

Loeys-Dietz Syndrome Core Panel, Sequencing

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Loeys-Dietz syndrome (LDS) is a connective tissue disorder causing a wide range of vascular, skeletal, craniofacial, cutaneous, allergic/inflammatory, gastrointestinal, and ocular abnormalities. Pathogenic variants in the *TGFBR1* and *TGFBR2* genes cause most cases of LDS. Quality of life may be significantly affected depending on the type and severity of symptoms, and average life expectancy is decreased due to the risk of arterial aneurysms. The most critical aspect of medical management and screening for individuals with LDS is cardiovascular evaluation in order to monitor risks of aneurysms, dissections, and ruptures. Significant variation in clinical features is common, even among family members with LDS.

Disease Overview

Incidence

Unknown

Symptoms

Vascular	<ul style="list-style-type: none"> • Aortic dilatation or dissection • Dissections or aneurysms in other arteries • Arterial aneurysm and tortuosity
Musculoskeletal	<ul style="list-style-type: none"> • Scoliosis • Arachnodactyly • Talipes equinovarus • Joint laxity or contracture • Pectus excavatum or carinatum • Cervical spine malformation and/or instability • Osteoarthritis
Craniofacial	<ul style="list-style-type: none"> • Hypertelorism • Craniosynostosis • Cleft palate/bifid uvula
Cutaneous	<ul style="list-style-type: none"> • Translucent, velvety skin, with noticeable veins • Dystrophic scars • Easy bruising • Striae
Allergic/inflammatory disease	<ul style="list-style-type: none"> • Seasonal allergies • Asthma • Food allergies • Eosinophilic esophagitis/gastritis • Eczema • Inflammatory bowel disease
Ocular	<ul style="list-style-type: none"> • Blue sclerae

Featured ARUP Testing

[Loeys-Dietz Syndrome Core Panel, Sequencing 3003947](#)

Method: Massively Parallel Sequencing

- Preferred test to diagnose LDS in individuals who meet diagnostic criteria.
- Use to determine if at-risk family members have a *TGFBR1* or *TGFBR2* gene variant when familial variant is unknown and affected relatives are not available for testing.

If a familial sequence variant has been previously identified, targeted sequencing for that variant may be appropriate; refer to the [Laboratory Test Directory](#) for additional information.

Diagnostic Criteria

A diagnosis can be established in an individual with no family history of LDS when a pathogenic variant causative for LDS is identified in *SMAD2*, *SMAD3*, *TGFB2*, *TGFB3*, *TGFBR1*, or *TGFBR2*, and there is either:

- Aortic root enlargement with a z-score of at least 2.0, type A dissection.

OR

- A combination of craniofacial, skeletal, cutaneous, and vascular findings characteristic of LDS.

In asymptomatic individuals with a positive family history, a diagnosis of LDS can be made based on molecular genetic testing alone.

Genetics

Causative Genes

TGFBR1, *TGFBR2*, *TGFB2*, *TGFB3*, *SMAD2*, and *SMAD3*

Inheritance

Autosomal dominant; 75% of cases are due to de novo variants

Penetrance

Nearly complete

Test Interpretation

Sensitivity/Specificity

Up to 75-85% by sequencing of *TGFBR1* and *TGFBR2*¹

Analytic Sensitivity/Specificity

For massively parallel sequencing:

Variant Class	Analytic Sensitivity (PPA) Estimate ^a (%)	Analytic Sensitivity (PPA) 95% Credibility Region ^a (%)
SNVs	99.2	96.9-99.4
Deletions 1-10 bp	93.8	84.3-98.2
Deletions 11-44 bp	99.9	87.8-100
Insertions 1-10 bp	94.8	86.8-98.5
Insertions 11-23 bp	99.9	62.1-100

^aGenes included on this test are a subset of a larger methods-based validation from which the PPA values are derived.

bp, base pairs; PPA, positive percent agreement; SNVs, single nucleotide variants

Results

Result	Result Description	Interpretive Data
Positive	Pathogenic variant detected	Confirms a diagnosis of LDS in a symptomatic individual
Negative	No variant detected	Reduces risk, but does not exclude a diagnosis of LDS in a symptomatic individual
Inconclusive	Sequence variant of unknown clinical significance may be detected	Uncertain whether variant is causative for LDS

Limitations

- A negative result does not exclude a diagnosis of Loeys-Dietz syndrome or other related disorders.
- Diagnostic errors can occur due to rare sequence variations.
- Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation.
- The following will not be evaluated:
 - Variants outside the coding regions and intron-exon boundaries of *TGFBR1* and *TGFBR2*
 - Regulatory region and deep intronic variants
 - Noncoding transcripts
 - Large deletions/duplications in any of the tested genes
- The following may not be detected:
 - Deletions/duplications/insertions of any size by massively parallel sequencing
 - Some variants due to technical limitations in the presence of pseudogenes, repetitive, or homologous regions
 - Low-level somatic variants

References

1. Loeys BL, Dietz HC. [Loeys-Dietz syndrome](#). In: Adam MP, Ardinger HH, Pagon RA, et al, eds. *GeneReviews*. University of Washington, Seattle. Last updated Mar 2018; accessed Jun 2021.

Related Information

[Aortopathy Panel, Sequencing and Deletion/Duplication](#)
[Marfan Syndrome \(FBN1\) Sequencing and Deletion/Duplication](#)

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