MAYO CLINIC LABORATORIES

Test Definition: DICET

DICER1 Mutation Analysis, Next-Generation Sequencing, Tumor

Overview

Useful For

Identifying specific mutations within the *DICER1* gene to assist in tumor diagnosis/classification

Genetics Test Information

This test uses targeted next-generation sequencing to evaluate for somatic mutations within the *DICER1* gene. See Targeted Genes and Methodology Details for *DICER1* Mutation Analysis for details regarding the targeted gene regions evaluated by this test.

This test is performed to evaluate for somatic mutations within solid tumor samples. This test **does not assess** for germline alterations within the *DICER1* gene.

Additional Tests

Test Id	Reporting Name	Available Separately	Always Performed
SLIRV	Slide Review in MG	No, (Bill Only)	Yes

Testing Algorithm

When this test is ordered, slide review will always be performed at an additional charge.

Special Instructions

- Tissue Requirements for Solid Tumor Next-Generation Sequencing
- Targeted Genes and Methodology Details for DICER1 Mutation Analysis

Method Name

Sequence Capture and Targeted Next-Generation Sequencing (NGS)

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

Multiple oncology (cancer) gene panels are available. For more information see Hematology, Oncology, and Hereditary Test Selection Guide.

Necessary Information

A pathology report (final or preliminary), at minimum containing the following information, **must accompany specimen for testing to be performed**:

1. Patient name
2. Block number-must be on all blocks, slides, and paperwork (can be handwritten on the paperwork)
3. Tissue collection date
4. Source of the tissue

Specimen Required

This assay requires at least 20% tumor nuclei.

-Preferred amount of tumor area with sufficient percent tumor nuclei: tissue 216 mm(2)

-Minimum amount of tumor area: tissue 36 mm(2)

-These amounts are cumulative over up to 10 unstained slides and must have adequate percent tumor nuclei.

-Tissue fixation: 10% neutral buffered formalin, not decalcified

-For specimen preparation guidance, see Tissue Requirement for Solid Tumor Next-Generation Sequencing. In this document, the sizes are given as 4 mm x 4 mm x 10 slides as preferred: approximate/equivalent to 144 mm(2) and the minimum as 3 mm x 1 mm x 10 slides: approximate/equivalent to 36 mm(2).

Preferred: Submit 3, if available, or 2 of the following specimens.
Acceptable: Submit **at least one** of the following specimens**.**

Specimen Type: Tissue block
Collection Instructions: Submit a formalin-fixed, paraffin-embedded tissue block with acceptable amount of tumor tissue.

Specimen Type: Tissue slide
Slides: 1 Hematoxylin and eosin stained and 10 unstained
Collection Instructions:
Submit the following slides:
1 slide stained with hematoxylin and eosin
AND
10 unstained, nonbaked slides with 5-micron thick sections of the tumor tissue.
Note: The total amount of required tumor nuclei can be obtained by scraping up to 10 slides from the same block.
Additional Information: Hematoxylin and eosin-stained and unstained slides will not be returned.

Specimen Type: Cytology slide (direct smears or ThinPrep)
Slides: 1 to 3 Slides
Collection Instructions: Submit 1 to 3 slides stained and coverslipped with a preferred total of 5000 nucleated cells, or a minimum of at least 3000 nucleated cells.
Note: Glass coverslips are preferred; plastic coverslips are acceptable but will result in longer turnaround times.
Additional Information: Cytology slides will not be returned. An image of the slides will be stored per regulatory requirements.

Forms

If not ordering electronically, complete, print, and send an Oncology Test Request (T729) with the specimen.

Specimen Minimum Volume
See Specimen Required

Reject Due To
All specimens will be evaluated at Mayo Clinic Laboratories for test suitability

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Ambient (preferred)		
	Refrigerated		

Clinical & Interpretive

Clinical Information
This test uses formalin-fixed paraffin-embedded tissue or cytology slides to assess for somatic mutations involving the *DICER1* gene known to be associated with multiple tumor types. *DICER1* mutations are a diagnostic marker of embryonal rhabdomyosarcoma and Sertoli-Leydig cell tumors.(1) In central nervous system tumors, *DICER1* mutations are a diagnostic molecular biomarker for primary intracranial sarcoma, *DICER1*-mutant, embryonal tumor with multilayered rosettes and pituitary blastoma.(2) *DICER1* mutations also occur in a subset of pineoblastoma, typically in the context of *DICER1* tumor-predisposition syndrome. *DICER1* tumor-predisposition syndrome is an inherited predisposition to pleuropulmonary blastoma, cystic nephroma, Wilms' Tumor, anaplastic sarcoma of the kidney, ovarian Sertoli-Leydig cell tumor, and cervical embryonal rhabdomyosarcoma.

Reference Values
An interpretive report will be provided.

Interpretation
The interpretation of molecular biomarker analysis includes an overview of the results and the associated diagnostic, prognostic, and therapeutic implications.

Cautions
This test cannot differentiate between somatic and germline alterations. Additional testing may be necessary to clarify the significance of results if there is a potential hereditary risk.

DNA variants of uncertain significance may be identified.

A negative result does not rule out the presence of a variant that may be present below the limits of detection of this assay. In a specimen with 20% or more tumor content, the analytical sensitivity of this assay for sequence reportable alterations is 5% mutant allele frequency with a minimum coverage of 500X.

Point mutations and small deletion-insertion mutations (delins) will be detected in the *DICER1* gene only. This test may

detect single exon deletions but does not detect multi-exon deletions, duplications, larger-scale genomic copy number variants, copy neutral loss of heterozygosity, or epigenetic modifications such as promoter methylation. Delins of 1000 bp or less are detectable with at least 50 or more supporting reads.

Variant allele frequency (VAF) is the percentage of sequencing reads supporting a specific variant divided by the total sequencing reads at that position. In somatic testing, VAF should be interpreted in the context of several factors, including, but not limited to, tumor purity/heterogeneity/copy number status (ploidy, gains/losses, loss of heterozygosity) and sequencing artifact/misalignment.(3,4)

Rare alterations (ie, polymorphisms) may be present that could lead to false-negative or false-positive results.

Test results should be interpreted in the context of clinical, tumor sampling, histopathological, and other laboratory data. If results obtained do not match other clinical or laboratory findings, contact the laboratory for discussion. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

Reliable results are dependent on adequate specimen collection and processing. This test has been validated on cytology slides and formalin-fixed, paraffin-embedded tissues; other types of fixatives are discouraged. Improper treatment of tissues, such as decalcification, may cause polymerase chain reaction failure.

Supportive Data

Performance Characteristics
The limit of detection for calling a somatic variant (single nucleotide variants [SNV] and deletions-insertions [delins]) is 5% variant allele frequency (VAF) and having at least 500x deduplicated coverage.

Verification studies demonstrated concordance between this test and the reference method for detection of SNV and delins is 98.5% (673/683) and 98.4% (122/124) of variants, respectively. Concordance for the detection of delins was 99.0% (100/101) in variants 1 to 10 base pairs (bp) in size, 93.3% (14/15) in variants 11 to 50 bp in size, and 100% (8/8) in variants over 50 bp in size.

To ensure accuracy, this test will be performed on cases that are estimated by a pathologist to have at least 20% tumor cells.

Clinical Reference

1. WHO Classification of Tumours Editorial Board. Female genital tumours. 5th ed. World Health Organization; 2020. WHO Classification of Tumours. Vol 4
2. WHO Classification of Tumours Editorial Board: Central nervous system tumours. 5th ed. World Health Organization; 2021. WHO Classification of Tumours. Vol 6
3. Strom SP. Current practices and guidelines for clinical next-generation sequencing oncology testing. Cancer Biol Med. 2016;13(1):3-11. doi:10.28092/j.issn.2095-3941.2016.0004
4. Spurr L, Li M, Alomran N, et al. Systematic pan-cancer analysis of somatic allele frequency. Sci Rep. 2018;8(1):7735. Published 2018 May 16. doi:10.1038/s41598-018-25462-0
5. Caroleo AM, De loris MA, Boccuto L, et al. DICER1 syndrome and cancer predisposition: From a rare pediatric tumor to lifetime risk. Front Oncol. 2021;10:614541
6. Li BK, Vasiljevic A, Dufour C, et al. Pineoblastoma segregates into molecular sub-groups with distinct clinico-pathologic

features: a rare brain tumor consortium registry study. Acta Neuropathol. 2020 Feb;139(2):223-241
7. Koelsche C, Mynarek M, Schrimpf D, et al. Primary intracranial spindle cell sarcoma with rhabdomyosarcoma-like features share a highly distinct methylation profile and DICER1 mutations. Acta Neuropathol. 2018;136(2):327-337
8. de Kock L, Yoon JY, Apellaniz-Ruiz M, et al. Significantly greater prevalence of DICER1 alterations in uterine embryonal rhabdomyosarcoma compared to adenosarcoma. Mod Pathol. 2020;33:1207-1219
9. McCluggage WG, Apellaniz-Ruiz M, Chong AL, et al. Embryonal rhabdomyosarcoma of the ovary and fallopian tube: Rare neoplasms associated with germline and somatic DICER1 mutations. Am J Surg Pathol. 2020;44:738-747
10. de Kock L, Terzic T, McCluggage WG, et al. DICER1 mutations are consistently present in moderately and poorly differentiated sertoli-leydig cell tumors. Am J Surg Pathol. 2017;41:1178-1187

Performance

Method Description
Next-generation sequencing is performed to evaluate the presence of a mutation in all coding regions of the *DICER1* gene. See Targeted Genes and Methodology Details for *DICER1* Mutation Analysis for details regarding the targeted gene regions identified by this test.(Unpublished Mayo method)

A pathology review and macro dissection to enrich for tumor cells is performed prior to slide scraping.

PDF Report
No

Day(s) Performed
Monday through Friday

Report Available
12 to 20 days

Specimen Retention Time
Tissue blocks: Unused portions of blocks will be returned; Tissue slides: Hematoxylin and eosin-stained and unstained slides will not be returned. Unused slides are stored for at least 5 years; Extracted DNA: 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 Definition: DICET

DICER1 Mutation Analysis, Next-Generation Sequencing, Tumor

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

88381-Microdissection, manual
81479

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
DICET	DICER1 Mutation Analysis, Tumor	105585-4

Result ID	Test Result Name	Result LOINC® Value
619668	Result	82939-0
619669	Interpretation	69047-9
619670	Additional Information	48767-8
619671	Specimen	31208-2
619672	Tissue ID	80398-1
619673	Method	85069-3
619674	Disclaimer	62364-5
619675	Released By	18771-6