

PCRmax Ltd <sup>TM</sup> qPCR test

# **Serratia marcescens**

Porin (ompC) gene

150 tests



For general laboratory and research use only

# Introduction to *Serratia marcescens*

*Serratia marcescens* is a species of Gram-negative, rod-shaped bacterium that is a facultative anaerobe. *S. marcescens* is involved in nosocomial infections, particularly catheter-associated bacteremia, urinary tract infections and wound infections as well as respiratory tract infections of hospitalized adults and gastrointestinal system of children. The genome consists of a single circular chromosome 5.1Mb in size with a GC content of 59%. *Serratia marcescens* is motile and travels by several different means. A single *Serratia marcescens* bacterium can swim with the use of its flagellum. As a group they can swarm together on agar of lower concentrations (0.5-0.8%). The swarmer cells can range in length from 5-30  $\mu\text{m}$  and they are highly flagellated and nonseptated. *Serratia marcescens* have about 100 – 1000 flagella per swimmer cell.

*Serratia marcescens* is commonly found in soil, water, plants and animals. Although *S. marcescens* is a pathogenic microorganism, it is only so with immunocompromised individuals such as those found in hospitals where many of the documented infections take place. The mode of transmission of this microorganism is by either direct contact, or by catheters, droplets, saline irrigation solutions, and other solutions that are believed to be sterile. *Serratia* infects the bloodstream, lower respiratory tract, urinary tract, surgical wounds, and skin and soft tissues in adult patients. Outbreaks of *S. marcescens* meningitis, wound infections, and arthritis have occurred in pediatric wards. A lipopolysaccharides (LPS) layer is attached to the outer membrane of the Gram negative bacteria. The LPS acts as an endotoxin. The release of LPS would over-stimulate the host defenses and cause them to undergo lethal endotoxic shock. The presence of LPS therefore makes it difficult to kill *Serratia marcescens* without causing the death of the host's cells. The ability of the pathogen to form a biofilm also makes treatment difficult.

Normally, *Serratia marcescens* causes generic infections in wound sites, as well as the urinary tract, respiratory system and eyes. For a urinary tract infection, the symptoms might include itching, burning discharge, and pain in the kidneys. Symptoms of respiratory infection include sore throat and nasal and chest congestion. At its most severe, *Serratia marcescens* can cause pneumonia, meningitis, arthritis and other serious illnesses.

# Specificity

The PCR Max qPCR Kit for *Serratia marcescens* (*S.marcescens*) genomes is designed for the in vitro quantification of *S.marcescens* genomes. The kit is designed to have the broadest detection profile possible whilst remaining specific to the *S.marcescens* genome.

The primers and probe sequences in this kit have 100% homology with a broad range of *S.marcescens* sequences based on a comprehensive bioinformatics analysis.

If you require further information, or have a specific question about the detection profile of this kit then please send an e.mail to [CPtechsupport@coleparmer.com](mailto:CPtechsupport@coleparmer.com) and our bioinformatics team will answer your question.

## Kit contents

- **S.marcescens specific primer/probe mix (150 reactions BROWN)**  
FAM labelled
- **S.marcescens positive control template (for Standard curve RED)**
- **Internal extraction control primer/probe mix (150 reactions BROWN)**  
VIC labelled as standard
- **Internal extraction control DNA (150 reactions BLUE)**
- **Endogenous control primer/probe mix (150 reactions BROWN)**  
FAM labelled
- **RNase/DNase free water (WHITE)**  
for resuspension of primer/probe mixes
- **Template preparation buffer (YELLOW)**  
for resuspension of and internal extraction control template, positive control template and standard curve preparation

## Reagents and equipment to be supplied by the user

### Real-time PCR Instrument

#### DNA extraction kit

This kit is designed to work well with all processes that yield high quality DNA with minimal PCR inhibitors.

#### Lyophilised 2X qPCR Master Mix

This kit is designed to be compatible with all commercially available master mixes that run with standard cycling conditions.

#### Pipettors and Tips

#### Vortex and centrifuge

#### Thin walled 1.5 ml PCR reaction tubes

## Kit storage and stability

This kit is stable at room temperature but should be stored at -20°C on arrival. Once the lyophilised components have been resuspended they should not be exposed to temperatures above -20°C for longer than 30 minutes and unnecessary repeated freeze/thawing should be avoided. The kit is stable for six months from the date of resuspension under these circumstances.

If a standard curve dilution series is prepared this can be stored frozen for an extended period. If you see any degradation in this serial dilution a fresh standard curve can be prepared from the positive control.

PCRmax does not recommend using the kit after the expiry date stated on the pack.

## Suitable sample material

All kinds of sample material suited for PCR amplification can be used. Please ensure the samples are suitable in terms of purity, concentration, and DNA integrity (An internal PCR control is supplied to test for non specific PCR inhibitors). Always run at least one negative control with the samples. To prepare a negative-control, replace the template DNA sample with RNase/DNase free water.

## Dynamic range of test

Under optimal PCR conditions PCRmax *S.marcescens* detection kits have very high priming efficiencies of >95% and can detect less than 100 copies of target template.

## Notices and disclaimers

This product is developed, designed and sold for research purposes only. It is not intended for human diagnostic or drug purposes or to be administered to humans unless clearly expressed for that purpose by the Food and Drug Administration in the USA or the appropriate regulatory authorities in the country of use. During the warranty period Master Mix detection kits allow precise and reproducible data recovery combined with excellent sensitivity. For data obtained by violation to the general GLP guidelines and the manufacturer's recommendations the right to claim under guarantee is expired. PCR is a proprietary technology covered by several US and foreign patents. These patents are owned by Roche Molecular Systems Inc. and have been sub-licensed by PE Corporation in certain fields. Depending on your specific application you may need a license from Roche or PE to practice PCR. Additional information on purchasing licenses to practice the PCR process may be obtained by contacting the Director of Licensing at Roche Molecular Systems, 1145 Atlantic Avenue, Alameda, CA 94501 or Applied Biosystems business group of the Applied Biosystems Corporation, 850 Lincoln Centre Drive, Foster City, CA 94404. In addition, the 5' nuclease assay and other homogeneous amplification methods used in connection with the PCR process may be covered by U.S. Patents 5,210,015 and 5,487,972, owned by Roche Molecular Systems, Inc, and by U.S. Patent 5,538,848, owned by The Perkin-Elmer Corporation.

## Trademarks

Master Mix™ is a trademark of Cole-Parmer Ltd.

The PCR process is covered by US Patents 4,683,195, and 4,683,202 and foreign equivalents owned by Hoffmann-La Roche AG. BI, ABI PRISM®, GeneAmp® and MicroAmp® are registered trademarks of the Applied Biosystems (Applied Biosystems Corporation). BIOMEK® is a registered trademark of Beckman Instruments, Inc.; iCycler™ is a registered trademark of Bio-Rad Laboratories, Rotor-Gene is a trademark of Corbett Research. LightCycler™ is a registered trademark of the Idaho Technology Inc. GeneAmp®, TaqMan® and AmpliTaqGold® are registered trademarks of Roche Molecular Systems, Inc., The purchase of the Master Mix reagents cannot be construed as an authorization or implicit license to practice PCR under any patents held by Hoffmann-LaRoche Inc.

# Principles of the test

## Real-time PCR

A *S.marcescens* specific primer and probe mix is provided and this can be detected through the FAM channel.

The primer and probe mix provided exploits the so-called TaqMan® principle. During PCR amplification, forward and reverse primers hybridize to the *S.marcescens* DNA. A fluorogenic probe is included in the same reaction mixture which consists of a DNA probe labeled with a 5`-dye and a 3`-quencher. During PCR amplification, the probe is cleaved and the reporter dye and quencher are separated. The resulting increase in fluorescence can be detected on a range of real-time PCR platforms.

## Positive control

For copy number determination and as a positive control for the PCR set up, the kit contains a positive control template. This can be used to generate a standard curve of *S. marcescens* copy number / Cq value. Alternatively the positive control can be used at a single dilution where full quantitative analysis of the samples is not required. Each time the kit is used, at least one positive control reaction must be included in the run. A positive result indicates that the primers and probes for detecting the target *S.marcescens* gene worked properly in that particular experimental scenario. If a negative result is obtained the test results are invalid and must be repeated. Care should be taken to ensure that the positive control does not contaminate any other kit component which would lead to false-positive results. This can be achieved by handling this component in a Post PCR environment. Care should also be taken to avoid cross-contamination of other samples when adding the positive control to the run. This can be avoided by sealing all other samples and negative controls before pipetting the positive control into the positive control well.

## Negative control

To validate any positive findings a negative control reaction should be included every time the kit is used. For this reaction the RNase/DNase free water should be used instead of template. A negative result indicates that the reagents have not become contaminated while setting up the run.

### **Internal DNA extraction control**

When performing DNA extraction, it is often advantageous to have an exogenous source of DNA template that is spiked into the lysis buffer. This control DNA is then co-purified with the sample DNA and can be detected as a positive control for the extraction process. Successful co-purification and real-time PCR for the control DNA also indicates that PCR inhibitors are not present at a high concentration.

A separate primer and probe mix are supplied with this kit to detect the exogenous DNA using real-time PCR. The primers are present at PCR limiting concentrations which allows multiplexing with the target sequence primers. Amplification of the control DNA does not interfere with detection of the *S.marcescens* target DNA even when present at low copy number. The Internal control is detected through the VIC channel and gives a Cq value of 28+/-3.

### **Endogenous control**

To confirm extraction of a valid biological template, a primer and probe mix is included to detect an endogenous gene. Detection of the endogenous control is through the FAM channel and it is NOT therefore possible to perform a multiplex with the *S.marcescens* primers. A poor endogenous control signal may indicate that the sample did not contain sufficient biological material.

# Resuspension Protocol

To minimize the risk of contamination with foreign DNA, we recommend that all pipetting be performed in a PCR clean environment. Ideally this would be a designated PCR lab or PCR cabinet. Filter tips are recommended for all pipetting steps.

- 1. Pulse-spin each tube in a centrifuge before opening.**  
This will ensure lyophilised primer and probe mix is in the base of the tube and is not spilt upon opening the tube.
- 2. Resuspend the primer/probe mixes in the RNase/DNase free water supplied, according to the table below:**  
To ensure complete resuspension, vortex each tube thoroughly.

Component - resuspend in water	Volume
<b>Pre-PCR pack</b>	
S.marcescens primer/probe mix (BROWN)	165 µl
Internal extraction control primer/probe mix (BROWN)	165 µl
Endogenous control primer/probe mix (BROWN)	165 µl

- 3. Resuspend the internal control template and positive control template in the template preparation buffer supplied, according to the table below:**  
To ensure complete resuspension, vortex the tube thoroughly.

Component - resuspend in template preparation buffer	Volume
<b>Pre-PCR heat-sealed foil</b>	
Internal extraction control DNA (BLUE)	600 µl
<b>Post-PCR heat-sealed foil</b>	
S.marcescens Positive Control Template (RED) *	500 µl

\* This component contains high copy number template and is a VERY significant contamination risk. It must be opened and handled in a separate laboratory environment, away from the other components.

## DNA extraction

The internal extraction control DNA can be added either to the DNA lysis/extraction buffer or to the DNA sample once it has been resuspended in lysis buffer.

**DO NOT add the internal extraction control DNA directly to the unprocessed biological sample as this will lead to degradation and a loss in signal.**

- 1. Add 4µl of the Internal extraction control DNA (BLUE) to each sample in DNA lysis/extraction buffer per sample.**
- 2. Complete DNA extraction according to the manufacturers protocols.**



# qPCR detection protocol

1. **For each DNA sample prepare a reaction mix according to the table below:**  
Include sufficient reactions for positive and negative controls.

Component	Volume
Lyophilised 2X qPCR Master Mix	10 $\mu$ l
S.marcescens primer/probe mix (BROWN)	1 $\mu$ l
Internal extraction control primer/probe mix (BROWN)	1 $\mu$ l
RNase/DNase free water (WHITE)	3 $\mu$ l
<b>Final Volume</b>	<b>15 <math>\mu</math>l</b>

2. **For each DNA sample prepare an endogenous control reaction according to the table below (Optional):**  
This control reaction will provide crucial information regarding the quality of the biological sample.

Component	Volume
Lyophilised 2X qPCR Master Mix	10 $\mu$ l
Endogenous control primer/probe mix (BROWN)	1 $\mu$ l
RNase/DNase free water (WHITE)	4 $\mu$ l
<b>Final Volume</b>	<b>15 <math>\mu</math>l</b>

3. **Pipette 15 $\mu$ l of each mix into individual wells according to your real-time PCR experimental plate set up.**
4. **Prepare sample DNA templates for each of your samples.**
5. **Pipette 5 $\mu$ l of DNA template into each well, according to your experimental plate set up.**  
For negative control wells use 5 $\mu$ l of RNase/DNase free water. The final volume in each well is 20 $\mu$ l.
6. **If a standard curve is included for quantitative analysis prepare a reaction mix according to the table below:**

Component	Volume
Lyophilised 2X qPCR Master Mix	10 $\mu$ l
S.marcescens primer/probe mix (BROWN)	1 $\mu$ l
RNase/DNase free water (WHITE)	4 $\mu$ l
<b>Final Volume</b>	<b>15 <math>\mu</math>l</b>

## 7. Preparation of standard curve dilution series.

- 1) Pipette 90µl of template preparation buffer into 5 tubes and label 2-6
- 2) Pipette 10µl of Positive Control Template (RED) into tube 2
- 3) Vortex thoroughly
- 4) Change pipette tip and pipette 10µl from tube 2 into tube 3
- 5) Vortex thoroughly

Repeat steps 4 and 5 to complete the dilution series

Standard Curve	Copy Number
Tube 1 Positive control (RED)	$2 \times 10^5$ per µl
Tube 2	$2 \times 10^4$ per µl
Tube 3	$2 \times 10^3$ per µl
Tube 4	$2 \times 10^2$ per µl
Tube 5	20 per µl
Tube 6	2 per µl

## 8. Pipette 5µl of standard template into each well for the standard curve according to your experimental plate set up.

The final volume in each well is 20µl.

## qPCR amplification protocol

Amplification conditions using Lyophilised 2X qPCR Master Mix.

	Step	Time	Temp
	Enzyme activation	2 min	95 °C
Cycling x50	Denaturation	10 s	95 °C
	DATA COLLECTION *	60 s	60 °C

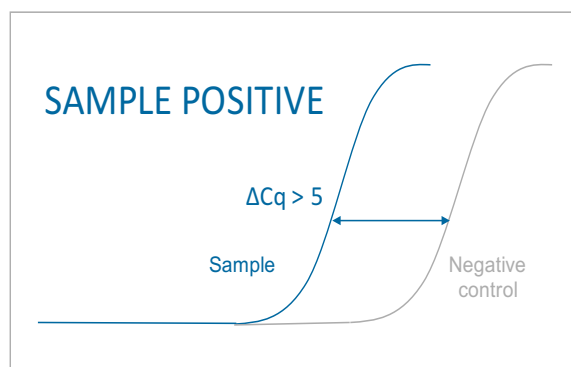
\* Fluorogenic data should be collected during this step through the FAM and VIC channels

# Interpretation of Results

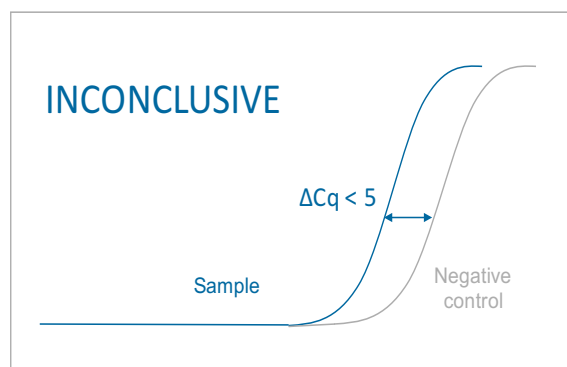
Target (FAM)	Internal control (VIC)	Positive control	Negative control	Interpretation
$\leq 30$	+ / -	+	-	<b>POSITIVE QUANTITATIVE RESULT</b> calculate copy number
$> 30$	+	+	-	<b>POSITIVE QUANTITATIVE RESULT</b> calculate copy number
$> 30$	-	+	-	<b>POSITIVE QUALITATIVE RESULT</b> do not report copy number as this may be due to poor sample extraction
-	+	+	-	<b>NEGATIVE RESULT</b>
+ / -	+ / -	+	$\leq 35$	<b>EXPERIMENT FAILED</b> due to test contamination
+ / -	+ / -	+	$> 35$	*
-	-	+	-	<b>SAMPLE PREPARATION FAILED</b>
+ / -	+ / -	-	+ / -	<b>EXPERIMENT FAILED</b>

Positive control template (RED) is expected to amplify between Cq 16 and 23. Failure to satisfy this quality control criterion is a strong indication that the experiment has been compromised.

\*Where the test sample is positive and the negative control is positive with a Cq  $> 35$ , the sample must be reinterpreted based on the relative signal strength of the two results:



If the sample amplifies  $> 5$  Cq earlier than the negative control then the sample should be reinterpreted (via the table above) with the negative control verified as negative.



If the sample amplifies  $< 5$  Cq earlier than the negative control then the positive sample result is invalidated and the result should be determined inconclusive due to test contamination. The test for this sample should be repeated.

**Internal PCR control**

The C<sub>q</sub> value obtained with the internal control will vary significantly depending on the extraction efficiency, the quantity of DNA added to the PCR reaction and the individual machine settings. C<sub>q</sub> values of 28±3 are within the normal range. When amplifying a *S. marcescens* sample with a high genome copy number, the internal extraction control may not produce an amplification plot. This does not invalidate the test and should be interpreted as a positive experimental result.

**Endogenous control**

The signal obtained from the endogenous control primer and probe set will vary according to the amount of biological material present in a given sample. An early signal indicates the presence of a good yield of biological material. A late signal suggests that little biological material is present in the sample.