Overview

Useful For
Aiding in the investigation of a potential outbreak by a single bacterial species
May assist in identification of recurrent infection in an individual patient

Reflex Tests

<table>
<thead>
<tr>
<th>Test ID</th>
<th>Reporting Name</th>
<th>Available Separately</th>
<th>Always Performed</th>
</tr>
</thead>
<tbody>
<tr>
<td>BIORE</td>
<td>Bioinformatics Reanalysis</td>
<td>No, (Bill Only)</td>
<td>No</td>
</tr>
<tr>
<td>RMALD</td>
<td>Ident by MALDI-TOF mass spec</td>
<td>No, (Bill Only)</td>
<td>No</td>
</tr>
<tr>
<td>ISAE</td>
<td>Aerobe Ident by Sequencing</td>
<td>No, (Bill Only)</td>
<td>No</td>
</tr>
<tr>
<td>REFID</td>
<td>Additional Identification Procedure</td>
<td>No, (Bill Only)</td>
<td>No</td>
</tr>
<tr>
<td>RMALA</td>
<td>Id MALDI-TOF Mass Spec Anaerobe</td>
<td>No, (Bill Only)</td>
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<tr>
<td>ANAID</td>
<td>Anaerobe Ident</td>
<td>No, (Bill Only)</td>
<td>No</td>
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<tr>
<td>ISAN</td>
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<td>No, (Bill Only)</td>
<td>No</td>
</tr>
</tbody>
</table>

Testing Algorithm
Organism identification is required. All bacteria submitted will be tested. Organism identifications that are incorrect or incomplete may result in no results at final analysis. Laboratory may perform matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) or other testing as listed in Reflex Tests to confirm identification, report this finding, and charge accordingly.

When reanalysis of previously submitted isolates for comparison to new isolates is requested, bioinformatics reanalysis will be added by Mayo Clinic Laboratories. Original patient submission information (names and order numbers) must be provided.

Special Instructions
- Infectious Specimen Shipping Guidelines

Method Name
Whole Genome Sequencing

NY State Available
No

Specimen

Specimen Type
**Advisory Information**

Currently, *Acinetobacter baumannii*, *Campylobacter jejuni/coli*, *Clostridioides (Clostridium) difficile*, *Enterobacter cloacaе*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Pseudomonas aeruginosa*, *Serratia marcescens*, *Staphylococcus aureus*, and *Streptococcus pyogenes* are being tested by this method.

For other bacterial species, order PFGE / Bacterial Typing by Pulsed-Field Gel Electrophoresis, Varies. PFGE orders for *A baumannii*, *C jejuni/coli*, *C difficile*, *E cloacaе*, *E faecalis*, *E faecium*, *E coli*, *K pneumoniae*, *L pneumophila*, *P aeruginosa*, *S marcescens*, *S aureus*, and *S pyogenes* will be automatically converted to BTWGS / Bacterial Strain Typing by Whole Genome Sequencing, Varies.

**Additional Testing Requirements**

If uncertain of organism identification, concomitantly order IDENT / Organism Referred for Identification, Aerobic Bacteria or ANIDE / Organism Referred for Identification, Anaerobic Bacteria.

**Shipping Instructions**

1. See [Infectious Specimen Shipping Guidelines](#) in Special Instructions for shipping information.

2. Place isolates in a large infectious container (T146) and label as an etiologic agent/infectious substance.

3. Place all isolates (all patients and/or sites to be compared) submitted for whole genome sequencing (WGS) together in 1 large bag, and send in the same shipping container. This is necessary for comparison of isolates by this method.

**Necessary Information**

1. **Organism identification and specimen source are required.**

2. *Acinetobacter baumannii*: Isolate must be *A baumannii*. Identification of *A baumannii* complex and *A baumannii/calcoaceticus* complex are not acceptable.


5. An email address registered on the Mayo Clinic Laboratories website is required for report delivery.

**Specimen Required**

**Aerobic Bacteria**

**Supplies:** Infectious Container, Large (T146)

**Container/Tube:** Agar slant

**Specimen Volume:** Isolates on separate agar slants in pure culture

**Collection Instructions:**
1. Isolate the bacteria (must be *Acinetobacter baumannii, Campylobacter jejuni/coli, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Klebsiella pneumoniae, Legionella pneumophila, Pseudomonas aeruginosa, Serratia marcescens, Staphylococcus aureus, or Streptococcus pyogenes*).

2. Bacterial isolate must be in pure culture, actively growing. **Do not submit mixed cultures.**

3. Each isolate must be submitted under a separate order.

**Anaerobic Bacteria: Clostridioides (Clostridium) difficile**

**Supplies:**
- Anaerobic Transport Tube (T588)
- Infectious Container, Large (T146)

**Specimen Type:** Pure culture of *C difficile*

**Container/Tube:**
- **Preferred:** Anaerobic transport tube
- **Acceptable:** Thioglycollate broth or any other suitable anaerobic transport system

**Specimen Volume:** Isolates in separate transport tubes in pure culture

**Collection Instructions:**
1. Isolate the bacteria (must be *Clostridioides (Clostridium) difficile*).

2. Do not submit growth directly from a CHROMagar plate; subculture to anaerobic media to obtain pure isolate, and confirm identification prior to submission.

3. Bacterial isolate must be in pure culture, actively growing. **Do not submit mixed cultures.**

4. Each isolate must be submitted under a separate order.

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

**Reject Due To**

| Other | Bacteria other than: *Acinetobacter baumannii, Campylobacter jejuni/coli, Clostridioides (Clostridium) difficile, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Klebsiella pneumoniae, Legionella pneumophila, Pseudomonas aeruginosa, Serratia marcescens, Staphylococcus aureus, Streptococcus pyogenes* Agar plate |
Specimen Stability Information

<table>
<thead>
<tr>
<th>Specimen Type</th>
<th>Temperature</th>
<th>Time</th>
<th>Special Container</th>
</tr>
</thead>
<tbody>
<tr>
<td>Varies</td>
<td>Ambient (preferred)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Refrigerated</td>
<td></td>
<td></td>
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Clinical and Interpretive

Clinical Information

Bacterial strain typing may be useful for determining strain relatedness in the setting of possible nosocomial transmission or community outbreaks. Serial isolates obtained from the same patient may be typed to assess similarity. Typing may allow discrimination of 2 or more isolates of the same species, which can inform recognition of an outbreak, nosocomial transmission, or identify a potential source of infection in an individual patient.

Pulse-field gel electrophoresis (PFGE) has traditionally been used for strain typing, but does not always discriminate between different bacterial strains (eg, 2 genetically dissimilar strains may have indistinguishable PFGE patterns). Whole genome sequencing offers a higher level of resolution of genetic relatedness of strains than PFGE does.

Reference Values

Reported as isolates are "related", "possibly related", or "unrelated" by whole genome sequencing.

Interpretation

The genomic sequence of individual isolates will be determined and compared to the genomic sequences of the other cosubmitted isolates. The report will indicate the degree of relatedness between the isolates. A link to the interpretive report will be sent to the registered email address provided by the client.

Cautions

Genomic relatedness does not prove that tested bacterial isolates are epidemiologically related. Establishment of an epidemiologic relationship requires correlation with clinical and epidemiological information. An epidemiological link may be ascribed if a common contact can be established between patients with bacterial strains demonstrating a high degree of genetic relatedness. Similar to other types of stain typing (eg, pulse-field gel electrophoresis: PFGE), sequence-based strain typing is most powerful in demonstrating genetic dissimilarity, decreasing the likelihood that the strains share a similar source.

Clinical Reference


Performance

Method Description

Following whole genome sequencing of each submitted isolate on a MiSeq (Illumina, San Diego, CA), sequences will be compared by core genome multilocus sequence typing (MLST) analysis using SeqSphere+ Software (Ridom GmbH, Munster, Germany). Allelic profiles will be used to generate a phylogenetic tree showing isolate relatedness. (Leopold SR, Goering RV, Witten A, et al: Bacterial whole-genome sequencing revisited: portable, scalable, and standardized analysis for typing and detection of virulence and antibiotic resistance genes. J Clin Microbiol 2014 Jul;52[7]:2365-2370)

PDF Report

No

Day(s) and Time(s) Test Performed

Varies; Batch tested 1 time per week

Analytic Time

30 days

Maximum Laboratory Time

40 days (testing may take longer if a large number of isolates is submitted)

Specimen Retention Time

1 month

Performing Laboratory Location

Rochester

Fees and Codes

Fees

- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their Regional Manager. For assistance, contact Customer Service.

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 U.S. Food and Drug Administration.

CPT Code Information

0010U-Bacterial Typing, Whole Genome Seq

87900-Bioinformatics Reanalysis (if appropriate)

87077-Ident by MALDI-TOF mass spec (if appropriate)

87153-Aerobe ident by sequencing (if appropriate)
87077-Additional identification procedure (if appropriate)

87076-Id MALDI-TOF mass spec anaerobe (if appropriate)

87076-Anaerobe Id (if appropriate)

87153-Anaerobe ident by sequencing (if appropriate)

**LOINC® Information**

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<thead>
<tr>
<th>Test ID</th>
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<th>Order LOINC Value</th>
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<tbody>
<tr>
<td>BTWGS</td>
<td>Bacterial Typing, Whole Genome Seq</td>
<td>90246-0</td>
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<tr>
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