Overview

Useful For
Detecting and identifying bacteria (including mycobacteria) from normally sterile sources, including synovial fluid; body fluids such as pleural, peritoneal, and pericardial fluids, cerebrospinal fluid; and both fresh and formalin-fixed paraffin-embedded tissues

This test is **not recommended** as a test of cure because nucleic acids may persist for long periods of time after successful treatment.

Testing Algorithm
If polymerase chain reaction (PCR) testing is negative, no sequencing is performed, and the test is resulted as negative.

If PCR testing is positive, sequencing is performed. Strong positive results are first submitted to Sanger sequencing, which can yield results in as few as 4 days. Weak positive results, or Sanger sequencing results that are mixed, are submitted to next-generation sequencing (ie, targeted metagenomics testing).

The following algorithms are available in Special Instructions:

- Infective Endocarditis: Diagnostic Testing for Identification of Microbiological Etiology
- Meningitis/Encephalitis Panel Algorithm

Special Instructions
- Infective Endocarditis: Diagnostic Testing for Identification of Microbiological Etiology
- Meningitis/Encephalitis Panel Algorithm

Highlights
This test is used for detection and identification of bacteria (including mycobacteria) in normally sterile specimens.

This test is optimal for situations in which bacteria (including mycobacteria) are visualized in the specimen but other laboratory methods have failed to yield a diagnosis.

Reflex Tests

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<th>Test Id</th>
<th>Reporting Name</th>
<th>Available Separately</th>
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Document generated May 10, 2022 at 06:29 AM
**Test Definition: BRBPS**  
Broad Range Bacteria PCR+Sequencing

<table>
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<tr>
<th>Method Name</th>
<th>Bacterial Ident by Sequencing</th>
<th>Ident by Next Generation Sequencing</th>
<th>Specimen Identification by PCR</th>
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**Method Name**  
16S Ribosomal RNA Gene Polymerase Chain Reaction (PCR) followed by Sequencing

**NY State Available**  
Yes

**Specimen**

**Specimen Type**  
Varies

**Necessary Information**  
Specimen source is required.

**Specimen Required**  
Fresh tissue is preferred over formalin-fixed, paraffin-embedded tissue.

Submit only 1 of the following specimens:

**Preferred Specimen Type:**

**Specimen Type:** Fresh tissue or biopsy

**Sources:** Normally sterile tissue such as bone, lymph node, joint, heart valve, brain, viscera, organ, lung

**Container/Tube:** Sterile container

**Specimen Volume:** Entire collection or 5 mm(3)-approximately the size of a pencil eraser

**Collection Instructions:**
1. Collect fresh tissue specimen.

2. Submit tissue only, do not add fluid to tissue.

3. Freeze specimen.

**Specimen Stability Information:** Frozen <14 days (preferred)/Refrigerated <14 days

**Alternate Specimen Type:**

**Preferred: Paraffin-embedded tissue block:**

**Supplies:** Tissue Block Container (T553)

**Specimen Type:** Formalin-fixed, paraffin-embedded (FFPE) tissue block

**Sources:** Normally sterile or deep tissues such as bone, lymph node, joint, heart valve, brain, viscera, organ, lung

**Container/Tube:** Tissue block

**Collection Instructions:** Submit a formalin-fixed, paraffin-embedded tissue block to be cut and returned.

**Specimen Stability Information:** Ambient (preferred)/Refrigerated

**Acceptable: Paraffin-embedded tissue block:**

**Specimen Type:** Section (scrolls) of FFPE tissue block

**Sources:** Normally sterile or deep tissues such as bone, lymph node, joint, heart valve, brain, viscera, organ, lung

**Container/Tube:** Sterile container for each individual cut section (scroll)

**Collection Instructions:** Perform microtomy and prepare five separate 10-micron sections. **Each section (scroll) must be placed in a separate sterile container for submission.**

**Specimen Stability Information:** Ambient (preferred)/Refrigerated

**Specimen Type:** Fluid

**Sources:** Normally sterile body fluids such as cerebrospinal, vitreous humor, pleural, abdominal, peritoneal, ascites, pericardial, pelvic
**Test Definition: BRBPS**

Broad Range Bacteria PCR+Sequencing

**Container/Tube:** Screw-capped, sterile container

**Specimen Volume:** 1 mL

**Collection Instructions:**

1. Collect fresh fluid specimen.

2. Freeze specimen.

**Specimen Stability Information:** Frozen <14 days (preferred)/Refrigerated <14 days

**Specimen Type:** Synovial fluid

**Container/Tube:**

**Preferred:** Red top or sterile container

**Acceptable:** Lavender top (EDTA), pink top (EDTA), royal blue top (EDTA), or sterile vial containing EDTA-derived aliquot

**Specimen Volume:** 1 mL

**Collection Instructions:** Send specimen in original tube (preferred).

**Specimen Stability Information:** Frozen <14 days (preferred)/Refrigerated <14 days

**Forms**

If not ordering electronically, complete, print, and send a Microbiology Test Request (T244) with the specimen.

**Reject Due To**

- Tissue in formalin, formaldehyde, acetone, or any other fluid
- Bone marrow
- Decalcified bone
- Slides
- Skin biopsy
- Colon biopsy

**Specimen Minimum Volume**

Fluid: 0.5 mL

Fresh tissue or biopsy: 5 mm(3)

Paraffin-embedded tissue block: two 10-micron sections

**Specimen Stability Information**
**Clinical Information**

Cultures from patients with suspected bacterial infection involving normally sterile sites may fail to provide bacterial (including mycobacterial) growth for identification due to the presence of fastidious or slow-growing bacteria or as a result of antecedent antimicrobial chemotherapy. Polymerase chain reaction amplification of a portion of the 16S ribosomal RNA (rRNA) gene followed by sequencing of the amplified product can be used to detect bacterial (including mycobacterial) nucleic acids in such situations, enabling a diagnosis. Sterile sources accepted for testing may have more than one bacterial species present or the presence of copy variants of the 16S rRNA gene within a single bacterial species, confounding Sanger sequencing analysis. Next-generation sequencing can be useful in such cases. Ideal specimens are those in which bacteria (includes mycobacteria) are visualized by microscopy. Heart valves from patients with endocarditis with positive Gram stains are, for example, especially suitable.

**Reference Values**

No bacterial DNA detected

**Interpretation**

A positive broad-range polymerase chain reaction (PCR)/sequencing result indicates that bacterial nucleic acid of the specified organism was detected, which may be due to bacterial infection or environmental or contaminating nucleic acids in the specimen.

A negative broad-range PCR/sequencing result indicates the absence of detectable bacterial (including mycobacterial) nucleic acids in the specimen but does not rule-out false-negative results that may occur due to sampling error, sequence variability underlying the primers, the presence of bacterial nucleic acids in quantities less than the limit of detection of the assay, or inhibition of PCR. If PCR testing appears to be negative but there is evidence of PCR inhibition, testing will be repeated. If inhibition is again detected, the result will be reported as "PCR inhibition present."

**Cautions**

This test does not detect nonbacterial organisms (eg, viruses, fungi, helminths, protozoa), but does detect mycobacteria. False-positive results are theoretically possible if patient specimens are contaminated with bacterial nucleic acids either from the environment or from patient microbiota (eg, skin microbiota contamination).

This test is validated for normally sterile sources.
In extenuating circumstances, sequencing, especially next-generation sequencing, may be associated with an extended turnaround time, approaching or possibly exceeding the published maximum laboratory time (28 days).

**Supportive Data**

One hundred thirty positive patient specimens were available for accuracy studies and correlated with results of culture, organism-specific polymerase chain reaction (PCR), or previous broad-range bacterial PCR and sequencing. In addition, 63 negative samples from previous Sanger sequence-based testing were used in verification. All samples were tested with both Sanger and next-generation sequencing (NGS) technologies enabling resolution of poor-quality Sanger results and identifying polybacterial presence in some samples. Using criteria established in verification, sensitivity of the assay is 99% and specificity is 97%. Some samples were spiked with gram-negative or gram-positive bacteria due to the scarcity of clinically positive samples. Testing demonstrated 100% correlation with expected results from spiked material.

The limit of detection was less than 65 colony forming units per PCR reaction for all sources as determined by spiking *Streptococcus gallolyticus* and *Escherichia coli* into PCR-negative fresh tissue, synovial fluid, formalin-fixed, paraffin-embedded tissue, sonicate fluid, body fluid, and cerebrospinal fluid.

Specificity was tested using a panel of 10 nucleic acid extracts from viral, fungal, and parasitic organisms. No cross-reactivity to these organisms was observed.

Inclusivity studies were performed by amplifying 42 genomic DNA samples representing diverse types of bacteria (including mycobacteria) expected to be present in the specimen types acceptable for this assay. All bacteria and mycobacteria were detected and correctly identified by both Sanger and NGS.

An additional study of 15 specimens previously characterized only as polybacterial revealed the ability of NGS to detect and differentiate multiple bacteria for reporting. The laboratory section director is responsible for reporting of polybacterial results.

**Clinical Reference**


**Performance**

**Method Description**

This test utilizes specimen processing, DNA extraction, and polymerase chain reaction (PCR) of a highly variable fragment of the 16S ribosomal RNA (rRNA) gene. The variability of the targeted V1-V3 region allows for taxonomically specific reporting. If positive by PCR based on signal strength, the amplified DNA is sequenced to obtain identification of the source organism. If PCR is negative, no sequencing is performed. PCR inhibition is detected with a second PCR reaction and amplification is performed on a LightCycler. Only high-quality consensus sequence of 400 base pairs or more (usable data for both forward and reverse direction) is used for Sanger sequencing identification. If sequence data is not interpretable using Sanger sequencing, next-generation sequencing (NGS) is performed. Quality filtering is performed for NGS and only results with 100X coverage are used in analysis. Positive and negative controls are used throughout all processes to ensure assay performance. Sequence quality (specimen score) and data analysis for organism identification is accomplished with Pathogenomix RipSeq software.(Unpublished Mayo method)

**PDF Report**

No

**Specimen Retention Time**

1 week

**Performing Laboratory Location**

Rochester

**Fees & Codes**

**Test Classification**

This test was developed, and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the US Food and Drug Administration.
Test Definition: BRBPS
Broad Range Bacteria PCR+Sequencing

CPT Code Information
87801-Broad Range Bacterial PCR and Sequencing
87798-Bacterial Idnt by Sequencing (if appropriate)
87798-Specimen Identification by PCR (if appropriate)
87798-Ident by Next Generation Sequencing (if appropriate)
87483-Meningitis Encephalitis Panel, PCR (if appropriate)

LOINC® Information

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