

Overview

Useful For

Providing a genetic evaluation for patients with a personal or family history suggestive of long QT syndrome (LQTS)

Establishing a diagnosis of LQTS

Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in 10 genes associated with long QT syndrome (LQTS): *CACNA1C*, *CALM1*, *CALM2*, *CALM3*, *KCNE1*, *KCNH2*, *KCNJ2*, *KCNQ1*, *SCN5A*, and *TRDN*. See [Targeted Genes and Methodology Details for Long QT Syndrome Gene Panel](#) and Method Description for additional details.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for LQTS.

[Prior Authorization](#) is available for this assay.

Special Instructions

- [Informed Consent for Genetic Testing](#)
- [Hereditary Cardiomyopathies and Arrhythmias: Patient Information](#)
- [Informed Consent for Genetic Testing \(Spanish\)](#)
- [Targeted Genes and Methodology Details for Long QT Syndrome Gene Panel](#)
- [Long QT Syndrome Gene Panel \(LQTSG\) Prior Authorization Ordering Instructions](#)

Method Name

Sequence Capture and Targeted Next-Generation Sequencing followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing.

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

This test is intended for genetic screening for and diagnosis of long QT syndrome.

For Brugada syndrome genetic testing, order *SCN5A* / Brugada Syndrome Multi-Gene Panel, Blood.

For comprehensive inherited cardiac arrhythmia genetic testing, order CARGG / Comprehensive Arrhythmia Gene Panel, Varies.

Customization of this panel and single gene analysis for any gene present on this panel are available. For more information see CGPH / Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies.

Targeted testing for familial variants (also called site-specific or known mutations testing) is available for the genes on this panel. See FMTT / Familial Variant, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.

Shipping Instructions

Specimen preferred to arrive within 96 hours of collection.

Necessary Information

[Prior Authorization](#) is available, **but not required**, for this test. If proceeding with the prior authorization process, submit the required form with the specimen.

Specimen Required

Patient Preparation: A previous bone marrow transplant from an allogenic donor will interfere with testing. Call 800-533-1710 for instructions for testing patients who have received a bone marrow transplant.

Specimen Type: Whole blood

Container/Tube:

Preferred: Lavender top (EDTA) or yellow top (ACD)

Acceptable: Any anticoagulant

Specimen Volume: 3 mL

Collection Instructions:

1. Invert several times to mix blood
2. Send whole blood specimen in original tube. **Do not aliquot.**

Specimen Stability Information: Ambient (preferred)/Refrigerated

Forms

. **New York Clients-Informed consent is required.** Document on the request form or electronic order that a copy is on file. The following documents are available:

-[Informed Consent for Genetic Testing](#) (T576)

-[Informed Consent for Genetic Testing \(Spanish\)](#) (T826)

2. [Hereditary Cardiomyopathies and Arrhythmias Patient Information](#)

3. [Long QT Syndrome Gene Panel \(LQTSG\) Prior Authorization Ordering Instructions](#)

4. If not ordering electronically, complete, print, and send a [Cardiovascular Test Request Form](#) (T724) with the specimen.

Specimen Minimum Volume

[1 mL](#)

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	Varies		

Clinical & Interpretive

Clinical Information

Long QT syndrome (LQTS) is a genetic cardiac arrhythmia condition characterized by QT prolongation and T-wave abnormalities on an electrocardiogram (ECG). LQTS may result in or present with recurrent syncope, ventricular arrhythmia (commonly torsade de pointes), sudden cardiac arrest, and sudden cardiac death. Some subtypes of LQTS are also referred to as Romano-Ward syndrome (RWS).(1)

LQTS has a prevalence of approximately 1:2000 and is caused by loss-of-function, disease-causing variants in genes that encode cardiac ion channels or associated proteins. It is estimated that up to 75% of individuals meeting clinical diagnostic criteria for LQTS are found to harbor a disease-causing variant in one of three genes: *KCNQ1*, *KCNH2*, and *SCN5A*.(2) Disease-causing variants in additional genes contribute to a minority of LQTS cases.(2) In most cases, LQTS follows an autosomal dominant pattern of inheritance.

Jervell and Lange-Nielsen syndrome (JLNS) is a rare condition characterized by prolonged QT interval and congenital profound bilateral sensorineural hearing loss. JLNS follows an autosomal recessive inheritance pattern and is caused by homozygous or compound heterozygous disease-causing variants in either *KCNQ1* or *KCNE1*.(1)

Andersen-Tawil syndrome is a rare condition characterized by prolonged QT interval, ventricular arrhythmias, episodic muscle weakness, and congenital anomalies that may include facial dysmorphism, clinodactyly, hand/foot syndactyly, short stature, and scoliosis. Andersen-Tawil syndrome follows an autosomal dominant inheritance pattern and is caused by disease-causing variants in the *KCNJ2* gene.(3)

Timothy syndrome is a rare, systemic condition involving prolonged QT interval in association with seizures, neurodevelopmental delays, recurrent infections, and congenital anomalies that may include hand/foot syndactyly, structural heart defects, and facial dysmorphism. Timothy syndrome follows an autosomal dominant patten of inheritance and is caused by disease-causing variants in the *CACNA1C* gene.(4)

Genetic testing in LQTS is recommended and supported by multiple consensus statements to confirm the clinical diagnosis, assist with risk stratification, guide management, and identify at-risk family members. Even individuals with a normal QT interval may still be at risk for a cardiac event and sudden cardiac death and, thus, ECG analysis alone is insufficient to rule out the diagnosis and genetic testing is necessary to confirm the presence or absence of disease in at-risk family members.(1-4)

Reference Values

An interpretive report will be provided.

Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(5) Variants are classified based on known, predicted, or possible pathogenicity and reported with

interpretive comments detailing their potential or known significance.

Cautions**Clinical Correlations:**

Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Detection of a reportable variant in an affected family member would allow for more informative testing of at-risk individuals.

To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact the Mayo Clinic Laboratories genetic counselors at 800-533-1710.

Technical Limitations:

Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some target regions; assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.

This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

Deletion/Duplication Analysis:

This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural rearrangements (such as translocations and inversions) may not be detected.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.

Genes may be added or removed based on updated clinical relevance. Refer to the [Targeted Genes and Methodology Details for Long QT Syndrome Gene Panel](#) for the most up to date list of genes included in this test. For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent blood transfusion, results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who

have received a bone marrow transplant.

Reclassification of Variants:

At this time, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare providers to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time.

Variant Evaluation:

Evaluation and categorization of variants is performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.⁽⁵⁾ Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.

Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgment.

Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. Incidental findings may include, but are not limited to, results related to the sex chromosomes. These findings will be carefully reviewed to determine whether they will be reported.

Clinical Reference

1. Alders M, Bikker H, Christiaans I: Long QT syndrome. In: Adam MP, Ardinger HH, Pagon RA, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 2003 . Updated February 8, 2018. Accessed July 27, 2022. Available at www.ncbi.nlm.nih.gov/books/NBK1129/
2. Giudicessi JR, Ackerman MJ: Genetic testing in heritable cardiac arrhythmia syndromes: differentiating pathogenic mutations from background genetic noise. Curr Opin Cardiol. 2013 Jan;28(1):63-71. doi:10.1097/HCO.0b013e32835b0a41
3. Veerapandiyani A, Statland JM, Tawil R: Andersen-Tawil syndrome. In: Adam MP, Ardinger HH, Pagon RA, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 2004. Updated June 7, 2018. Accessed July 27, 2022. Available at www.ncbi.nlm.nih.gov/books/NBK1264/
4. Napolitano C, Timothy KW, Bloise R, Priori SG: CACNA1C-related disorders. In: Adam MP, Ardinger HH, Pagon RA, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 2006. Updated February 11, 2021. Accessed July 27, 2022. Available at www.ncbi.nlm.nih.gov/books/NBK1403/
5. Richards S, Aziz N, Bale S, et al: Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med. 2015 May;17(5):405-424

Performance**Method Description**

Next-generation sequencing (NGS) and/or Sanger sequencing is performed to test for the presence of variants in coding regions and intron/exon boundaries of the genes analyzed, as well as some other regions that have known disease-causing variants. The human genome reference GRCh37/hg19 build was used for sequence read alignment. At least 99% of the bases are covered at a read depth over 30X. Sensitivity is estimated at above 99% for single nucleotide variants, above 94% for deletion-insertions (delins) less than 40 base pairs (bp), above 95% for deletions up to 75 bp and insertions up to 47 bp. NGS and/or a polymerase chain reaction-based quantitative method is performed to test for the presence of deletions and duplications in the genes analyzed.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine content, and repetitive sequences. See [Targeted Genes and Methodology Details for Long QT Syndrome Gene Panel](#) for details regarding the targeted genes analyzed for each test and specific gene regions not routinely covered. (Unpublished Mayo method)

Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

Genes analyzed: *CACNA1C*, *CALM1*, *CALM2*, *CALM3*, *KCNE1*, *KCNH2*, *KCNJ2*, *KCNQ1*, *SCN5A*, and *TRDN*

PDF Report

Supplemental

Day(s) Performed

Varies

Report Available

28 to 42 days

Specimen Retention Time

Whole blood: 2 weeks (if available); 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 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

81403
81406 x2
81407
81479
81479 (if appropriate for government payers)

Prior Auhtorization

Insurance preauthorization is available for this testing; forms are available.

Patient financial assistance may be available to those who qualify. Patients who receive a bill from Mayo Clinic Laboratories will receive information on eligibility and how to apply.

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
LQTSG	Long QT Syndrome Gene Panel	55146-5

Result ID	Test Result Name	Result LOINC® Value
617352	Test Description	62364-5
617353	Specimen	31208-2
617354	Source	31208-2
617355	Result Summary	50397-9
617356	Result	82939-0
617357	Interpretation	69047-9
617358	Additional Results	82939-0
617359	Resources	99622-3
617360	Additional Information	48767-8
617361	Method	85069-3
617362	Genes Analyzed	48018-6
617363	Disclaimer	62364-5
617364	Released By	18771-6