MAYO CLINIC LABORATORIES

Test Definition: BA190

BCR::ABL1, p190, mRNA Detection, Reverse Transcription-PCR (RT-PCR), Quantitative, Monitoring Assay, Varies

Overview

Useful For

Therapeutic monitoring of *BCR::ABL1* p190 (e1a2)-positive hematologic neoplasms (eg, acute lymphoblastic leukemia, chronic myeloid leukemia)

This test **should not be used** to screen for *BCR::ABL1* fusion forms at the time of diagnosis or quantitative therapeutic monitoring of p210 or rare fusion forms.

Testing Algorithm

For information see *BCR::ABL1* Ordering Guide for Blood and Bone Marrow.

Special Instructions

- Hematopathology Patient Information
- BCR::ABL1 Ordering Guide for Blood and Bone Marrow

Method Name

Quantitative Reverse Transcription-Polymerase Chain Reaction (RT-PCR)

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

This test is intended for therapeutic monitoring of patients with known e1a2 *BCR::ABL1* (p190) fusion form and **should not** be used to screen for *BCR::ABL1* fusion forms at the time of diagnosis.

To screen for *BCR::ABL1* fusion forms at diagnosis, order one of the following:
BADX / *BCR::ABL1*, Qualitative, Diagnostic Assay, Varies
BCRFX / *BCR::ABL1* Qualitative Diagnostic Assay with Reflex to *BCR::ABL1* p190 Quantitative Assay or *BCR::ABL1* p210 Quantitative Assay, Varies.

To monitor patients carrying *BCR::ABL1* fusion forms coding for p210 (e13/e14a2), order BCRAB / *BCR::ABL1*, p210, mRNA Detection, Reverse Transcription-PCR (RT-PCR), Quantitative, Monitoring Chronic Myeloid Leukemia (CML), Varies.

To monitor patients carrying rare *BCR::ABL1* fusion forms coding for e19a2, e13/e14a3, e1a3, e6a2, e19a3, e8a2, e12a2, e6a3, e8a3, and e12a3, order BARQ / *BCR::ABL1*, Rare Fusion Monitoring, Quantitative, Varies.

Shipping Instructions

Refrigerate specimens must arrive within 5 days of collection, and ambient specimens must arrive within 72 hours of collection. Collect and package specimen as close to shipping time as possible.

Necessary Information

Pertinent clinical history including patient diagnosis of chronic myeloid leukemia or other *BCR*::*ABL1*-positive neoplasm information **is required.**

Specimen Required

Submit only 1 of the following specimens:

Preferred:
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 whole blood specimen in original tube. **Do not aliquot.**
3. Label specimen as whole 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 bone marrow specimen in original tube. **Do not aliquot.**
3. Label specimen as bone marrow.

Forms

1. Hematopathology Patient Information (T676)
2. If not ordering electronically, complete, print, and send a Hematopathology/Cytogenetics Test Request (T726) with the specimen.

Specimen Minimum Volume

Whole blood: 8 mL; Bone marrow: 2 mL

Reject Due To

Gross hemolysis	Reject
Moderately to severely clotted	Reject

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Refrigerated (preferred)	5 days	PURPLE OR PINK TOP/EDTA
	Ambient	72 hours	PURPLE OR PINK TOP/EDTA

Clinical & Interpretive

Clinical Information

Messenger RNA (mRNA) transcribed from *BCR*::*ABL1* (fusion of the breakpoint cluster region gene [*BCR*] at chromosome 22q11 to the Abelson gene [*ABL1*] at chromosome 9q34) is detected in all patients with chronic myeloid leukemia (CML) and a subset of patients with both acute lymphoblastic leukemia (ALL) and acute myeloid leukemia (AML). Although breakpoints in the *BCR* and *ABL1* genes may occur in a variety of locations, splicing of the primary RNA transcripts result in only 8 fusion site variants (e1/a2, e6/a2, e13/a2, e14/a2, e19/a2, and e1/a3, e13/a3, e14/a3), which incorporate the entire sequence of the exons on both sides of the fusion site. The e1/a2 and e1/a3 fusion forms produce a 190-kDa protein designated p190. This *BCR*::*ABL1* protein form is found in approximately 75% of patients with childhood ALL and approximately 50% of patients with adult ALL, with the majority arising from e1/a2 mRNA. The p190 is also the predominant fusion form in a small subset of patients with CML, although the vast majority of CML cases contain the p210 protein, typically from e13/a2 or e14/a2 mRNA fusions. Other fusion forms are very rare.

Quantitative reverse-transcription polymerase chain reaction is the most sensitive method for monitoring *BCR*::*ABL1* levels during treatment. This test detects mRNA coding for the most common p190 fusion form (e1/a2).

Reference Values

The presence or absence of the *BCR*::*ABL1* messenger RNA fusion form producing the p190 fusion protein is reported. If positive, the level is reported as the ratio of *BCR*::*ABL1* (p190) transcript to *ABL1* transcript in the form of a percentage.

Interpretation

An interpretive report will be provided which includes the ratio of *BCR*::*ABL1* (p190) transcript to *ABL1* transcript in the form of a percentage, if positive.

Cautions

This test detects only the e1/a2 *BCR*::*ABL1* (p190) fusion form. Other fusion forms are not detected by this assay, including those containing the *BCR* e13 and e14 exons, which code for the p210 protein commonly found in chronic

myeloid leukemia (CML), and the rare e1/a3 (p190) fusion form.

The precision of this assay at very low *BCR*::*ABL1* levels is less reliable, such that inter-run variation can be more variable. If the results are being used to make major therapeutic decisions, significant changes during monitoring should be verified with a subsequent specimen.

Results of this assay cannot be directly compared with results generated from other polymerase chain reaction (PCR) assays, including identical assays performed in other laboratories. Monitoring should be performed using the same method and laboratory for each subsequent specimen.

The results of this assay cannot be directly compared with *BCR*::*ABL1* results obtained using fluorescence in situ hybridization (FISH) technology. FISH measures DNA alleles and this PCR-based assay measures messenger RNA (mRNA) transcripts. Because a single DNA allele can produce many mRNA transcripts, the values are not directly comparable.

Blood is the specimen of choice for monitoring. While most patients show similar *BCR*::*ABL1* levels in blood and bone marrow drawn at the same time, some patients have a consistent difference in the levels in blood and bone marrow such that altering specimen types during monitoring can lead to confusion.

Assay precision does not appear to be significantly affected by specimen transport or moderate delays in processing. However, in specimens with very low levels of *BCR*::*ABL1*, these conditions may cause sufficient RNA degradation to produce false-negative results. Thus, specimens should be shipped as quickly as possible. Ambient specimens over 3 days old and refrigerate specimens over 5 days old at the time of receipt are unacceptable.

Clinical Reference

1. Hughes TP, Kaeda J, Branford S, et al. Frequency of major molecular responses to imatinib or interferon alfa plus cytarabine in newly diagnosed chronic myeloid leukemia. N Engl J Med. 2003;349(15):1423-1432
2. Radich JP, Gooley T, Bryant E, et al. The significance of *BCR-ABL* molecular detection in chronic myeloid leukemia patients "late," 18 months or more after transplantation. Blood. 2001;98(6):1701-1707
3. Olavarria E, Kanfer E, Szydlo R, et al. Early detection of *BCR-ABL* transcripts by quantitative reverse transcriptase-polymerase chain reaction predicts outcome after allogeneic stem cell transplantation for chronic myeloid leukemia. Blood. 2001;97(6):1560-1565
4. Tefferi A. The classic myeloproliferative neoplasms: Chronic myelogenous leukemia, polycythemia vera, essential thrombocythemia, and primary myelofibrosis. In: Valle DL, Antonarakis S, Ballabio A, Beaudet AL, Mitchell GA, eds. The Online Metabolic and Molecular Bases of Inherited Disease. McGraw-Hill; 2019. Accessed September 10, 2026. Available at https://ommbid.mhmedical.com/content.aspx?sectionid=225078035&bookid=2709

Performance

Method Description

Total RNA is extracted and reverse transcribed to complementary DNA. Quantitative real time polymerase chain reaction is performed and p190/*ABL* quantitative levels are determined using TaqMan-type probe technology. The data

is analyzed for relative quantification with calibrator normalization and efficiency correction. The reference gene, *ABL1,* is used to control for RNA degradation in the sample and the calibrator is used to control for inter-run variations. A normalized ratio of *BCR*::*ABL1* (p190) mRNA:*ABL1* mRNA is obtained and reported in the form of a percentage.(Unpublished Mayo method)

PDF Report
Supplemental

Day(s) Performed
Monday through Friday

Report Available
4 to 8 days

Specimen Retention Time
Whole blood/Bone marrow: 2 weeks; Extracted RNA 3 months

Performing Laboratory Location
Mayo Clinic Laboratories - Rochester Main Campus

Fees & 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 account representative. 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. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information
81207

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
BA190	BCR/ABL1, p190, Quant, Monitor	21823-0

Result ID	Test Result Name	Result LOINC® Value
MP002	Specimen Type	31208-2
19765	Interpretation	69047-9

39470	BCR/ABL1 p190 Result	No LOINC Needed