

Primerdesign™ Ltd

# Brucella genus (all species)

L-glutamine: 2-deoxy-scyllo-inosose amino-transferase

genesig® Standard Kit

150 tests

GENESIG

Kits by Primerdesign

For general laboratory and research use only

# Introduction to Brucella genus (all species)

The Brucella genus is a genus of Gram-negative, non-motile bacteria that are rod shaped. Species within this genus cause Brucellosis in many species of mammals. Brucella species have a genome of around 3.2M nucleotides in length split over two circular chromosomes.

All Brucella species cause infections in specific animal groups that lead to similar diseases. Differences between the bacterium within this genus can be found in genes coding for surface exposed proteins. *B. suis* infects swine, whereas *B. melitensis* infects goats and camels *B. canis* infects dogs. Cattle are mainly infected by *B. abortus*, with *B. ovis* infecting sheep and *B. pinnipediae* recently thought to infect marine mammals. These bacterial species cause male infertility resulting from orchitis and epididymitis and may also cause abortion in females due to endometritis and placentitis.

These bacteria are also capable of infecting humans and can be transmitted via inhalation of infected animal waste products, direct contact with open wounds or ingestion of contaminated food substances such as un-pasteurised milk. In humans, Brucella infection can result in headache, fatigue, fever, sweating, weight loss and muscle pain. The human infection can be treated by a course of antibiotics in combination to prevent symptoms.

# Specificity

The Primerdesign genesig Kit for Brucella genus (all species) (Brucella\_spp) genomes is designed for the in vitro quantification of Brucella\_spp 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.

The primers have 100% homology with over 95% of Brucella reference sequences included in the NCBI database and therefore have a very broad detection profile (CP001488.1, AE008917.1, P000887.1, CP000911.1, CP000872.1, CP000708.1, AE014291.4AF047478.1, AM040264.1, AE017223.1).

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

- **Brucella\_spp specific primer/probe mix (150 reactions BROWN)**  
FAM labelled
- **Brucella\_spp 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 Brucella\_spp 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 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

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# Principles of the test

## Real-time PCR

A *Brucella\_spp* 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 *Brucella\_spp* 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 *Brucella\_spp* 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 *Brucella\_spp* 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>                   |        |
| Brucella_spp 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>                     |        |
| Brucella_spp 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                      |
|---|-----------------------------|
| oasig or PrecisionPLUS 2X qPCR Master Mix | 10 $\mu$ l                  |
| Brucella_spp 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> |

- 2. Pipette 15 $\mu$ l 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 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.
- 5. If a standard curve is included for quantitative analysis, prepare a reaction mix according to the table below:**

| Component                                 | Volume                      |
|---|-----------------------------|
| oasig or PrecisionPLUS 2X qPCR Master Mix | 10 $\mu$ l                  |
| Brucella_spp 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> |



## 6. Preparation of a 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               |

7. 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 oasis 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><br>calculate copy number |
| -      | +                | -                | <b>NEGATIVE RESULT</b>                                       |
| + / -  | +                | $\leq 35$        | <b>EXPERIMENT FAILED</b><br>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.