glass or metal than fonts made of stone, for example.

Testing of the selected bacterial isolates for antibiotic resistance to nine antibiotics showed that the majority of the strains tested were sensitive to tetracycline (12.5 mg/l) and chloramphenicol (25 mg/l) and resistant to cefotaxime (2 mg/l) and colistin (3.5 mg/l) (Fig. 8). The use of colistin has increased recently mainly because of the emergence of multidrug-resistant Gram-negative bacteria. It is used as a last resort antibiotic against most *Enterobacterales* species and non-fermenting Gram-negative bacteria such as *Acinetobacter baumannii* and *Pseudomonas aeruginosa*. Conversely, colistin is not active against Gram-positive bacteria, Gram-negative cocci, and anaerobic bacteria (Torres et al. 2021). However, such a high level of resistance (63,9% of bacterial isolates) could be alarming. The European Committee on Antimicrobial Susceptibility Testing (EUCAST) minimal inhibitory concentration (MIC) breakpoints for colistin (EUCAST 2022) for interpretation are for *Acinetobacter* spp. and *Enterobacterales* ≤ 2 mg l⁻¹ susceptible (S), > 2 mg l⁻¹ resistant (R), while for *Pseudomonas* spp. ≤ 4 mg l⁻¹ susceptible, > 4 mg l⁻¹ resistant. However, the Clinical and Laboratory Standards Institute (CLSI) recommends higher susceptibility breakpoints for *P. aeruginosa* (S ≤ 2 mg l⁻¹, R ≥ 8 mg l⁻¹) and for *Enterobacterales* and *Acinetobacter* spp. (S ≤ 2 mg l⁻¹, R ≥ 4 mg l⁻¹) (CLSI 2020). According to CLSI recommendations, the colistin concentration in the culture medium was too low to correctly assess susceptibility to colistin. The same may be

true for cefotaxime, where the EUCAST recommendations are for *Enterobacterales* and other non-species related ($S \leq 1 \text{ mg l}^{-1}$, $R \geq 2 \text{ mg l}^{-1}$) (EUCAST 2022), whereas the CLSI breakpoint recommendations are for aerobic bacteria ($S \leq 1 \text{ mg l}^{-1}$, $R \geq 4 \text{ mg l}^{-1}$) (Humphries et al. 2019). The observed high resistance in *Pseudomonas aeruginosa* and *Stenotrophomonas maltophilia* strains, both of which are most commonly associated with respiratory infections in humans, is somewhat expected and consistent with the literature, as these multidrug-resistant species are intrinsically resistant to a variety of antibiotics (Brooke 2012, Luczkiewicz et al. 2015).

According to our results, the risk of bacterial infection from holy water is modest, especially if only applied to unbroken skin. Many of the isolated bacteria from holy water may actually have been introduced by churchgoers. This is especially true for those bacteria that are considered part of skin microbiota and are not normally associated with aqueous environments. However, the unpredictability of contamination source of holy water means that the water may sporadically contain more problematic species than the ones identified in this study, or strains of the species found here, but with higher resistance to antibiotics. Therefore, sprinkling or other actions that can lead to inhalation or ingestion of the holy water or its introduction into eyes is not recommended, particularly for immunocompromised individuals, the elderly, neonates, and patients with severe burns, trauma, postoperative wounds, or intravenous access.

Conclusions

Holy water may pose a risk of infection with pathogenic microorganisms. Adding salt (NaCl) to holy water is an accepted practice in Catholic churches, but the concentrations required to limit most microbial growth (20% w/v or more) are often incompatible with the protection of fonts as part of the cultural heritage. Since the complete removal of water from fonts would likely be poorly accepted for religious reasons, the recommended practice to limit the transmission of potentially pathogenic microorganisms is regular and rigorous cleaning of the fonts, use of vessels with easy-to-clean

surfaces and regular replacement, e.g., after several days during non-holiday period, and daily after attending Mass in churches during church holidays. The public, especially individuals with increased susceptibility for infection, can protect themselves by avoiding the contact of the holy water with eyes, nose, mouth, ears and broken skin, and by practising good hand hygiene.

Povzetek

V Sloveniji se je po zadnjem popisu prebivalstva iz leta 2002 za katoličane opredelilo 57,8 % prebivalcev (Črnič in sod. 2013). Tako kot v drugih krščanskih religijah je za katoličane blagoslovljena voda tista, ki jo je blagoslovil duhovnik in se uporablja pri svetem krstu ter za blagoslov ljudi, živali, cerkva, domov in predmetov (Jurado in sod. 2002, Kirschner in sod. 2012). Nekatere študije so blagoslovljeno vodo prepoznale kot potencialni vir okužbe s patogenimi organizmi (Rees in Allen 1996, Greaves in Porter 1992, Michel in sod. 2013, Gajurel in Deresinski 2021). Zaradi zaskrbljenosti zaradi COVID-19 so številne cerkve izpraznile kropilnike za blagoslovljeno vodo, v nekaterih cerkvah so celo namestili brezkontaktno razdelilnike blagoslovljene vode (Pullella 2020, Drogo 2022). V tej raziskavi smo preučevali mikrobiološko kakovost blagoslovljene vode, s poudarkom na bakterijah, v kropilnikih in rezervarjih desetih izbranih rimskokatoliških cerkva v Ljubljani in njeni okolici. Da bi ocenili potencialno tveganje za zdravje, smo bakterijske seve, izolirane iz blagoslovljene vode, identificirali in preučili njihovo odpornost proti izbranim antibiotikom.

Obremenitev blagoslovljene vode z aerobnimi bakterijami smo določili z metodo štetja na ploščah. V večini proučevanih cerkva je bilo število kolonijskih enot (CFU) na ml vzorca večje v blagoslovljeni vodi iz kropilnikov ($10^2 - 10^5 \text{ CFU ml}^{-1}$; sl. 2) kot v rezervoarjih ($10^1 - 10^3 \text{ CFU ml}^{-1}$; sl. 3), kar je pričakovano, saj imajo obiskovalci cerkve neposreden vsakodnevni stik s blagoslovljeno vodo iz kropilnikov. Obremenitev z bakterijami se je razlikovala med različnimi cerkvami in tudi med različnimi vzorčnji ene same cerkve. Ugotovljena relativno zmerna bakterijska kontaminacija blagoslovljene vode iz kropilnikov je

skladna s prejšnjimi študijami iz cerkva na Dunaju v Avstriji (Kirschner in sod. 2012) in na območju Villingen-Schwenningen v Nemčiji (König in sod. 2017), kjer so uporabili podobne pogoje gojenja (bogato gojišče, inkubacija pri 37 °C). Na Dunaju so imeli vsi vzorci blagoslovljene vode iz preiskovanih cerkva in bolnišničnih kapelic visoko število heterotrofnih mikrobov pri 37 °C, do 3×10^7 CFU ml⁻¹, več kot v naši študiji, medtem ko je bila na območju Villingen-Schwenningena (Nemčija) povprečna mikrobna obremenitev blagoslovljene vode z aerobi $5,85 \pm 3,98 \times 10^3$ CFU ml⁻¹. V študiji blagoslovljene vode iz kropilnikov cerkva v Sevilli v Španiji je bilo število aerobnih ter koliformnih bakterij v nekaterih cerkvah previsoko, da bi jih lahko prešteli (»too numerous too count«, TNTC) (Jurado in sod. 2002). Na obremenitev z bakterijami zagotovo vpliva število obiskovalcev ter pogostost čiščenja in menjave vode v kropilnikih (König in sod. 2017, Jurado in sod. 2002). Tovrstni podatki bi nam pomagali razumeti razlike med bakterijsko obremenitvijo blagoslovljene vode iz kropilnikov preučevanih cerkva v Ljubljani, vendar ti podatki niso bili na voljo. Kljub temu naši rezultati potrjujejo, da je pogosto pomakanje prstov vernikov v vodo kropilnika ob vstopu in izstopu iz cerkve verjetno glavni razlog za večjo bakterijsko obremenitev v kropilnikih v primerjavi z rezervoarji. Na ta način se mikrobi – in tudi hranila za njihovo rast – prenesejo s kože v blagoslovljeno vodo (Kirschner in sod. 2012).

Rimskokatoliška cerkev priporoča dodajanje blagoslovljene soli (NaCl) vodi ob blagoslovu (Kirschner in sod. 2012). Sol smo določili le v vzorcih blagoslovljene vode iz dveh cerkva, njena koncentracija pa je bila nizka in se je gibala od 0,2 do 1,5 % NaCl (m/v) (Tab.1). V večini cerkva je bila koncentracija natrija enakega reda velikosti kot v vodovodni vodi. V študiji iz Španije so merili sposobnost preživetja izbranih bakterijskih vrst kot funkcijo različnih koncentracij NaCl. Pri koncentraciji NaCl 20 % ali več naj bi tako patogene kot nepatogene bakterije lizirale (Jurado in sod. 2002). Do tega procesa, imenovanega plazmoliza, pride zaradi izhajanja vode, ki povzroči zmanjšanje volumna citoplazme. To lahko privede do umika celične stene, ocepitve in gubanja plazmaleme ter prekinitve proteinskih kompleksov, ki segajo čez celično steno (Wood 2011). V študiji Hrenovic

in Ivankovic (2009), kjer so testirali preživetje *E. coli* in *Acinetobacter junii* pri različnih koncentracijah NaCl, je bilo popolno uničenje *E. coli* pri koncentraciji 20 % NaCl doseženo po 72 urah. Da bi preprečili kontaminacijo blagoslovljene vode, bi tako morali dodati večje količine NaCl, kot smo jih zaznali v naših vzorcih, saj bi le tako popolnoma zavrla rast večine mikroorganizmov. Visoke koncentracije NaCl pa lahko poškodujejo kropilnike, zato moramo uporabo NaCl skrbno uravnovežiti z varovanjem kulturne dediščine (Jurado in sod. 2002). Druga alternativa je, da blagoslovljeno vodo dnevno menjamo in redno čistimo kropilnike.

Iz 56 vzorcev blagoslovljene vode smo osamili 585 bakterijskih izolatov, ter jih identificirali na podlagi homolognih zaporedij gena za 16S rRNA v podatkovni zbirki GenBank. Združbo aerobnih gojljivih bakterij iz blagoslovljene vode so sestavljale predvsem bakterijske vrste iz razredov *Gammaproteobacteria* in *Actinomycetes* (slika 4). Sestava bakterijske združbe se je razlikovala med cerkvami, pa tudi med kropilnikom in rezervoarjem posamezne cerkve. Nekateri rodovi so bili prisotni samo v blagoslovljeni vodi iz kropilnikov (*Delftia*, *Kocuria*, *Sphingobacterium*, *Staphylococcus*), v blagoslovljeni vodi iz kropilnikov, rezervoarjev in vodovodne vode pa smo identificirali vrste le dveh rodov (*Acinetobacter*, *Pseudomonas*) (sl. 5). Verjetno so nekatere od identificiranih bakterij iz kropilnikov izvirale s kože obiskovalcev cerkve. V mikrobioti kože človeških rok, ki so jo preučevali s sekvenciranjem pomnožkov, so bile najdene vrste iz bakterijskih debel *Pseudomonadota*, *Actinomycetota* in *Bacillota*, ki so predstavljale 94 % vseh identificiranih bakterijskih vrst, z najbolj razširjenimi rodovi *Cutibacterium* (31,6 % vseh zaporedij; *Actinomycetota*), *Streptococcus* (17,2 %; *Bacillota*), *Staphylococcus* (8,3 %; *Bacillota*), *Corynebacterium* (4,3 %; *Actinomycetota*) in *Lactobacillus* (3,1 %; *Bacillota*) (Egert in Simmering 2016, Byrd in sod. 2018, Carmona-Cruz in sod. 2022). V skladu s predhodnimi študijami (Rees in Allen 1996, Jurado in sod. 2002, Kirschner in sod. 2012, König in sod. 2017) smo odkrili tudi bakterije fekalnega izvora, to so enterokoki in enterobakterije, čeprav v zelo nizkem številu. Tako je bil predstavnik fekalnih indikatorskih bakterij *Enterococcus* sp. najden le

v enem vzorcu blagoslovljene vode iz rezervoarja, *Citrobacter freundii* in *Enterobacter cloacae* pa v dveh vzorcih vode iz kropilnikov.

Z uporabo metod strojnega učenja smo želeli raziskati pojavljanje bakterijskih vrst kot funkcije lokacije vzorčenja (kropilnik ali rezervoar). Nekaterе bakterijske vrste so se pojavljale le v blagoslovljeni vodi iz kropilnikov (*Acinetobacter beijerinckii*, *Acinetobacter haemolyticus*, *Brevundimonas aurantiaca*, *Brevundimonas mediterranea*, *Staphylococcus warneri*), medtem ko so bile druge, kot je *Microbacterium maritypicum*, bolj pogoste v rezervoarjih blagoslovljene vode (sl. 6). Večina teh bakterij ima razmeroma nizek patogeni potencial in nekatere od njih veljajo za kožne komensale. Rod *Acinetobacter* (*Pseudomonadota*) se običajno nahaja v vodnem okolju, pri čemer je večina vrst nepatogenih. Najpogostejša vrsta, ki povzroča okužbe, je *A. baumannii*, sledijo pa ji vrste, ki jih najdemo tudi na človeški koži, kot sta *A. calcoaceticus* in *A. hwoffii*, ki je bil prav tako izoliran iz naših vzorcev blagoslovljene vode. To so večinoma oportunistični patogeni, ki povzročajo okužbe, zlasti pri bolnikih z oslabljenim imunskim sistemom. Druge vrste, vključno z *A. haemolyticus*, *A. johnsonii*, *A. junii*, *A. nosocomialis*, *A. pittii*, *A. schindleri* in *A. ursingii*, naj bi le redko povzročale okužbe (Wong in sod. 2017). *Brevundimonas* spp. (*Pseudomonadota*) so rod nefermentirajočih gramnegativnih bakterij in so, zlasti *Brevundimonas diminuta* in *Brevundimonas vesicularis*, le malo klinično pomembne (Ryan in Pembroke 2018). Vrste rodu *Microbacterium* (*Actinomycetota*), ki so grampozitivne paličice in ne tvorijo spor, so prav tako redko povezovali z okužbami pri ljudeh. Vse več raziskav pa kaže, da so vrste rodu *Microbacterium* oportunistični človeški patogeni, ki lahko na primer povzročijo infektivni endokarditis, povezan z bakteriemijo, povzročeno z *Microbacterium maritypicum* (Yeung in sod. 2020). Po drugi strani pa *Staphylococcus warneri*, koagulazno negativni stafilokok (CNS), ki ga pogosto najdemo v mikrobioti človeških in živalskih epitelijev in sluznic, velja za oportunističnega patogena, ki povzroča resne okužbe pri ljudeh in živalih (Liu in sod. 2020).

Hierarhično združevanje smo uporabili za ugotavljanje podobnosti med mesti vzorčenja (kropilniki in rezervoarji) na podlagi matrike

pojavljanja različnih bakterijskih vrst. Nekateri rezervoarji so se združevali skupaj z vodovodno vodo, kar kaže, da pomemben del bakterijske združbe v teh rezervoarjih izvira iz vodovodne vode (sl. 7). Vendar to ne velja za vse vzorčne cerkve. Morda nepričakovano tudi nismo opazili združevanja vzorcev iz rezervoarjev in kropilnikov posamezne cerkve. Ker so bili kropilniki v preučevanih cerkvah izdelani iz kamna, porcelana, stekla in kovine, smo ugotavljali, ali obstaja povezava med materialom kropilnika in prisotnostjo posameznih bakterijskih vrst. Čeprav so bile določene bakterijske vrste izolirane samo iz nekovinskih kropilnikov, žal nismo ugotovili povezave med materialom posode (kovina, kamen, steklo, porcelan) in prisotnostjo določenih bakterijskih vrst. Material posode z blagoslovljeno vodo vpliva na rast mikroorganizmov z gladkostjo površine. Bolj grobe površine zagotavljajo boljšo podlago za pritrnitev mikrobov in tvorbo biofilma. Mikroorganizmi se hitreje prilepijo na hidrofobne in nepolarne materiale (plastika) kot na hidrofilne materiale (steklo ali kovina) (Donlan 2002). Da bi zmanjšali onesnaženje blagoslovljene vode, bi bilo bolje uporabiti kropilnike na primer iz stekla ali kovine kot iz kamna.

Protimikrobno testiranje izbranih bakterijskih izolatov proti devetim antibiotikom je pokazalo, da je večina testiranih sevov občutljivih proti tetraciklinu (12,5 mg/l) in kloramfenikolu (25 mg/l) ter odpornih proti cefotaksimu (2 mg/l) in kolistinu (3,5 mg/l) (sl. 8). Uporaba kolistina se je v zadnjem času povečala predvsem zaradi pojava gramnegativnih bakterij, odpornih proti več antibiotikom. Uporablja se kot antibiotik zadnje obrambne linije proti večini vrst reda *Enterobacterales* in nefermentirajočih gramnegativnih bakterij, kot sta *Acinetobacter baumannii* in *Pseudomonas aeruginosa*. Nasprotno pa kolistin ne deluje proti grampozitivnim bakterijam, gramnegativnim kokom in anaerobnim bakterijam (Torres in sod. 2021). Zato bi lahko bila tako visoka stopnja odpornosti (63,9 % bakterijskih izolatov) zaskrbljujoča. Smernice mejnih vrednosti minimalne inhibitorne koncentracije (MIC) za kolistin (EUCAST 2022) po EUCAST (European Committee on Antimicrobial Susceptibility Testing) so za *Acinetobacter* spp. in *Enterobacterales* ≤ 2 mg l⁻¹ občutljiv (S), > 2 mg l⁻¹ odporen (R),

medtem ko za *Pseudomonas* spp. velja ≤ 4 mg l⁻¹ občutljiv, > 4 mg l⁻¹ odporen. Vendar Inštitut za klinične in laboratorijske standarde (CLSI) priporoča višje mejne vrednosti občutljivosti za *P. aeruginosa* ($S \leq 2$ mg l⁻¹, $R \geq 8$ mg l⁻¹) ter za *Enterobacterales* in *Acinetobacter* spp. ($S \leq 2$ mg l⁻¹, $R \geq 4$ mg l⁻¹) (CLSI 2020). Glede na smernice CLSI je bila koncentracija kolistina v gojišču prenizka za pravilno oceno občutljivosti proti kolistinu. Enako bi lahko veljalo za cefotaksim, kjer so smernice EUCAST za *Enterobacterales* in druge nesorodne vrste ($S \leq 1$ mg l⁻¹, $R \geq 2$ mg l⁻¹) (EUCAST 2022), medtem ko so smernice CLSI za mejne vrednosti za aerobne bakterije ($S \leq 1$ mg l⁻¹, $R \geq 4$ mg l⁻¹) (Humphries in sod. 2019). Opažena visoka odpornost sevov vrst *Pseudomonas aeruginosa* in *Stenotrophomonas maltophilia*, ki sta najpogosteje povezani z okužbami dihal pri ljudeh, je pričakovana in skladna z objavami, saj sta ti vrsti intrinzično odporni proti več antibiotikom (Brooke 2012, Luczkiewicz in sod. 2015).

Glede na naše rezultate je tveganje za bakterijsko okužbo z blagoslovljeno vodo majhno, še posebej, če se jo nanaša samo na nepoškodovano kožo. Precej izoliranih bakterij iz blagoslovljene vode so najbrž vanjo vnesli obiskovalci cerkve. To še posebej velja za tiste bakterije, ki so prepoznane kot del mikrobiote kože in običajno niso povezane z vodnim okoljem. Vendar pa nepredvidljivost vira kontaminacije blagoslovljene vode pomeni, da lahko voda občasno vsebuje več problematičnih vrst od tistih, opredeljenih v tej študiji, ali sevov vrst, ki jih najdemo tukaj, vendar z večjo odpornostjo proti antibiotikom. Zato načini uporabe blagoslovljene vode, ki bi lahko vodili do vdihavanja, zaužitja vode ali njenega vnosa v oči ali druga tkiva,

niso priporočljivi, zlasti za imunsko oslABLJENE posameznike, starejše, novorojenčke in bolnike s hudimi opeklinami, poškodbami, pooperativnimi ranami ali z vzpostavljeno periferno vensko potjo.

Blagoslovljena voda tako lahko predstavlja nevarnost okužbe s patogenimi mikroorganizmi. Ker bi bila popolna odstranitev vode iz kropilnikov verjetno slabo sprejeta zaradi verskih razlogov, je priporočena praksa za omejitev prenosa potencialno patogenih mikroorganizmov redno in temeljito čiščenje kropilnikov, uporaba posod s površinami, ki jih je enostavno čistiti, in redna oziroma vsakodnevna zamenjava vode, zlasti po povečanem obisku cerkva (npr. ob cerkvenih praznikih). Javnost, zlasti posamezniki s povečano dovzetnostjo za okužbe, se lahko zaščitijo tako, da se izogibajo stiku blagoslovljene vode z očmi, nosom, usti, ušesi in poškodovano kožo ter z vzdrževanjem dobre higijene rok.

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Supplementary material

Table S1: List of identified bacterial isolates from holy water of fonts and reservoirs.

Table S2: List of the isolates selected for the antimicrobial susceptibility testing with the corresponding antimicrobial profile.

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Supplementary information

Table S1: List of identified bacterial isolates from holy water of fonts and reservoirs.

Risk group determined according to TRBA 466 Classification of Prokaryotes (Bacteria and Archaea) into Risk Groups (Federal Institute for Occupational Safety and Health. <https://www.baua.de/EN/Service/Legislative-texts-and-technical-rules/Rules/TRBA/TRBA-466.html>).

Tabela S1: Seznam identificiranih bakterijskih izolatov iz blagoslovljene vode kropilnikov in rezervoarjev.

Mycosmo culture collection no. (exb)	Genbank	Identity	Risk group	Phylum, class, order, family	Sample	Medium and growth temperature
L-5025	<i>Kocuria salsicia</i>	99.72	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	FC_1	blood agar, 37 °C
L-5026	<i>Brevundimonas aurantiaca</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_1	blood agar, 37 °C
L-5027	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	99.9	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_1	blood agar, 37 °C
L-5028	<i>Staphylococcus lugdunensis</i>	100	2	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	FC_1	blood agar, 37 °C
L-5029	<i>Kocuria arsenatis/ Kocuria rhizophila</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	FC_1	blood agar, 37 °C
L-5030	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_1	blood agar, 37 °C
L-5031	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	99.9	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_1	UriSelect4 agar, 37 °C
L-5032	<i>Brevundimonas aurantiaca</i>	99.91	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_1	UriSelect4 agar, 37 °C
L-5033	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	FC_R1	blood agar, 37 °C
L-5034	<i>Ralstonia pickettii</i>	99.7	2	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiaceae</i>	FC_R1	blood agar, 37 °C
L-5035	<i>Pseudomonas alcaliphila/ Pseudomonas oleovorans</i>	99.89	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	FC_R1	blood agar, 37 °C

L-5036	<i>Pseudomonas chloritidismutans</i> / <i>Pseudomonas knackmussii</i>	99.81	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5037	<i>Ralstonia pickettii</i>	99.82	2	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Burkholderiaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5038	<i>Microbacterium invictum</i>	98.42	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	FC_R1	blood agar, 37 °C
L-5039	<i>Pseudomonas chloritidismutans</i> / <i>Pseudomonas knackmussii</i>	99.81	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	FC_R1	blood agar, 37 °C
L-5040	<i>Brevibacterium sanguinis</i>	100	2	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Brevibacteriaceae</i>	FC_R1	blood agar, 37 °C
L-5041	<i>Ralstonia pickettii</i>	99.79	2	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Burkholderiaceae</i>	FC_R1	blood agar, 37 °C
L-5042	<i>Microbacterium maritypicum</i>	99.82	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	FC_R1	blood agar, 37 °C
L-5043	<i>Microbacterium maritypicum</i>	99.8	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5044	<i>Pseudomonas chloritidismutans</i> / <i>Pseudomonas knackmussii</i>	99.81	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5045	<i>Pseudomonas chengduensis</i>	99.82	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5046	<i>Pseudomonas chengduensis</i>	99.89	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5047	<i>Microbacterium invictum</i>	98.35	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5048	<i>Pseudomonas chengduensis</i>	100	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	FC_R1	UriSelect4 agar, 37 °C
L-5049	<i>Rothia kristinae</i>	99.56	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Micrococcineae</i>	FC_2	blood agar, 37 °C
L-5050	<i>Brevundimonas vesicularis</i> / <i>Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Caulobacterales, Caulobacteraceae</i>	FC_2	blood agar, 37 °C
L-5051	<i>Brevundimonas vesicularis</i> / <i>Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Caulobacterales, Caulobacteraceae</i>	FC_2	UriSelect4 agar, 37 °C

L-5052	<i>Sphingomonas hankookensis</i>	99.41	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5053	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5054	<i>Actinomyces haliotis</i>	99.97	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Actinomycetaceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5055	<i>Rothia amarae</i>	97.88	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5056	<i>Rothia terrae</i>	98.96	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	FC_2	blood agar, 37 °C
L-5057	<i>Staphylococcus haemolyticus</i>	99.82	2	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	FC_2	blood agar, 37 °C
L-5058	<i>Rothia kristinae</i>	99.63	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	FC_2	blood agar, 37 °C
L-5059	<i>Brevundimonas aurantiaca</i>	99.9	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_2	blood agar, 37 °C
L-5060	<i>Brevundimonas aurantiaca</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5061	<i>Staphylococcus haemolyticus</i>	99.91	2	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5062	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5063	<i>Rothia kristinae</i>	99.63	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5064	<i>Rothia kristinae</i>	99.63	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	FC_2	UriSelect4 agar, 37 °C
L-5067	<i>Microbacterium testaceum</i>	99.05	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	FC_R2	blood agar, 37 °C
L-5068	<i>Brevibacterium sanguinis</i>	99.72	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	FC_R2	blood agar, 37 °C
L-5069	<i>Brevibacterium sanguinis</i>	99.72	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	FC_R2	UriSelect4 agar, 37 °C
L-5070	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	99.79	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	FC_R2	blood agar, 37 °C
L-5071	<i>Chryseobacterium shandongense</i>	99.91	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	FC_R2	UriSelect4 agar, 37 °C
L-5072	<i>Brevibacterium casei</i>	99.22	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	FC_R2	UriSelect4 agar, 37 °C

L-5073	<i>Sphingobacterium daejeonense</i>	99.63	1	Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae	FC_R2	UriSelect4 agar, 37 °C
L-5074	<i>Pseudomonas rhodesiae</i>	100	1	Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae	FC_R2	UriSelect4 agar, 37 °C
L-5075	<i>Pseudomonas chloritidismutans/ Pseudomonas knackmussii</i>	99.81	1	Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae	FC_R2	UriSelect4 agar, 37 °C
L-5076	<i>Stenotrophomonas maltophilia</i>	99.35	2	Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae	FC_R2	UriSelect4 agar, 37 °C
L-5077	<i>Microbacterium saccharophilum</i>	99.14	1	Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae	FC_R2	UriSelect4 agar, 37 °C
L-5078	<i>Pseudomonas chengduensis</i>	99.8	1	Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae	FC_R2	UriSelect4 agar, 37 °C
L-5079	<i>Pseudomonas chloritidismutans/ Pseudomonas knackmussii</i>	99.81	1	Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae	FC_R2	UriSelect4 agar, 37 °C
L-5080	<i>Acinetobacter haemolyticus</i>	99.2	2	Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae	SC_1	blood agar, 37 °C
L-5081	<i>Brevundimonas mediterranea</i>	100	1	Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae	SC_1	blood agar, 37 °C
L-5082	<i>Acinetobacter johnsonii</i>	99.61	2	Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae	SC_1	blood agar, 37 °C
L-5083	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	99.61	2	Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae	SC_1	blood agar, 37 °C
L-5084	<i>Sphingomonas hankookensis</i>	99.42	1	Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae	SC_1	blood agar, 37 °C
L-5085	<i>Sphingomonas hankookensis</i>	99.42	1	Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae	SC_1	blood agar, 37 °C
L-5086	<i>Sphingomonas hankookensis</i>	99.42	1	Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae	SC_1	blood agar, 37 °C

L-5087	<i>Sphingomonas hankookensis</i>	99.42	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SC_1	blood agar, 37 °C
L-5089	<i>Sphingomonas hankookensis</i>	98.87	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SC_1	UriSelect4 agar, 37 °C
L-5090	<i>Staphylococcus vitulinus</i>	99.91	1	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	SC_1	UriSelect4 agar, 37 °C
L-5091	<i>Acinetobacter haemolyticus</i>	99.14	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_1	UriSelect4 agar, 37 °C
L-5092	<i>Sphingomonas hankookensis</i>	99.51	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SC_1	UriSelect4 agar, 37 °C
L-5093	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacteriales, Caulobacteraceae</i>	SC_1	UriSelect4 agar, 37 °C
L-5094	<i>Acinetobacter johnsonii</i>	99.57	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_1	UriSelect4 agar, 37 °C
L-5095	<i>Staphylococcus vitulinus</i>	99.9	1	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	SC_1	UriSelect4 agar, 37 °C
L-5097	<i>Pseudomonas peli</i>	99.63	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SC_R1	blood agar, 37 °C
L-5098	<i>Bacillus drentensis/ Bacillus infantis</i>	99.7	1	<i>Bacillota, Bacilli, Bacillales, Bacillaceae</i>	UC_1	blood agar, 37 °C
L-5099	<i>Microbacterium testaceum</i>	99.12	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_1	blood agar, 37 °C
L-5100	<i>Aquincola tertiaricarbonis</i>	98.25	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_1	blood agar, 37 °C
L-5101	<i>Aquincola tertiaricarbonis</i>	98.4	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_1	blood agar, 37 °C
L-5102	<i>Microbacterium testaceum</i>	99.15	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_1	UriSelect4 agar, 37 °C
L-5103	<i>Aquincola tertiaricarbonis</i>	98.18	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_1	UriSelect4 agar, 37 °C

L-5104	<i>Aquicola tertiarycarbonis</i>	98.24	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_R1	blood agar, 37 °C
L-5105	<i>Microbacterium lacus</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R1	blood agar, 37 °C
L-5107	<i>Aquicola tertiarycarbonis</i>	98.29	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_R1	UriSelect4 agar, 37 °C
L-5108	<i>Enterococcus ureilyticus</i>	99.9	1	<i>Bacillota, Bacilli, Lactobacillales, Enterococcaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5109	<i>Cellulosimicrobium funkei</i>	99.72	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Promicromonosporaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5110	<i>Microbacterium maritypicum</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5111	<i>Microbacterium saccharophilum</i>	98.28	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5112	<i>Aquicola tertiarycarbonis</i>	98.38	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_R1	UriSelect4 agar, 37 °C
L-5113	<i>Microbacterium maritypicum</i>	99.8	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5114	<i>Kocuria carniphila</i>	99.72	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5115	<i>Acinetobacter johnsonii</i>	99.78	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5116	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5117	<i>Pseudomonas koreensis</i>	99.65	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5120	<i>Janibacter indicus</i>	99.09	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Intrasporangiaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5121	<i>Rothia amarae</i>	98.04	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	UC_R1	UriSelect4 agar, 37 °C
L-5122	<i>Acinetobacter beijerinckii</i>	98.93	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_1	blood agar, 37 °C
L-5123	<i>Acinetobacter johnsonii</i>	99.9	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_1	blood agar, 37 °C

L-5124	<i>Acinetobacter johnsonii</i>	98.76	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	VC_1	blood agar, 37 °C
L-5125	<i>Acinetobacter johnsonii</i>	99	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	VC_1	blood agar, 37 °C
L-5126	<i>Acinetobacter johnsonii</i>	99.9	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5127	<i>Chryseobacterium hispalense</i>	99.79	1	<i>Bacteroidota, Flavobacteriia,</i> <i>Flavobacteriales, Weeksellaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5128	<i>Microbacterium maritipicum</i>	99.81	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5129	<i>Kocuria carniphila</i>	99.71	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Micrococcaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5130	<i>Pseudomonas koreensis</i>	99.62	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5131	<i>Acinetobacter johnsonii</i>	99.89	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5132	<i>Pseudomonas rhodesiae</i>	100	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5133	<i>Acinetobacter johnsonii</i>	99.89	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	VC_1	UriSelect4 agar, 37 °C
L-5134	<i>Barriostimonas humi</i>	99.9	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Dermacoccaceae</i>	VC_R1	blood agar, 37 °C
L-5136	<i>Novosphingobium aquaticum/</i> <i>Novosphingobium subterraneum/</i> <i>Novosphingobium lentum</i>	97.82	1	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Sphingomonadales,</i> <i>Erythrobacteraceae</i>	VC_R1	blood agar, 37 °C
L-5137	<i>Ponticoccus gilvus</i>	100	1	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Rhodobacterales,</i> <i>Rhodobacteraceae</i>	VC_R1	blood agar, 37 °C
L-5139	<i>Microbacterium maritipicum</i>	100	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	VC_R1	blood agar, 37 °C
L-5140	<i>Bacillus aerius</i>	99.68	1	<i>Bacillota, Bacilli,</i> <i>Bacillales, Bacillaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5141	<i>Microbacterium chocolatum</i>	98.6	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5142	<i>Microbacterium chocolatum</i>	98.6	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	VC_R1	UriSelect4 agar, 37 °C

L-5143	<i>Acinetobacter johnsonii</i>	98.82	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5144	<i>Cellulosimicrobium funkei</i>	99.53	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5145	<i>Microbacterium maritypicum</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5146	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	99.9	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5147	<i>Rothia amarae</i>	99.89	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5149	<i>Naumannella halotolerans</i>	100	1	<i>Actinomycetota, Actinomycetes, Propionibacteriales, Propionibacteriaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5150	<i>Sphingomonas panaciterrae</i>	99.8	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	VC_R1	UriSelect4 agar, 37 °C
L-5151	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_1	blood agar, 37 °C
L-5153	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_1	UriSelect4 agar, 37 °C
L-5154	<i>Pseudomonas rhodesiae</i>	99.81	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_1	UriSelect4 agar, 37 °C
L-5155	<i>Staphylococcus epidermidis</i>	99.89	2	<i>Firmicutes, Bacilli, Bacillales, Staphylococcaceae</i>	TC_1	UriSelect4 agar, 37 °C
L-5156	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_1	UriSelect4 agar, 37 °C
L-5157	<i>Acinetobacter johnsonii</i>	99.6	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_1	blood agar, 37 °C
L-5158	<i>Acinetobacter johnsonii</i>	98.98	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_1	blood agar, 37 °C
L-5159	<i>Microbacterium testaceum</i>	99.04	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_1	blood agar, 37 °C
L-5160	<i>Brevundimonas aurantiaca</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	KC_1	blood agar, 37 °C

L-5161	<i>Acidovorax facilis</i>	99.44	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	KC_1	blood agar, 37 °C
L-5162	<i>Chryseobacterium shandongense</i>	99.36	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	KC_1	blood agar, 37 °C
L-5163	<i>Acinetobacter beijerinckii</i>	99.41	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_1	blood agar, 37 °C
L-5164	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	KC_1	UriSelect4 agar, 37 °C
L-5165	<i>Acinetobacter johnsonii</i>	99.45	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_1	UriSelect4 agar, 37 °C
L-5166	<i>Acinetobacter johnsonii</i>	99.32	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_1	UriSelect4 agar, 37 °C
L-5167	<i>Microbacterium testaceum</i>	98.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_1	UriSelect4 agar, 37 °C
L-5168	<i>Brevundimonas aurantiaca</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	KC_1	UriSelect4 agar, 37 °C
L-5169	<i>Acidovorax facilis</i>	99.42	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	KC_1	UriSelect4 agar, 37 °C
L-5170	<i>Kocuria uropygioeca/Kocuria uropygialis</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	KC_1	UriSelect4 agar, 37 °C
L-5171	<i>Acinetobacter beijerinckii</i>	99.45	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	BC_1	blood agar, 37 °C
L-5173	<i>Acinetobacter beijerinckii</i>	99.61	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	BC_1	UriSelect4 agar, 37 °C
L-5174	<i>Sphingobium hydrophobicum</i>	99.5	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	BC_1	UriSelect4 agar, 37 °C
L-5177	<i>Sphingomonas paucimobilis</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	BC_R1	UriSelect4 agar, 37 °C
L-5178	<i>Microbacterium testaceum</i>	99.13	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_1	blood agar, 37 °C
L-5179	<i>Brevundimonas mediterranea</i>	99.72	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	DC_1	blood agar, 37 °C

L-5180	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_1	blood agar, 37 °C
L-5181	<i>Kocuria uropygioeca</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	DC_1	blood agar, 37 °C
L-5182	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	97.7	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	DC_1	blood agar, 37 °C
L-5183	<i>Acinetobacter johnsonii</i>	99.73	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	DC_1	UriSelect4 agar, 37 °C
L-5184	<i>Microbacterium testaceum</i>	98.24	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_1	UriSelect4 agar, 37 °C
L-5185	<i>Microbacterium testaceum</i>	99.15	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_1	UriSelect4 agar, 37 °C
L-5186	<i>Microbacterium testaceum</i>	99.1	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_1	UriSelect4 agar, 37 °C
L-5187	<i>Stenotrophomonas rhizophila</i>	99.61	1	<i>Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae</i>	DC_R1	blood agar, 37 °C
L-5188	<i>Sphingobium hydrophobicum</i>	99.9	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	DC_R1	blood agar, 37 °C
L-5189	<i>Stenotrophomonas chelatiphaga</i>	99.55	1	<i>Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae</i>	DC_R1	blood agar, 37 °C
L-5190	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R1	UriSelect4 agar, 37 °C
L-5191	<i>Sphingobium hydrophobicum</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	DC_R1	UriSelect4 agar, 37 °C
L-5192	<i>Microbacterium testaceum</i>	99.08	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_R1	UriSelect4 agar, 37 °C
L-5193	<i>Stenotrophomonas rhizophila</i>	99.61	1	<i>Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae</i>	DC_R1	UriSelect4 agar, 37 °C
L-5194	<i>Stenotrophomonas rhizophila</i>	99.67	1	<i>Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae</i>	DC_R1	UriSelect4 agar, 37 °C
L-5195	<i>Microbacterium testaceum</i>	99.17	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_R1	UriSelect4 agar, 37 °C

L-5196	<i>Acidovorax facilis</i>	99.34	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_R1	UriSelect4 agar, 37 °C
L-5197	<i>Sphingobium hydrophobicum</i>	99.81	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SI_1	blood agar, 37 °C
L-5198	<i>Sphingobium hydrophobicum</i>	99.9	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SI_1	blood agar, 37 °C
L-5200	<i>Sphingobium hydrophobicum</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SI_1	UriSelect4 agar, 37 °C
L-5201	<i>Chryseobacterium sediminis</i>	98.17	1	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	SI_1	blood agar, 37 °C
L-5202	<i>Rothia aeria</i>	99.63	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	SI_1	blood agar, 37 °C
L-5203	<i>Staphylococcus warneri</i>	99.91	1	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	SI_1	UriSelect4 agar, 37 °C
L-5204	<i>Rothia amarae</i>	97.99	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	SI_1	UriSelect4 agar, 37 °C
L-5205	<i>Microbacterium paraoxydans</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_1	UriSelect4 agar, 37 °C
L-5207	<i>Staphylococcus haemolyticus</i>	99.91	2	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	SI_1	UriSelect4 agar, 37 °C
L-5208	<i>Pseudomonas koreensis</i>	99.63	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SI_R1	blood agar, 37 °C
L-5209	<i>Microbacterium maritipicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R1	blood agar, 37 °C
L-5210	<i>Aerococcus urinaeequi</i>	99.91	1	<i>Bacillota, Bacilli, Bacillales, Aerococcaceae</i>	SI_R1	blood agar, 37 °C
L-5211	<i>Sphingomonas olei/Sphingomonas panaciterrae</i>	100	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SI_R1	blood agar, 37 °C
L-5212	<i>Pseudomonas koreensis</i>	99.54	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SI_R1	UriSelect4 agar, 37 °C
L-5213	<i>Microbacterium maritipicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R1	UriSelect4 agar, 37 °C
L-5214	<i>Brachybacterium paraconglomeratum</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Dermabacteraceae</i>	SI_R1	UriSelect4 agar, 37 °C

L-5215	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R1	UriSelect4 agar, 37 °C
L-5216	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R1	UriSelect4 agar, 37 °C
L-5217	<i>Acinetobacter johnsonii</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_1	blood agar, 37 °C
L-5218	<i>Pseudomonas koreensis</i>	99.9	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_1	blood agar, 37 °C
L-5220	<i>Acinetobacter johnsonii</i>	99.13	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_1	blood agar, 37 °C
L-5221	<i>Rothia amarae</i>	98.04	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	RC_1	blood agar, 37 °C
L-5222	<i>Acinetobacter haemolyticus</i>	99.86	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_1	blood agar, 37 °C
L-5223	<i>Microbacterium lacus</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_1	blood agar, 37 °C
L-5224	<i>Pseudomonas koreensis</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_1	UriSelect4 agar, 37 °C
L-5225	<i>Acinetobacter johnsonii</i>	99.42	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_1	UriSelect4 agar, 37 °C
L-5226	<i>Brevundimonas diminuta</i>	99.53	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	RC_1	UriSelect4 agar, 37 °C
L-5227	<i>Delftia lacustris</i>	100	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_1	UriSelect4 agar, 37 °C
L-5228	<i>Acinetobacter johnsonii</i>	99.45	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_1	UriSelect4 agar, 37 °C
L-5229	<i>Stenotrophomonas bentonitica</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Lysobacteriales, Lysobacteraceae</i>	RC_1	UriSelect4 agar, 37 °C
L-5230	<i>Pseudomonas koreensis</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_1	UriSelect4 agar, 37 °C
L-5231	<i>Pseudomonas helmanticensis</i>	99.82	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_R1	blood agar, 37 °C

L-5232	<i>Acinetobacter johnsonii</i>	99.73	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	RC_R1	blood agar, 37 °C
L-5234	<i>Microbacterium paraoxydans</i>	99.82	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	RC_R1	blood agar, 37 °C
L-5235	<i>Pseudomonas turukhanskensis</i>	99.62	-	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	RC_R1	blood agar, 37 °C
L-5236	<i>Microbacterium maritipicum</i>	100	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	RC_R1	blood agar, 37 °C
L-5238	<i>Sphingomonas panaciterrae</i>	99.9	-	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Sphingomonadales,</i> <i>Sphingomonadaceae</i>	RC_R1	blood agar, 37 °C
L-5239	<i>Microbacterium maritipicum</i>	100	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	RC_R1	blood agar, 37 °C
L-5240	<i>Pseudomonas turukhanskensis</i>	99.62	-	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	RC_R1	blood agar, 37 °C
L-5241	<i>Tsakumurella pulmonis</i>	100	2	<i>Actinomycetota, Actinomycetes,</i> <i>Mycobacteriales, Tsakumurellaceae</i>	RC_R1	blood agar, 37 °C
L-5242	<i>Pseudomonas putida</i>	99.2	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	RC_R1	blood agar, 37 °C
L-5243	<i>Pseudomonas chloritidismutans</i>	99.73	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	RC_R1	blood agar, 37 °C
L-5244	<i>Acinetobacter johnsonii</i>	99.72	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5245	<i>Acinetobacter johnsonii</i>	99.72	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5246	<i>Microbacterium maritipicum</i>	100	1	<i>Actinomycetota, Actinomycetes,</i> <i>Micrococcales, Microbacteriaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5247	<i>Acinetobacter johnsonii</i>	99.81	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5248	<i>Brevundimonas vesicularis/</i> <i>Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Caulobacterales, Caulobacteraceae</i>	RC_R1	UriSelect4 agar, 37 °C

L-5249	<i>Pseudomonas koreensis</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5250	<i>Stenotrophomonas maltophilia</i>	99.54	2	<i>Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5251	<i>Sphingomonas olei</i>	99.81	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5252	<i>Acinetobacter johnsonii</i>	99.6	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5253	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5254	<i>Brachybacterium conglomeratum</i>	99.8	1	<i>Actinomycetota, Actinomycetes, Actinomycetales, Dermabacteraceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5255	<i>Microbacterium paraoxydans</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_R1	UriSelect4 agar, 37 °C
L-5256	<i>Acinetobacter haemolyticus</i>	99.11	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_2	blood agar, 37 °C
L-5257	<i>Acinetobacter johnsonii</i>	99.6	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_2	blood agar, 37 °C
L-5258	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_2	blood agar, 37 °C
L-5259	<i>Stenotrophomonas maltophilia/ Pseudomonas hibiscicola</i>	98.96	2	<i>Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae</i>	SC_2	UriSelect4 agar, 37 °C
L-5260	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_2	blood agar, 37 °C
L-5261	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_2	blood agar, 37 °C
L-5262	<i>Brevundimonas aurantiaca</i>	99.91	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_2	blood agar, 37 °C
L-5263	<i>Curtobacterium oceanosedimentum</i>	99.63	-	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SC_2	UriSelect4 agar, 37 °C
L-5264	<i>Asticcacaulis excentricus</i>	99.62	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_2	UriSelect4 agar, 37 °C

L-5265	<i>Acinetobacter haemolyticus</i>	99.26	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_2	UriSelect4 agar, 37 °C
L-5266	<i>Brevundimonas aurantiaca</i>	99.9	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacteriales, Caulobacteraceae</i>	SC_2	UriSelect4 agar, 37 °C
L-5267	<i>Sphingomonas hankookensis</i>	99.13	1	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	SC_2	UriSelect4 agar, 37 °C
L-5268	<i>Pantoea dispersa</i>	99.17	1	<i>Pseudomonadota, Gammaproteobacteria, Enterobacteriales, Erwiniaceae</i>	SC_R2	blood agar, 37 °C
L-5269	<i>Stenotrophomonas pavanii/ Stenotrophomonas maltophilia/ Pseudomonas geniculata</i>	99.79	2	<i>Pseudomonadota, Gammaproteobacteria, Lysobacteriales, Lysobacteraceae</i>	SC_R2	blood agar, 37 °C
L-5270	<i>Curtobacterium oceanosedimentum</i>	99.73	-	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SC_R2	blood agar, 37 °C
L-5271	<i>Curtobacterium oceanosedimentum</i>	99.81	-	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SC_R2	blood agar, 37 °C
L-5272	<i>Cellulomonas pakistanensis</i>	99.89	1	<i>Actinomycetota, Actinomycetes, Actinomycetales, Cellulomonadaceae</i>	SC_R2	blood agar, 37 °C
L-5273	<i>Pantoea dispersa</i>	99.19	1	<i>Pseudomonadota, Gammaproteobacteria, Enterobacteriales, Erwiniaceae</i>	SC_R2	UriSelect4 agar, 37 °C
L-5274	<i>Pantoea dispersa</i>	99.02	1	<i>Pseudomonadota, Gammaproteobacteria, Enterobacteriales, Erwiniaceae</i>	SC_R2	UriSelect4 agar, 37 °C
L-5275	<i>Pseudomonas oryzihabitans</i>	99.54	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SC_R2	UriSelect4 agar, 37 °C
L-5276	<i>Curtobacterium citreum</i>	99.43	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SC_R2	UriSelect4 agar, 37 °C
L-5278	<i>Microbacterium foliorum</i>	99.44	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SC_R2	UriSelect4 agar, 37 °C
L-5279	<i>Acinetobacter haemolyticus</i>	99.17	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	FC_3	blood agar, 37 °C
L-5280	<i>Delftia acidovorans</i>	99.91	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	FC_3	blood agar, 37 °C
L-5281	<i>Delftia acidovorans</i>	99.91	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	FC_3	blood agar, 37 °C

L-5282	<i>Acinetobacter haemolyticus</i>	99.23	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	FC_3	blood agar, 37 °C
L-5283	<i>Acinetobacter johnsonii</i>	99.54	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	FC_3	blood agar, 37 °C
L-5284	<i>Acinetobacter haemolyticus</i>	99.25	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	FC_3	UriSelect4 agar, 37 °C
L-5285	<i>Acinetobacter johnsonii</i>	99.72	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	FC_3	UriSelect4 agar, 37 °C
L-5286	<i>Acinetobacter johnsonii</i>	99.82	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	FC_3	UriSelect4 agar, 37 °C
L-5288	<i>Microbacterium testaceum</i>	98.99	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5289	<i>Microbacterium zeae/ Microbacterium proteolyticum</i>	98.48	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5290	<i>Microbacterium zeae/ Microbacterium proteolyticum</i>	98.42	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5291	<i>Brevibacterium sanguinis</i>	99.9	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5292	<i>Pseudomonas aeruginosa</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	FC_R3	blood agar, 37 °C
L-5293	<i>Pseudomonas chloritidismutans</i>	99.81	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	FC_R3	blood agar, 37 °C
L-5294	<i>Microbacterium zeae/ Microbacterium proteolyticum</i>	98.42	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5295	<i>Sphingomonas koreensis</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5296	<i>Acinetobacter johnsonii</i>	99.9	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5297	<i>Brevibacterium sanguinis</i>	99.72	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5298	<i>Microbacterium zeae/ Microbacterium proteolyticum</i>	98.61	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	FC_R3	UriSelect4 agar, 37 °C

L-5299	<i>Aquicola tertiaricarbonis</i>	98.23	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_2	blood agar, 37 °C
L-5300	<i>Aquicola tertiaricarbonis</i>	98.23	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_2	blood agar, 37 °C
L-5301	<i>Microbacterium lacus</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_2	blood agar, 37 °C
L-5302	<i>Aquicola tertiaricarbonis</i>	98.27	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_2	UriSelect4 agar, 37 °C
L-5303	<i>Aquicola tertiaricarbonis</i>	98.22	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_2	UriSelect4 agar, 37 °C
L-5304	<i>Aquicola tertiaricarbonis</i>	98.23	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_2	blood agar, 37 °C
L-5305	<i>Acinetobacter johnsonii</i>	99.81	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_2	blood agar, 37 °C
L-5306	<i>Limnobacter thiooxidans</i>	99.53	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiaceae</i>	UC_2	blood agar, 37 °C
L-5307	<i>Aquicola tertiaricarbonis</i>	98.19	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_2	blood agar, 37 °C
L-5308	<i>Aquicola tertiaricarbonis</i>	98.25	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_2	UriSelect4 agar, 37 °C
L-5313	<i>Aquicola tertiaricarbonis</i>	98.21	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_R2	blood agar, 37 °C
L-5314	<i>Microbacterium paraoxydans</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R2	blood agar, 37 °C
L-5317	<i>Aquicola tertiaricarbonis</i>	98.21	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_R2	blood agar, 37 °C

L-5318	<i>Aquincola tertiarycarbonis</i>	98.1	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	UC_R2	UriSelect4 agar, 37 °C
L-5319	<i>Kocuria arsenatis/Kocuria rhizophila</i>	99.71	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcaceae</i>	UC_R2	UriSelect4 agar, 37 °C
L-5320	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R2	UriSelect4 agar, 37 °C
L-5321	<i>Chryseobacterium echinoideorum</i>	99.54	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	VC_2	blood agar, 37 °C
L-5322	<i>Sphingobacterium faecium</i>	99.11	1	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	VC_2	blood agar, 37 °C
L-5323	<i>Acinetobacter johnsonii</i>	99.71	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_2	blood agar, 37 °C
L-5324	<i>Sphingomonas panni</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	VC_2	blood agar, 37 °C
L-5325	<i>Chryseobacterium hominis</i>	99.63	2	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	VC_2	blood agar, 37 °C
L-5327	<i>Chryseobacterium echinoideorum</i>	99.53	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	VC_2	UriSelect4 agar, 37 °C
L-5328	<i>Chryseobacterium hominis</i>	98.32	2	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	VC_2	UriSelect4 agar, 37 °C
L-5329	<i>Sphingobacterium faecium</i>	99.62	1	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	VC_2	UriSelect4 agar, 37 °C
L-5330	<i>Brevundimonas bullata</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	VC_2	UriSelect4 agar, 37 °C
L-5331	<i>Pelomonas aquatica</i>	98.99	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	VC_2	UriSelect4 agar, 37 °C
L-5332	<i>Acinetobacter johnsonii</i>	99.81	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_2	UriSelect4 agar, 37 °C
L-5333	<i>Microbacterium aurum</i>	99.8	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	VC_R2	blood agar, 37 °C
L-5334	<i>Limnobacter thiooxidans</i>	99.68	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiaceae</i>	VC_R2	blood agar, 37 °C
L-5335	<i>Pelomonas puraquae</i>	99.34	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	VC_R2	blood agar, 37 °C

L-5336	<i>Pelomonas aquatica</i>	99.18	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	VC_R2	blood agar, 37 °C
L-5337	<i>Novosphingobium lentum</i>	99.86	1	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Sphingomonadales,</i> <i>Erythrobacteraceae</i>	VC_R2	blood agar, 37 °C
L-5338	<i>Pelomonas aquatica</i>	99.15	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	VC_R2	blood agar, 37 °C
L-5339	<i>Pelomonas aquatica</i>	99.01	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	VC_R2	UriSelect4 agar, 37 °C
L-5340	<i>Pelomonas aquatica</i>	99.16	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	TC_2	blood agar, 37 °C
L-5341	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	TC_2	blood agar, 37 °C
L-5342	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	TC_2	blood agar, 37 °C
L-5343	<i>Pseudomonas xanthomarina</i>	98.97	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	TC_2	blood agar, 37 °C
L-5344	<i>Pseudomonas chloritidismutans</i>	99.9	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	TC_2	UriSelect4 agar, 37 °C
L-5345	<i>Pseudomonas xanthomarina</i>	98.97	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	TC_2	UriSelect4 agar, 37 °C
L-5346	<i>Pseudomonas rhodesiae</i>	99.81	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	TC_2	UriSelect4 agar, 37 °C
L-5347	<i>Staphylococcus hominis</i>	99.9	2	<i>Bacillota, Bacilli, Bacillales,</i> <i>Staphylococcaceae</i>	TC_2	UriSelect4 agar, 37 °C
L-5348	<i>Pseudomonas chloritidismutans</i>	99.81	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	TC_2	UriSelect4 agar, 37 °C

L-5349	<i>Pseudomonas zhaodongensis</i>	99.48	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_2	blood agar, 37 °C
L-5350	<i>Pseudomonas knackmussii</i>	99.9	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_2	blood agar, 37 °C
L-5351	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_2	blood agar, 37 °C
L-5352	<i>Pelomonas aquatica</i>	99.16	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	TC_2	blood agar, 37 °C
L-5353	<i>Pelomonas aquatica</i>	96.94	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	TC_2	UriSelect4 agar, 37 °C
L-5354	<i>Pseudomonas xanthomarina</i>	98.97	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_2	UriSelect4 agar, 37 °C
L-5355	<i>Microbacterium testaceum</i>	98.98	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_2	blood agar, 37 °C
L-5356	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_2	blood agar, 37 °C
L-5357	<i>Pelomonas aquatica</i>	99.07	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_2	blood agar, 37 °C
L-5358	<i>Microbacterium testaceum</i>	99.08	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_2	blood agar, 37 °C
L-5359	<i>Pelomonas aquatica</i>	99.15	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_2	UriSelect4 agar, 37 °C
L-5360	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_2	UriSelect4 agar, 37 °C
L-5361	<i>Sphingobium hydrophobicum</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	DC_2	UriSelect4 agar, 37 °C
L-5362	<i>Microbacterium testaceum</i>	99.11	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_2	UriSelect4 agar, 37 °C
L-5363	<i>Staphylococcus warneri</i>	100	1	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	DC_2	blood agar, 37 °C

L-5364	<i>Citrobacter freundii</i>	99.24	2	<i>Pseudomonadota, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae</i>	DC_2	blood agar, 37 °C
L-5365	<i>Pelomonas aquatica</i>	99.15	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_2	blood agar, 37 °C
L-5366	<i>Pelomonas aquatica</i>	99.08	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_2	UriSelect4 agar, 37 °C
L-5367	<i>Microbacterium testaceum</i>	99.08	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_2	UriSelect4 agar, 37 °C
L-5368	<i>Acinetobacter johnsonii</i>	99.81	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	DC_2	UriSelect4 agar, 37 °C
L-5369	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R2	blood agar, 37 °C
L-5370	<i>Sphingobium hydrophobicum</i>	100	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	DC_R2	blood agar, 37 °C
L-5371	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R2	UriSelect4 agar, 37 °C
L-5372	<i>Sphingobium hydrophobicum</i>	99.9	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	DC_R2	UriSelect4 agar, 37 °C
L-5373	<i>Sphingobium hydrophobicum</i>	99.81	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	DC_R2	UriSelect4 agar, 37 °C
L-5374	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_R2	blood agar, 37 °C
L-5375	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R2	blood agar, 37 °C
L-5376	<i>Microbacterium maritypicum</i>	99.9	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_R2	blood agar, 37 °C
L-5377	<i>Pelomonas aquatica</i>	99.23	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_R2	blood agar, 37 °C
L-5378	<i>Acidovorax facilis</i>	99.44	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_R2	blood agar, 37 °C

L-5379	<i>Pelomonas aquatica</i>	99.08	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	DC_R2	blood agar, 37 °C
L-5380	<i>Stenotrophomonas rhizophila</i>	99.62	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Lysobacterales, Lysobacteraceae</i>	DC_R2	blood agar, 37 °C
L-5381	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	DC_R2	blood agar, 37 °C
L-5382	<i>Pelomonas aquatica</i>	99.04	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	DC_R2	UriSelect4 agar, 37 °C
L-5383	<i>Pelomonas aquatica</i>	99.15	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	DC_R2	UriSelect4 agar, 37 °C
L-5384	<i>Stenotrophomonas rhizophila</i>	99.63	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Lysobacterales, Lysobacteraceae</i>	DC_R2	UriSelect4 agar, 37 °C
L-5386	<i>Pelomonas puraquae</i>	99.26	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	DC_R2	UriSelect4 agar, 37 °C
L-5387	<i>Pseudomonas rhodesiae</i>	99.82	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	KC_2	blood agar, 37 °C
L-5388	<i>Pseudomonas koreensis</i>	100	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	KC_2	blood agar, 37 °C
L-5390	<i>Pseudomonas oryzihabitans</i>	99.45	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	KC_2	blood agar, 37 °C
L-5391	<i>Acinetobacter johnsonii</i>	99.45	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	KC_2	blood agar, 37 °C
L-5392	<i>Pelomonas puraquae</i>	98.46	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	KC_2	UriSelect4 agar, 37 °C
L-5393	<i>Pelomonas aquatica</i>	99.17	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Comamonadaceae</i>	KC_2	UriSelect4 agar, 37 °C
L-5394	<i>Pseudomonas koreensis</i>	100	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	KC_2	UriSelect4 agar, 37 °C

L-5395	<i>Pelomonas aquatica</i>	97.36	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	KC_2	UriSelect4 agar, 37 °C
L-5396	<i>Pelomonas puraquae</i>	99.21	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	KC_2	blood agar, 37 °C
L-5397	<i>Acinetobacter lwoffii</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_2	UriSelect4 agar, 37 °C
L-5398	<i>Chryseobacterium shandongense</i>	99.36	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	KC_R2	UriSelect4 agar, 37 °C
L-5399	<i>Chryseobacterium shandongense</i>	99.36	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	KC_R2	UriSelect4 agar, 37 °C
L-5400	<i>Chryseobacterium shandongense</i>	99.38	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	KC_R2	blood agar, 37 °C
L-5401	<i>Acinetobacter lwoffii</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_R2	blood agar, 37 °C
L-5402	<i>Pelomonas aquatica</i>	98.89	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	KC_R2	blood agar, 37 °C
L-5403	<i>Microbacterium maritypicum</i>	99.71	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_R2	UriSelect4 agar, 37 °C
L-5404	<i>Microbacterium hominis</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_2	blood agar, 37 °C
L-5405	<i>Acinetobacter johnsonii</i>	99.73	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_2	blood agar, 37 °C
L-5408	<i>Pelomonas aquatica</i>	99.01	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_2	blood agar, 37 °C
L-5409	<i>Pelomonas aquatica</i>	98.77	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_2	UriSelect4 agar, 37 °C
L-5411	<i>Pseudomonas koreensis</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_2	UriSelect4 agar, 37 °C
L-5412	<i>Staphylococcus lentus</i>	100	1	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	RC_2	UriSelect4 agar, 37 °C
L-5413	<i>Pelomonas aquatica</i>	99.17	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_2	UriSelect4 agar, 37 °C
L-5414	<i>Staphylococcus warneri</i>	99.91	1	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	RC_2	UriSelect4 agar, 37 °C
L-5416	<i>Pelomonas puraquae</i>	99.23	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_2	UriSelect4 agar, 37 °C

L-5417	<i>Acinetobacter johnsonii</i>	99.9	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_2	UriSelect4 agar, 37 °C
L-5418	<i>Sphingomonas panni</i>	99.81	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SI_2	blood agar, 37 °C
L-5419	<i>Pseudomonas koreensis</i>	99.62	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SI_2	blood agar, 37 °C
L-5421	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SI_2	UriSelect4 agar, 37 °C
L-5422	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SI_2	UriSelect4 agar, 37 °C
L-5423	<i>Microbacterium maritypicum</i>	99.73	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R2	blood agar, 37 °C
L-5424	<i>Pseudomonas koreensis</i>	99.8	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SI_R2	UriSelect4 agar, 37 °C
L-5425	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R2	UriSelect4 agar, 37 °C
L-5426	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R2	blood agar, 37 °C
L-5427	<i>Pseudomonas baetica</i>	99.35	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SI_R2	blood agar, 37 °C
L-5428	<i>Microbacterium maritypicum</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R2	blood agar, 37 °C
L-5429	<i>Pseudomonas baetica</i>	99.42	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SI_R2	blood agar, 37 °C
L-5430	<i>Microbacterium maritypicum</i>	99.63	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R2	blood agar, 37 °C
L-5431	<i>Pseudomonas koreensis</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	SI_R2	UriSelect4 agar, 37 °C
L-5432	<i>Microbacterium maritypicum</i>	99.79	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R2	UriSelect4 agar, 37 °C
L-5433	<i>Microbacterium maritypicum</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	SI_R2	UriSelect4 agar, 37 °C

L-5434	<i>Brevundimonas vesicularis</i> / <i>Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Caulobacterales</i> , <i>Caulobacteraceae</i>	BC_2	blood agar, 37 °C
L-5435	<i>Brevundimonas mediterranea</i>	100	1	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Caulobacterales</i> , <i>Caulobacteraceae</i>	BC_2	blood agar, 37 °C
L-5436	<i>Staphylococcus warneri</i>	100	1	<i>Bacillota</i> , <i>Bacilli</i> , <i>Bacillales</i> , <i>Staphylococcaceae</i>	BC_2	UriSelect4 agar, 37 °C
L-5437	<i>Brevundimonas vesicularis</i> / <i>Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Caulobacterales</i> , <i>Caulobacteraceae</i>	BC_2	UriSelect4 agar, 37 °C
L-5438	<i>Streptococcus mitis</i>	88.36	2	<i>Bacillota</i> , <i>Bacilli</i> , <i>Lactobacillales</i> , <i>Streptococcaceae</i>	BC_2	blood agar, 37 °C
L-5439	<i>Rothia mucilaginosa</i>	99.27	2	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Micrococceinae</i>	BC_2	UriSelect4 agar, 37 °C
L-5440	<i>Acinetobacter parvus</i>	99.63	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	Tap water	blood agar, 37 °C
L-5441	<i>Methyloburbum populi</i> / <i>Methyloburbum thiocyanatum</i>	99.81	1	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Hyphomicrobiales</i> , <i>Methylobacteriaceae</i>	Tap water	blood agar, 37 °C
L-5442	<i>Sphingopyxis alaskensis</i>	100	1	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Sphingomonadales</i> , <i>Sphingomonadaceae</i>	Tap water	blood agar, 37 °C
L-5443	<i>Ottowia shaoguanensis</i>	96.96	-	<i>Pseudomonadota</i> , <i>Betaproteobacteria</i> , <i>Burkholderiales</i> , <i>Comamonadaceae</i>	Tap water	blood agar, 37 °C
L-5444	<i>Pseudomonas peli</i>	99.91	1	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	Tap water	blood agar, 37 °C
L-5445	<i>Sphingopyxis alaskensis</i>	100	1	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Sphingomonadales</i> , <i>Sphingomonadaceae</i>	Tap water	blood agar, 37 °C
L-5446	<i>Methyloburbum populi</i> / <i>Methyloburbum thiocyanatum</i>	99.79	1	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Rhizobiales</i> , <i>Methylobacteriaceae</i>	Tap water	UriSelect4 agar, 37 °C
L-5464	<i>Massilia varians</i>	99.72	1	<i>Pseudomonadota</i> , <i>Betaproteobacteria</i> , <i>Burkholderiales</i> , <i>Oxalobacteraceae</i>	VC_3	blood agar, 37 °C
L-5465	<i>Acinetobacter johnsonii</i>	99.35	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	VC_3	blood agar, 37 °C

L-5466	<i>Acinetobacter johnsonii</i>	99.29	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_3	blood agar, 37 °C
L-5467	<i>Pseudomonas oryzihabitans</i>	99.45	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	VC_3	blood agar, 37 °C
L-5469	<i>Sphingobacterium multivorum</i>	99.9	2	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5470	<i>Acinetobacter johnsonii</i>	99.53	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5471	<i>Sphingobacterium multivorum</i>	99.91	2	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5472	<i>Massilia varians</i>	99.73	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Oxalobacteraceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5473	<i>Acinetobacter johnsonii</i>	98.26	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5474	<i>Pseudomonas putida</i>	99.91	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5475	<i>Acinetobacter johnsonii</i>	99.46	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5476	<i>Sphingomonas olei</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	VC_3	blood agar, 37 °C
L-5477	<i>Sphingobacterium hotanense</i>	99.9	1	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5478	<i>Pseudomonas plecoglossicida</i>	99.81	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5479	<i>Limnobacter thiooxidans</i>	99.72	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiaceae</i>	VC_R3	blood agar, 37 °C
L-5480	<i>Limnobacter thiooxidans</i>	99.61	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiaceae</i>	VC_R3	blood agar, 37 °C
L-5481	<i>Barrientosiimonas humi</i>	99.9	1	<i>Actinomycetota, Actinomycetes, Actinomycetales, Dermacoccaceae</i>	VC_R3	blood agar, 37 °C

L-5482	<i>Cellulosimicrobium funkei</i>	99.51	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Promicromonosporaceae</i>	VC_R3	blood agar, 37 °C
L-5483	<i>Microbacterium paraoxydans</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	VC_R3	UriSelect4 agar, 37 °C
L-5484	<i>Cellulosimicrobium funkei</i>	99.9	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Promicromonosporaceae</i>	VC_R3	UriSelect4 agar, 37 °C
L-5485	<i>Epidermidibacterium keratini</i>	100	-	<i>Actinomycetota, Actinomycetes, Geodermatophilales, Antricoccaceae</i>	VC_R3	UriSelect4 agar, 37 °C
L-5486	<i>Pseudomonas chloritidismutans</i>	99.9	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5487	<i>Sphingobacterium cellulitidis</i>	100	1	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5488	<i>Sphingobacterium multivorum</i>	100	2	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5489	<i>Pseudoxanthomonas japonensis</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Lysobacterales, Lysobacteraceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5490	<i>Acinetobacter johnsonii</i>	99.73	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5491	<i>Pseudomonas chloritidismutans</i>	99.82	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5492	<i>Brevundimonas olei</i>	100	-	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5493	<i>Pseudomonas chloritidismutans</i>	99.81	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_3	blood agar, 37 °C
L-5494	<i>Enterobacter cloacae</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae</i>	TC_3	blood agar, 37 °C
L-5495	<i>Tsakamurella tyrosinosolvens</i>	100	2	<i>Actinomycetota, Actinomycetes, Mycobacteriales, Tsakamurellaceae</i>	TC_3	blood agar, 37 °C
L-5496	<i>Pseudomonas chloritidismutans</i>	99.81	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_3	blood agar, 37 °C

L-5497	<i>Brachybacterium paraconglomeratum</i>	99.89	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Dermabacteraceae</i>	TC_3	blood agar, 37 °C
L-5498	<i>Sphingobacterium cellulitidis</i>	100	1	<i>Bacteroidota, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae</i>	TC_3	blood agar, 37 °C
L-5500	<i>Pseudomonas chloritidismutans</i>	99.81	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	TC_3	UriSelect4 agar, 37 °C
L-5501	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_3	UriSelect4 agar, 37 °C
L-5502	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_3	UriSelect4 agar, 37 °C
L-5503	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_3	blood agar, 37 °C
L-5504	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_3	blood agar, 37 °C
L-5505	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R3	blood agar, 37 °C
L-5506	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R3	blood agar, 37 °C
L-5507	<i>Acidovorax temperans</i>	99.64	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	DC_R3	blood agar, 37 °C
L-5508	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_R3	blood agar, 37 °C
L-5509	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R3	UriSelect4 agar, 37 °C
L-5510	<i>Microbacterium maritypicum</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	DC_R3	UriSelect4 agar, 37 °C
L-5511	<i>Pseudomonas baetica</i>	99.28	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	DC_R3	UriSelect4 agar, 37 °C

L-5513	<i>Brevundimonas aurantiaca</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacteriales, Caulobacteraceae</i>	KC_3	blood agar, 37 °C
L-5514	<i>Microbacterium testaceum</i>	99.14	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_3	blood agar, 37 °C
L-5515	<i>Microbacterium hatanonis</i>	99.44	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_3	blood agar, 37 °C
L-5516	<i>Microbacterium chocolatum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_3	blood agar, 37 °C
L-5517	<i>Microbacterium chocolatum</i>	99.9	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_3	blood agar, 37 °C
L-5518	<i>Microbacterium testaceum</i>	99.17	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_3	UriSelect4 agar, 37 °C
L-5519	<i>Acinetobacter hwoffii</i>	99.71	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_3	UriSelect4 agar, 37 °C
L-5520	<i>Brevundimonas bullata</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacteriales, Caulobacteraceae</i>	KC_3	UriSelect4 agar, 37 °C
L-5521	<i>Pseudomonas chloritidismutans</i>	99.8	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	KC_3	blood agar, 37 °C
L-5522	<i>Acinetobacter hwoffii</i>	99.9	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_3	blood agar, 37 °C
L-5523	<i>Acinetobacter johnsonii</i>	99.54	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_3	blood agar, 37 °C
L-5525	<i>Pseudomonas rhodesiae</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	KC_3	blood agar, 37 °C
L-5526	<i>Acinetobacter johnsonii</i>	99.48	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	KC_3	UriSelect4 agar, 37 °C
L-5527	<i>Pseudomonas koreensis</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	KC_3	UriSelect4 agar, 37 °C
L-5528	<i>Chryseobacterium shandongense</i>	99.36	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	KC_R3	blood agar, 37 °C
L-5530	<i>Micrococcus aloeverae</i>	99.79	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	KC_R3	blood agar, 37 °C
L-5531	<i>Staphylococcus epidermidis</i>	99.82	2	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	KC_R3	blood agar, 37 °C
L-5532	<i>Chryseobacterium shandongense</i>	99.36	-	<i>Bacteroidota, Flavobacteriia, Flavobacteriales, Weeksellaceae</i>	KC_R3	UriSelect4 agar, 37 °C

L-5533	<i>Micrococcus yunnanensis</i>	99.68	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	KC_R3	UriSelect4 agar, 37 °C
L-5534	<i>Acinetobacter haemolyticus</i>	99.04	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_3	blood agar, 37 °C
L-5535	<i>Sphingomonas panni</i>	100	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SC_3	blood agar, 37 °C
L-5537	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_3	blood agar, 37 °C
L-5538	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_3	UriSelect4 agar, 37 °C
L-5539	<i>Acinetobacter haemolyticus</i>	99.18	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_3	UriSelect4 agar, 37 °C
L-5540	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_3	UriSelect4 agar, 37 °C
L-5541	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_3	UriSelect4 agar, 37 °C
L-5542	<i>Sphingomonas hankookensis</i>	99.42	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SC_3	UriSelect4 agar, 37 °C
L-5543	<i>Acinetobacter haemolyticus</i>	99.12	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_3	UriSelect4 agar, 37 °C
L-5544	<i>Staphylococcus warneri</i>	99.91	1	<i>Bacillota, Bacilli, Bacillales, Staphylococcaceae</i>	SC_3	blood agar, 37 °C
L-5545	<i>Acinetobacter haemolyticus</i>	99.27	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	SC_3	blood agar, 37 °C
L-5547	<i>Sphingomonas panni</i>	99.82	1	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SC_R3	blood agar, 37 °C
L-5548	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	SC_R3	blood agar, 37 °C
L-5550	<i>Acidovorax temperans</i>	99.65	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	SC_R3	UriSelect4 agar, 37 °C

L-5551	<i>Brevundimonas vesicularis</i> / <i>Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Caulobacterales</i> , <i>Caulobacteraceae</i>	SC_R3	UriSelect4 agar, 37 °C
L-5552	<i>Acinetobacter haemolyticus</i>	99.26	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	FC_3	blood agar, 37 °C
L-5553	<i>Rothia kristinae</i>	99.63	1	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Microbacteriaceae</i>	FC_3	blood agar, 37 °C
L-5554	<i>Acinetobacter johnsonii</i>	99.9	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	FC_3	blood agar, 37 °C
L-5556	<i>Acinetobacter haemolyticus</i>	99.2	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	FC_3	UriSelect4 agar, 37 °C
L-5557	<i>Rothia amarae</i>	99.9	1	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Micrococcineae</i>	FC_3	UriSelect4 agar, 37 °C
L-5559	<i>Acinetobacter haemolyticus</i>	99.12	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	FC_3	UriSelect4 agar, 37 °C
L-5560	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	FC_R3	blood agar, 37 °C
L-5561	<i>Microbacterium zeae</i>	98.63	1	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Microbacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5562	<i>Microbacterium lacus</i>	99.91	1	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Microbacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5563	<i>Brevibacterium sanguinis</i>	99.71	2	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Brevibacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5564	<i>Brevibacterium sanguinis</i>	99.72	2	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Brevibacteriaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5565	<i>Pseudomonas alcaligenes</i>	98.79	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5566	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5567	<i>Stenotrophomonas maltophilia</i>	99.91	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Lysobacterales</i> , <i>Lysobacteraceae</i>	FC_R3	blood agar, 37 °C
L-5568	<i>Rhodococcus corynebacterioides</i>	99.81	1	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Mycobacteriales</i> , <i>Nocardiaceae</i>	FC_R3	blood agar, 37 °C
L-5569	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	FC_R3	blood agar, 37 °C

L-5570	<i>Brevibacterium sanguinis</i> / <i>Brevibacterium celere</i> / <i>Brevibacterium antiquum</i> / <i>Brevibacterium aurantiacum</i> / <i>Brevibacterium casei</i>	100	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	FC_R3	blood agar, 37 °C
L-5571	<i>Pseudomonas peli</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5572	<i>Brevibacterium sanguinis</i>	99.7	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	FC_R3	UriSelect4 agar, 37 °C
L-5573	<i>Brevundimonas mediterranea</i>	99.91	1	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	BC_3	blood agar, 37 °C
L-5574	<i>Aquicola tertiarycarbonis</i>	98.24	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiales incertae sedis</i>	BC_3	blood agar, 37 °C
L-5575	<i>Brevundimonas vesicularis</i> / <i>Brevundimonas nasdae</i>	99.91	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	BC_3	blood agar, 37 °C
L-5576	<i>Brevundimonas vesicularis</i> / <i>Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	BC_3	UriSelect4 agar, 37 °C
L-5577	<i>Acinetobacter lwoffii</i>	99.48	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_3	blood agar, 37 °C
L-5578	<i>Acinetobacter johnsonii</i>	99.91	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_3	blood agar, 37 °C
L-5579	<i>Microbacterium paraoxydans</i>	99.52	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_3	blood agar, 37 °C
L-5580	<i>Aeromonas media</i>	99.79	1	<i>Pseudomonadota, Gammaproteobacteria, Aeromonadales, Aeromonadaceae</i>	RC_3	blood agar, 37 °C
L-5581	<i>Pseudomonas plecoglossicida</i>	99.72	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_3	blood agar, 37 °C
L-5582	<i>Tsukamurella pulmonis</i>	100	2	<i>Actinomycetota, Actinomycetes, Mycobacteriales, Tsukamurellaceae</i>	RC_3	blood agar, 37 °C
L-5583	<i>Microbacterium foliorum</i>	99.53	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_3	blood agar, 37 °C
L-5584	<i>Acinetobacter lwoffii</i>	99.53	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_3	blood agar, 37 °C

L-5585	<i>Delftia lacustris</i>	99.91	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5586	<i>Acinetobacter johnsonii</i>	99.31	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5587	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5588	<i>Microbacterium paraoxydans</i>	99.82	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5589	<i>Acinetobacter johnsonii</i>	99.01	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5591	<i>Microbacterium schleiferi</i>	99.16	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_3	blood agar, 37 °C
L-5592	<i>Micrococcus yunnanensis</i>	99.72	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5593	<i>Delftia lacustris</i>	100	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5594	<i>Aeromonas salmonicida/ Aeromonas piscicola/ Aeromonas bestiarum</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Aeromonadales, Aeromonadaceae</i>	RC_3	UriSelect4 agar, 37 °C
L-5595	<i>Acidovorax soli</i>	98.6	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_R3	blood agar, 37 °C
L-5596	<i>Microbacterium phyllosphaerae</i>	99.72	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_R3	blood agar, 37 °C
L-5597	<i>Microbacterium maritypicum</i>	99.82	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_R3	blood agar, 37 °C
L-5598	<i>Exiguobacterium mexicanum</i>	99.82	1	<i>Bacillota, Bacilli, Bacillales, Bacillales Incertae Sedis XII</i>	RC_R3	blood agar, 37 °C
L-5599	<i>Acinetobacter johnsonii</i>	99.37	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_R3	blood agar, 37 °C
L-5600	<i>Acinetobacter johnsonii</i>	99.43	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_R3	blood agar, 37 °C
L-5601	<i>Acinetobacter hwoffii</i>	99.65	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_R3	blood agar, 37 °C
L-5602	<i>Brevibacterium casei</i>	99.52	2	<i>Actinomycetota, Actinomycetes, Micrococcales, Brevibacteriaceae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5603	<i>Sphingomonas panaciterrae</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	RC_R3	UriSelect4 agar, 37 °C

L-5604	<i>Acidovorax soli</i>	98.63	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5605	<i>Neomicrococcus aestuarii</i>	99.9	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5606	<i>Acinetobacter johnsonii</i>	99.71	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5607	<i>Acinetobacter hwoffii</i>	99.81	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5608	<i>Microbacterium maritypicum</i>	99.82	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5609	<i>Microbacterium maritypicum</i>	100	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5610	<i>Microbacterium paraoxydans</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	RC_R3	UriSelect4 agar, 37 °C
L-5611	<i>Comamonas testosteroni</i>	99.64	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	RC_R3	blood agar, 37 °C
L-5612	<i>Pseudomonas oryzihabitans</i>	99.45	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	RC_R3	blood agar, 37 °C
L-5613	<i>Acinetobacter hwoffii</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_3	blood agar, 37 °C
L-5614	<i>Massilia varians</i>	99.6	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Oxalobacteraceae</i>	UC_3	blood agar, 37 °C
L-5615	<i>Microbacterium maritypicum</i>	99.73	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_3	blood agar, 37 °C
L-5616	<i>Pseudomonas peli</i>	98.82	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_3	blood agar, 37 °C
L-5617	<i>Acinetobacter hwoffii</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_3	blood agar, 37 °C
L-5618	<i>Rothia amarae</i>	97.99	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	UC_3	UriSelect4 agar, 37 °C
L-5619	<i>Sphingomonas olei</i>	99.82	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5620	<i>Massilia varians</i>	99.79	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Oxalobacteraceae</i>	UC_3	UriSelect4 agar, 37 °C

L-5621	<i>Pseudomonas pseudoalcaligenes</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5622	<i>Massilia timonae</i>	99.89	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Oxalobacteraceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5623	<i>Acinetobacter hwoffii</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5624	<i>Pseudomonas stutzeri</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_3	blood agar, 37 °C
L-5625	<i>Sphingomonas olei/ Sphingomonas panaciterrae</i>	99.9	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	UC_3	blood agar, 37 °C
L-5626	<i>Massilia timonae</i>	99.89	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Oxalobacteraceae</i>	UC_3	blood agar, 37 °C
L-5627	<i>Rothia terrae</i>	99.26	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	UC_3	UriSelect4 agar, 37 °C
L-5628	<i>Pseudomonas oryzihabitans/ Pseudomonas psychrotolerans</i>	99.53	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5629	<i>Microbacterium maritipicum</i>	99.91	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5630	<i>Acinetobacter hwoffii</i>	99.8	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5631	<i>Massilia varians</i>	99.79	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Oxalobacteraceae</i>	UC_3	UriSelect4 agar, 37 °C
L-5633	<i>Pseudomonas peli</i>	99.07	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_R3	blood agar, 37 °C
L-5634	<i>Sphingomonas olei</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	UC_R3	blood agar, 37 °C
L-5635	<i>Acinetobacter hwoffii</i>	100	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_R3	blood agar, 37 °C

L-5636	<i>Pseudomonas peli</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_R3	blood agar, 37 °C
L-5637	<i>Brevundimonas vesicularis/ Brevundimonas nasdae</i>	100	2	<i>Pseudomonadota, Alphaproteobacteria, Caulobacterales, Caulobacteraceae</i>	UC_R3	blood agar, 37 °C
L-5638	<i>Sphingomonas olei/ Sphingomonas panaciterrae</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5639	<i>Pseudomonas peli</i>	100	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5640	<i>Acinetobacter schindleri</i>	98.68	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5643	<i>Acinetobacter lwoffii</i>	99.91	2	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Moraxellaceae</i>	UC_R3	blood agar, 37 °C
L-5644	<i>Sphingomonas olei/ Sphingomonas panaciterrae</i>	99.9	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	UC_R3	blood agar, 37 °C
L-5645	<i>Pseudomonas koreensis</i>	99.91	1	<i>Pseudomonadota, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5646	<i>Rothia terrae</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5647	<i>Rothia terrae</i>	99.72	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5648	<i>Microbacterium maritypicum</i>	99.81	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Microbacteriaceae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5649	<i>Limnobacter thiooxidans</i>	99.7	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Burkholderiaceae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5650	<i>Rothia kristinae</i>	99.54	1	<i>Actinomycetota, Actinomycetes, Micrococcales, Micrococcineae</i>	UC_R3	UriSelect4 agar, 37 °C
L-5651	<i>Hydrogenophaga palleronii</i>	99.91	1	<i>Pseudomonadota, Betaproteobacteria, Burkholderiales, Comamonadaceae</i>	SI_3	blood agar, 37 °C
L-5653	<i>Sphingobium hydrophobicum</i>	99.91	-	<i>Pseudomonadota, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>	SI_3	blood agar, 37 °C

L-5654	<i>Sphingomonas olei</i> / <i>Sphingomonas</i> <i>panaciterrae</i>	99.91	-	<i>Pseudomonadota</i> , <i>Alphaproteobacteria</i> , <i>Sphingomonadales</i> , <i>Sphingomonadaceae</i>	SI_3	blood agar, 37 °C
L-5655	<i>Aquicola</i> <i>tertiaricarbonis</i>	98.15	1	<i>Pseudomonadota</i> , <i>Betaproteobacteria</i> , <i>Burkholderiales</i> , <i>Burkholderiales</i> <i>incertae sedis</i>	SI_3	blood agar, 37 °C
L-5656	<i>Acinetobacter lwoffii</i>	99.82	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	SI_3	blood agar, 37 °C
L-5657	<i>Pseudomonas koreensis</i>	99.72	1	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	SI_3	blood agar, 37 °C
L-5658	<i>Aquicola</i> <i>tertiaricarbonis</i>	98.2	1	<i>Pseudomonadota</i> , <i>Betaproteobacteria</i> , <i>Burkholderiales</i> , <i>Burkholderiales</i> <i>incertae sedis</i>	SI_3	UriSelect4 agar, 37 °C
L-5659	<i>Chryseobacterium</i> <i>shandongense</i>	99.27	-	<i>Bacteroidota</i> , <i>Flavobacteriia</i> , <i>Flavobacteriales</i> , <i>Weeksellaceae</i>	SI_3	UriSelect4 agar, 37 °C
L-5660	<i>Pseudomonas koreensis</i>	99.55	1	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	SI_3	UriSelect4 agar, 37 °C
L-5661	<i>Acinetobacter johnsonii</i>	99.72	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	SI_3	UriSelect4 agar, 37 °C
L-5662	<i>Chryseobacterium</i> <i>aquaticum</i>	99.63	1	<i>Bacteroidota</i> , <i>Flavobacteriia</i> , <i>Flavobacteriales</i> , <i>Weeksellaceae</i>	SI_3	UriSelect4 agar, 37 °C
L-5663	<i>Acinetobacter</i> <i>beijerinckii</i>	99.37	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	SI_3	blood agar, 37 °C
L-5667	<i>Pseudomonas koreensis</i>	99.72	1	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Pseudomonadaceae</i>	SI_3	UriSelect4 agar, 37 °C
L-5668	<i>Rothia amarae</i>	97.9	1	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Micrococcineae</i>	SI_3	UriSelect4 agar, 37 °C
L-5671	<i>Acinetobacter johnsonii</i>	99.3	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	SI_R3	blood agar, 37 °C
L-5672	<i>Microbacterium</i> <i>maritypicum</i>	99.89	1	<i>Actinomycetota</i> , <i>Actinomycetes</i> , <i>Micrococcales</i> , <i>Microbacteriaceae</i>	SI_R3	blood agar, 37 °C
L-5673	<i>Acinetobacter johnsonii</i>	99.37	2	<i>Pseudomonadota</i> , <i>Gammaproteobacteria</i> , <i>Pseudomonadales</i> , <i>Moraxellaceae</i>	SI_R3	blood agar, 37 °C

L-5675	<i>Massilia varians</i>	99.34	1	<i>Pseudomonadota,</i> <i>Betaproteobacteria,</i> <i>Burkholderiales, Oxalobacteraceae</i>	SI_R3	UriSelect4 agar, 37 °C
L-5676	<i>Stenotrophomonas rhizophila</i>	99.63	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Lysobacterales, Lysobacteraceae</i>	SI_R3	UriSelect4 agar, 37 °C
L-5677	<i>Pseudomonas rhodesiae</i>	99.82	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	SI_R3	UriSelect4 agar, 37 °C
L-5678	<i>Bacillus aryabhatai</i>	99.9	1	<i>Bacillota, Bacilli,</i> <i>Bacillales, Bacillaceae</i>	SI_R3	UriSelect4 agar, 37 °C
L-5680	<i>Serratia quinivorans</i>	99.53	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Enterobacteriales, Yersiniaceae</i>	SI_R3	UriSelect4 agar, 37 °C
L-5681	<i>Pseudomonas rhodesiae</i>	99.73	1	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales,</i> <i>Pseudomonadaceae</i>	SI_R3	blood agar, 37 °C
L-5682	<i>Acinetobacter johnsonii</i>	99.24	2	<i>Pseudomonadota,</i> <i>Gammaproteobacteria,</i> <i>Pseudomonadales, Moraxellaceae</i>	VC_3	UriSelect4 agar, 37 °C
L-5683	<i>Sphingobium hydrophobicum</i>	99.81	-	<i>Pseudomonadota,</i> <i>Alphaproteobacteria,</i> <i>Sphingomonadales,</i> <i>Sphingomonadaceae</i>	DC_3	blood agar, 37 °C

Table S2: List of the isolates selected for the antimicrobial susceptibility testing with the corresponding antimicrobial profile. + indicates resistance; - indicates susceptibility.

Ampicillin (AMP) 100 mg/l; Chloramphenicol (CHL) 25 mg/l; Cefotaxime (CTX) 2 mg/l; Colistin (COL) 3.5 mg/l; Enrofloxacin (ENR) 0.5 mg/l; Erythromycin (ERY) 15 mg/l; Imipenem (IPM) 4 mg/l; Kanamycin (KAN) 50 mg/l; Tetracycline (TET) 10 mg/l.

Tabela S2: Seznam izolatov, izbranih za testiranje odpornosti proti antibiotikom, s protimikrobnim profilom. + označuje odpornost; - označuje občutljivost.

Mycosmo culture collection No. (EXB)	Bacterial strain	AMP 100 mg/l	TET 12,5 mg/l	IPM 4 mg/l	ERY 15 mg/l	CHL 25 mg/l	KAN 50 mg/l	CTX 2 mg/l	ENR 0.5 mg/l	COL 3.5 mg/l	LB
L-5122	<i>Acinetobacter beijerinckii</i>	-	-	-	-	-	-	-	-	+	+
L-5171	<i>Acinetobacter beijerinckii</i>	-	-	-	-	-	-	-	-	+	+
L-5091	<i>Acinetobacter haemolyticus</i>	-	-	-	-	-	-	+	-	+	+
L-5256	<i>Acinetobacter haemolyticus</i>	-	-	-	-	-	-	+	-	+	+
L-5279	<i>Acinetobacter haemolyticus</i>	-	-	-	-	-	-	+	-	+	+
L-5539	<i>Acinetobacter haemolyticus</i>	-	-	-	-	-	-	+	-	+	+
L-5559	<i>Acinetobacter haemolyticus</i>	-	-	-	-	-	-	+	-	+	+
L-5094	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5125	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5165	<i>Acinetobacter johnsonii</i>	-	-	-	+	-	-	+	+	+	+
L-5183	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5217	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5232	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5286	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5296	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5470	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5523	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5578	<i>Acinetobacter johnsonii</i>	-	-	-	-	-	-	+	-	-	+
L-5522	<i>Acinetobacter lwoffii</i>	-	-	-	-	-	-	-	-	-	+
L-5577	<i>Acinetobacter lwoffii</i>	-	-	-	-	-	-	+	-	-	+
L-5397	<i>Acinetobacter lwoffii/</i> <i>Prolinoborus fasciculus</i>	-	-	-	-	-	-	+	-	-	+
L-5401	<i>Acinetobacter lwoffii/</i> <i>Prolinoborus fasciculus</i>	-	-	-	-	-	-	+	-	-	+
L-5072	<i>Brevibacterium casei</i>	-	-	-	-	+	-	+	+	+	+

L-5181	<i>Kocuria uropygioeca</i>	-	-	-	-	-	-	-	+	+	+
L-5223	<i>Microbacterium lacus</i>	-	-	-	-	-	-	-	-	-	+
L-5587	<i>Microbacterium maritipicum</i>	-	-	-	+	-	-	-	-	+	+
L-5205	<i>Microbacterium paraoxydans</i>	-	-	-	+	-	+	+	-	+	+
L-5483	<i>Microbacterium paraoxydans</i>	-	-	-	+	-	+	+	-	+	+
L-5579	<i>Microbacterium paraoxydans</i>	-	-	-	-	-	-	+	-	+	+
L-5099	<i>Microbacterium testaceum</i>	-	-	-	-	-	-	-	+	+	+
L-5268	<i>Pantoea dispersa</i>	-	-	-	+	-	-	-	-	-	+
L-5292	<i>Pseudomonas aeruginosa</i>	+	+	+	+	+	+	+	-	-	+
L-5565	<i>Pseudomonas alcaligenes</i>	+	-	+	+	-	-	+	-	-	+
L-5243	<i>Pseudomonas chloritidismutans</i>	-	-	-	-	-	-	-	-	-	+
L-5293	<i>Pseudomonas chloritidismutans</i>	-	-	-	-	-	-	-	-	-	+
L-5344	<i>Pseudomonas chloritidismutans</i>	-	-	-	-	-	-	-	-	-	+
L-5521	<i>Pseudomonas chloritidismutans</i>	-	-	-	-	-	-	-	-	-	+
L-5527	<i>Pseudomonas koreensis</i>	+	-	-	+	+	-	+	-	-	+
L-5275	<i>Pseudomonas oryzihabitans</i>	-	-	-	-	-	-	-	-	-	+
L-5390	<i>Pseudomonas oryzihabitans</i>	-	-	-	+	-	-	+	+	-	+
L-5467	<i>Pseudomonas oryzihabitans</i>	-	-	-	+	-	-	+	-	-	+
L-5242	<i>Pseudomonas putida</i>	-	-	-	+	-	-	+	-	-	+
L-5474	<i>Pseudomonas putida</i>	+	-	-	+	-	-	+	-	-	+
L-5055	<i>Rothia amarae</i>	-	-	-	-	-	-	-	+	+	+
L-5204	<i>Rothia amarae</i>	-	-	-	-	-	-	-	+	+	+
L-5049	<i>Rothia kristinae</i>	-	-	-	-	-	-	-	+	+	+
L-5553	<i>Rothia kristinae</i>	-	-	-	-	-	-	-	+	+	+
L-5487	<i>Sphingobacterium cellulosum</i>	-	-	-	-	-	+	+	-	+	+

L-5469	<i>Sphingobacterium multivorum</i>	-	-	-	-	-	-	-	+	+	+
L-5488	<i>Sphingobacterium multivorum</i>	-	-	+	-	-	+	+	-	+	+
L-5177	<i>Sphingomonas paucimobilis</i>	-	-	-	-	-	-	-	-	+	+
L-5531	<i>Staphylococcus epidermidis</i>	-	-	-	+	-	-	-	-	+	+
L-5057	<i>Staphylococcus haemolyticus</i>	-	-	-	-	-	-	-	-	+	+
L-5207	<i>Staphylococcus haemolyticus</i>	-	-	-	+	-	-	-	-	+	+
L-5412	<i>Staphylococcus lentus</i>	-	-	-	-	-	-	+	-	+	+
L-5028	<i>Staphylococcus lugdunensis</i>	-	-	-	-	-	-	-	-	+	+
L-5076	<i>Stenotrophomonas maltophilia</i>	-	-	+	+	-	+	+	-	-	+
L-5250	<i>Stenotrophomonas maltophilia</i>	+	-	+	+	-	+	+	-	+	+
L-5259	<i>Stenotrophomonas maltophilia/ Pseudomonas hibiscicola</i>	-	-	+	+	-	+	+	-	-	+
L-5269	<i>Stenotrophomonas pavanii/ Stenotrophomonas maltophilia</i>	+	-	+	+	-	+	+	+	+	+