

Primerdesign™ Ltd

# Tannerella forsythia

## Heat shock protein 60 gene (hsp60 gene)

### genesig® Standard Kit

150 tests

G E N E S I G

Kits by Primerdesign

For general laboratory and research use only

# Introduction to *Tannerella forsythia*

*Tannerella Forsythia*, formerly known as *Bacteroides forsythus*, is a fusiform, fastidious, anaerobic, Gram-negative organism that resides in the deep periodontal pockets of humans. It belongs to the genus *Bacteroides* and forms a part of the oral microbiota. It is covered by a crystalline surface (S-layer) which is a 6-nm thick, closed, monolayer that is formed by co-assembly of the two S-layer glycoproteins. This organism is synergistic with *Porphyromonas gingivalis*, and the presence of both accelerates progression of the disease. Pathogenic factors include a trypsin-like protease (PrtH) and a variety of glycosidases. Other virulence factors include the cell surface adhesin, BspA, that mediates adherence to fibronectin and other extracellular matrix components. The genome is approximately 3405 kb long and contains 3034 predicted open reading frames.

Proteolytic enzymes in *Tannerella Forsythia* are responsible for degradation of host proteins, providing essential amino acids, peptides and haem for growth. They contribute to the bacterial virulence in a number of ways such as by degrading host periodontal tissues, activating host degradative enzymes, modifying host cell proteins to expose cryptotopes for bacterial colonization, cleaving components involved in innate and adaptive immunity and activating components involved in clotting/fibrinolysis. They have the ability to induce apoptosis and invade the periodontal pocket along with *P.gingivalis*, attacking the host's white blood cells. The induction of host cell apoptosis results in the elimination of host immune cells which further supports the bacterial colonization of the periodontal pockets. *T. forsythia* is generally sensitive to antibiotics that are active against anaerobes.

Periodontitis is the disruption of connective tissue attachment along with the adjacent alveolar bone. Some symptoms include development of new spaces between the teeth, change in the manner that the teeth fit together when biting and swelling of the gums. Periodontitis is significantly correlated with an overgrowth of a large number of anaerobic bacteria so this disease can be suppressed by good oral hygiene and by utilizing antimicrobial agents that target the participating anaerobes.

# Specificity

The Primerdesign genesig Kit for *Tannerella forsythia* (*T.forsythia*) genomes is designed for the in vitro quantification of *T.forsythia* genomes. The kit is designed to have a broad detection profile. Specifically, the primers represent 100% homology with over 95% of the NCBI database reference sequences available at the time of design.

The dynamics of genetic variation means that new sequence information may become available after the initial design. Primerdesign periodically reviews the detection profiles of our kits and when required releases new versions.

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

# Kit contents

- **T.forsythia specific primer/probe mix (150 reactions BROWN)**  
FAM labelled
- **T.forsythia positive control template (for Standard curve RED)**
- **RNase/DNase free water (WHITE)**  
for resuspension of primer/probe mixes
- **Template preparation buffer (YELLOW)**  
for resuspension of positive control template and standard curve preparation

## Reagents and equipment to be supplied by the user

### Real-time PCR Instrument

### Extraction kit

This kit is recommended for use with genesig Easy DNA/RNA extraction kit. However, it is designed to work well with all processes that yield high quality RNA and DNA with minimal PCR inhibitors.

### oasig™ lyophilised or Precision®PLUS 2X qPCR Master Mix

This kit is intended for use with oasig or PrecisionPLUS 2X qPCR Master Mix.

### 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 at a time 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.

Primerdesign 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. 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 genesig T.forsythia 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 Primerdesign genesig 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 Applera 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

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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 Applera Genomics (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 Primerdesign 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 *T.forsythia* 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 *T.forsythia* 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 qPCR 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 *T.forsythia* 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 *T.forsythia* 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.

# 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 kit components 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>	
T.forsythia primer/probe mix (BROWN)	165 µl

## 3. Resuspend the 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>Post-PCR heat-sealed foil</b>	
T.forsythia 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.

# 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
oasis or PrecisionPLUS 2X qPCR Master Mix	10 µl
T.forsythia primer/probe mix (BROWN)	1 µl
RNase/DNase free water (WHITE)	4 µl
<b>Final Volume</b>	<b>15 µl</b>

2. Pipette 15µl of this mix into each well according to your qPCR experimental plate set up.
3. Prepare DNA templates for each of your samples.
4. Pipette 5µl of DNA template into each well, according to your experimental plate set up.  
For negative control wells use 5µl of RNase/DNase free water. The final volume in each well is 20µl.
5. If a standard curve is included for quantitative analysis, prepare a reaction mix according to the table below:

Component	Volume
oasis or PrecisionPLUS 2X qPCR Master Mix	10 µl
T.forsythia primer/probe mix (BROWN)	1 µl
RNase/DNase free water (WHITE)	4 µl
<b>Final Volume</b>	<b>15 µl</b>

## 6. Preparation of a standard curve dilution series.

- 1) Pipette 90 $\mu$ l of template preparation buffer into 5 tubes and label 2-6
- 2) Pipette 10 $\mu$ l of Positive Control Template (**RED**) into tube 2
- 3) Vortex thoroughly
- 4) Change pipette tip and pipette 10 $\mu$ l 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 ( <b>RED</b> )	$2 \times 10^5$ per $\mu$ l
Tube 2	$2 \times 10^4$ per $\mu$ l
Tube 3	$2 \times 10^3$ per $\mu$ l
Tube 4	$2 \times 10^2$ per $\mu$ l
Tube 5	20 per $\mu$ l
Tube 6	2 per $\mu$ l

7. Pipette 5 $\mu$ l of standard template into each well for the standard curve according to your experimental plate set up.  
The final volume in each well is 20 $\mu$ l.

## qPCR amplification protocol

Amplification conditions using oasisig or PrecisionPLUS 2X qPCR Master Mix.

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

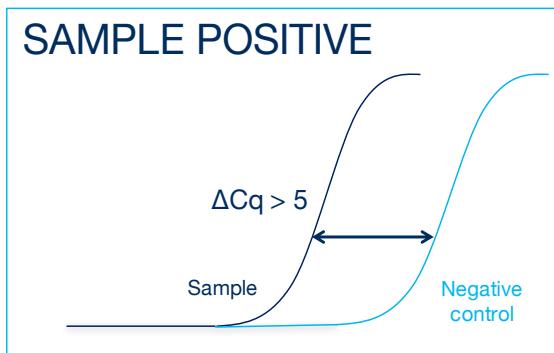
\* Fluorogenic data should be collected during this step through the FAM channel

# Interpretation of results

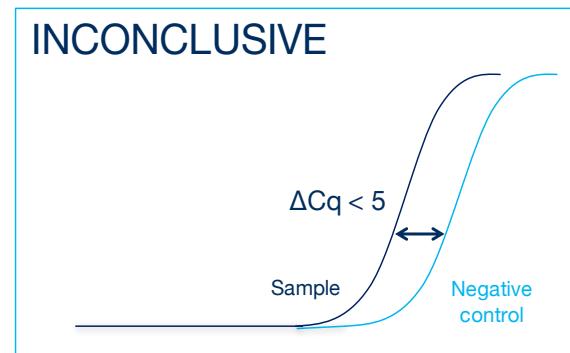
Target	Positive control	Negative control	Interpretation
+	+	-	<b>POSITIVE QUANTITATIVE RESULT</b> calculate copy number
-	+	-	<b>NEGATIVE RESULT</b>
+ / -	+	$\leq 35$	<b>EXPERIMENT FAILED</b> due to test contamination
+ / -	+	$> 35$	*
+ / -	-	+ / -	<b>EXPERIMENT FAILED</b>

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.