Overview

Useful For
Diagnostic workup of patients with a high probability of BCR-ABL1-positive hematopoietic neoplasms, predominantly chronic myelogenous leukemia and acute lymphoblastic leukemia

Testing Algorithm
The following algorithms are available in Special Instructions:

- Myeloproliferative Neoplasm: A Diagnostic Approach to Bone Marrow Evaluation
- Myeloproliferative Neoplasm: A Diagnostic Approach to Peripheral Blood Evaluation

Special Instructions
- Myeloproliferative Neoplasm: A Diagnostic Approach to Peripheral Blood Evaluation
- Myeloproliferative Neoplasm: A Diagnostic Approach to Bone Marrow Evaluation
- Hematopathology Patient Information
- BCR/ABL1 Ordering Guide for Blood and Bone Marrow

Method Name
Reverse Transcription-Polymerase Chain Reaction (RT-PCR) Multiplex PCR

NY State Available
Yes

Specimen

Specimen Type
Varies

Advisory Information
This test is only qualitative and should not be used for routine monitoring (ie, quantitative mRNA level).

Monitoring of most patients with chronic myeloid leukemia (CML) should be performed using BCRAB / BCR/ABL, p210, mRNA Detection, Reverse Transcription-PCR (RT-PCR), Quantitative, Monitoring Chronic Myelogenous Leukemia (CML), Varies.

Monitoring of patients known to carry a p190 fusion should be performed using BA190 / BCR/ABL, p190, mRNA Detection, Reverse Transcription-PCR (RT-PCR), Quantitative, Monitoring Assay, Varies.

For information on which test to order for various scenarios, see BCR/ABL1 Ordering Guide for Blood and Bone Marrow in Special Instructions.

Shipping Instructions
Refrigerate specimens must arrive within 5 days of collection, and ambient specimens must arrive with 3 days (72 hours) of collection. Collect and package specimens as close to shipping time as possible.

Necessary Information
The following information is required:
1. Pertinent clinical history including if the patient has a diagnosis of chronic myelogenous leukemia or other BCR/ABL1-positive neoplasm

2. Date of collection

3. Specimen source (blood or bone marrow)

**Specimen Required**
Submit only 1 of the following specimens:

**Specimen Type:** Whole blood

**Container/Tube:**
**Preferred:** Lavender top (EDTA)
**Acceptable:** Yellow top (ACD)

**Specimen Volume:** 10 mL

**Collection Instructions:**
1. Invert several times to mix blood.
2. Send specimen in original tube.
3. Label specimen as blood.

**Specimen Type:** Bone marrow

**Container/Tube:**
**Preferred:** Lavender top (EDTA)
**Acceptable:** Yellow top (ACD)

**Specimen Volume:** 4 mL

**Collection Instructions:**
1. Invert several times to mix bone marrow.
2. Send specimen in original tube.
3. Label specimen as bone marrow.

**Forms**
1. [Hematopathology Patient Information](#) (T676) in Special Instructions

2. If not ordering electronically, complete, print, and send a [Hematopathology/Cytogenetics Test Request](#) (T726) with the specimen.
**Test Definition: BADX**

**BCR/ABL1, RNA-Qual, Diagnostic**

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**Specimen Minimum Volume**

Peripheral blood: 4 mL  
Bone marrow: 2 mL

**Reject Due To**

<table>
<thead>
<tr>
<th>Gross hemolysis</th>
<th>Reject</th>
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</thead>
<tbody>
<tr>
<td>Other</td>
<td>Moderately to severely clotted</td>
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**Specimen Stability Information**

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<tr>
<th>Specimen Type</th>
<th>Temperature</th>
<th>Time</th>
<th>Special Container</th>
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<tbody>
<tr>
<td>Varies</td>
<td>Refrigerated (preferred)</td>
<td>5 days</td>
<td>PURPLE OR PINK TOP/EDTA</td>
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<tr>
<td></td>
<td>Ambient</td>
<td>72 hours</td>
<td>PURPLE OR PINK TOP/EDTA</td>
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**Clinical and Interpretive**

**Clinical Information**

The t(9;22)/BCR-ABL1 abnormality is associated with chronic myelogenous leukemia (CML) and "Philadelphia-positive" acute lymphoblastic leukemia of B-cell lineage (Ph+ ALL). Very rarely, this abnormality has also been identified in cases of acute myeloid leukemia and T-lymphoblastic leukemia/lymphoma. The fusion gene on the derivative chromosome 22q11 produces a chimeric BCR-ABL1 mRNA transcript and corresponding translated oncoprotein. Despite substantial breakpoint heterogeneity at the DNA level, a consistent set of BCR-ABL1 mRNA transcripts are produced that can be readily and sensitively detected by reverse transcription-PCR (RT-PCR) technique. In CML, breakpoints in BCR result in either exons 13 or 14 (e13, e14) joined to exon 2 of ABL1 (a2). The corresponding e13-a2 or e14-a2 BCR-ABL1 mRNAs produce a 210-kD protein (p210). Rare cases of CML are characterized by an e19-a2 type mRNA with a corresponding p230 protein. In Ph+ ALL, the majority of cases harbor an e1-a2 BCR-ABL1 mRNA transcript, producing a p190 protein. However, chimeric mRNA type is not invariably associated with disease type, as noted by the presence of p210-positive Ph ALL and very rare cases of p190-positive CML. Therefore, positive results from a screening (diagnostic) assay for BCR-ABL1 mRNA need to be correlated with clinical and pathologic findings.

In addition to the main transcript variants described above, rare occurrences of both CML and Ph+ ALL can have alternative break-fusion events resulting in unusual BCR-ABL1 transcript types. Examples include e6-a2 and BCR exon fusions to ABL1 exon a3 (eg, e13-a3, e14-a3, or e1-a3). In addition to detecting common BCR-ABL1 mRNA transcripts, this assay also can identify these rarer BCR-ABL1 transcript variants and is, therefore, a comprehensive screen for both usual and uncommon BCR-ABL1 gene fusions in hematopoietic malignancies. Given the nature of genetic events in tumors, however, this assay will not identify extremely rare and unexpected BCR-ABL1 events involving other exons (eg, case report level) and is, therefore, not absolutely specific, but is predicted to detect more than 99.5% of BCR-ABL1 events. Therefore, it is recommended that for diagnosis, RT-PCR plus a second method (eg, BCR-ABL1 FISH or cytogenetics) should be used. However, this RT-PCR assay is invaluable at diagnosis for identifying the precise BCR-ABL1 mRNA type (eg, for future quantitative assay disease monitoring), which cannot be done by complementary methods.

This assay is intended as a qualitative method, providing information on the presence (and specific mRNA type) or
absence of the BCR-ABL1 mRNA. Results from this test can be used to determine the correct subsequent assay for monitoring of transcript levels following therapy (e.g., BCRAB / BCR/ABL1, p210, mRNA Detection, Reverse Transcription-PCR (RT-PCR), Quantitative, Monitoring Chronic Myeloid Leukemia (CML), Varies; BA190 / BCR/ABL, p190, mRNA Detection, Reverse Transcription-PCR (RT-PCR), Quantitative, Monitoring Assay, Varies). Because the assay is analytically sensitive, it compensates for situations such as partially degraded RNA quality, or low cell number, but it is not intended for quantitative or monitoring purposes.

**Reference Values**
A qualitative result is provided that indicates the presence or absence of BCR/ABL1 mRNA. When positive, the fusion variant is also reported.

**Interpretation**
An interpretive report will be provided.

When positive, the test identifies the specific mRNA fusion variant present to guide selection of an appropriate monitoring assay.

Monitoring is available for common p210 or p190 fusion variant detected.

- Common fusion variants detected: e13-a2 or e14-a2 (p210), e1-a2 (p190), and e6-a2 (p205*)

- Rare fusion variants detected: e13-a3 (p210), e14-a3 (p210), e1-a3 (p190), e19-a2 (p230)

- Potential rare fusions detected: e12-a3, e19-a3

*This is formerly observed as the e6-a2 (p185) fusion form.

**Cautions**
No significant cautionary statements

**Clinical Reference**


**Performance**

**Method Description**
Total RNA is extracted from the patient's blood or bone marrow at the time of diagnosis and mRNA is reverse transcribed into cDNA. The cDNA is then subjected to PCR using 4 separate multiplex reactions. A qualitative result, which will include the relative ratio of target translocation mRNA to control GUSB gene mRNA, will be provided. Although this method employs a quantitative PCR platform, the results can be used to evaluate the relative expression levels of the translocation mRNA relative to control mRNA, thus, providing an improved measure of RNA quality in the assay. Reporting of results will be qualitative; either BCR-ABL1 mRNA positive/detected (with transcript type) or negative/not detected. (Unpublished Mayo method)
No

**Day(s) and Time(s) Test Performed**
Monday through Saturday; a.m.

**Analytic Time**
5 days

**Maximum Laboratory Time**
10 days

**Specimen Retention Time**
RNA 3 months

**Performing Laboratory Location**
Rochester

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**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**
81206
81207
81208

**LOINC® Information**

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<th>Order LOINC Value</th>
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<tr>
<td>BADX</td>
<td>BCR/ABL1, RNA-Qual, Diagnostic</td>
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<table>
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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](#).

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