# Test Definition: MDYSP

Inherited Muscular Dystrophy Gene Panel, Varies

## Overview

### Useful For

Establishing a molecular diagnosis for patients with muscular dystrophy

Identifying variants within genes known to be associated with muscular dystrophy, allowing for predictive testing of at-risk family members

### Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in 75 genes associated with muscular dystrophy: *ACTA1, ANO5, B3GALNT2, B4GAT1, BAG3, BIN1, BVES, CAPN3, CAV3, CAVIN1, CHKB, COL12A1, COL6A1, COL6A2, COL6A3, CRPPA, CRYAB, DAG1, DES, DMD, DNAJB6, DNM2, DPM1, DPM2, DPM3, DYSF, EMD, FHL1, FKRP, FKTN, FLNC, GAA, GMPPB, GNE, GOSR2, HNRNPA1, HNRNPA2B1, HNRNPDL, INPP5K, ITGA7, JAG2, LAMA2, LARGE1, LDB3, LMNA, MATR3, MSTO1, MYH7, MYOT, PLEC, POGLUT1, POMGNT1, POMGNT2, POMK, POMT1, POMT2, RXYLT1, SELENON, SGCA, SGCB, SGCD, SGCG, SQSTM1, SUN1, SUN2, SYNE1, TCAP, TIA1, TMEM43, TNPO3, TOR1AIP1, TRAPPC11, TRIM32, TTN*, and *VCP*. For more information see Method Description and Targeted Genes and Methodology Details for Inherited Muscular Dystrophy Gene Panel.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, recurrence risk assessment, familial screening, and genetic counseling for muscular dystrophy.

### Testing Algorithm

For information see Neuromuscular Myopathy Testing Algorithm

### Special Instructions

- Informed Consent for Genetic Testing
- Molecular Genetics: Neurology Patient Information
- Neuromuscular Myopathy Testing Algorithm
- Informed Consent for Genetic Testing (Spanish)
- Targeted Genes and Methodology Details for Inherited Muscular Dystrophy Gene Panel

### 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 does not currently test for facioscapulohumeral muscular dystrophy type 1, oculopharyngeal muscular dystrophy, or myotonic dystrophy types 1 and 2. Additional testing for these conditions would need to be ordered separately if clinically indicated.

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.

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.

## Specimen Required

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

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

**Specimen Type:** Whole blood
**Container/Tube:**
**Preferred:** Lavender top (EDTA) or yellow top (ACD)
**Acceptable:** None
**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) 4 days/Refrigerated 4 days/Frozen 4 days
**Additional Information**:
1. Specimens are preferred to be received within 4 days of collection. Extraction will be attempted for specimens received after 4 days, and DNA yield will be evaluated to determine if testing may proceed.
2. To ensure minimum volume and concentration of DNA is met, the requested volume must be submitted. Testing may be canceled if DNA requirements are inadequate.

**Specimen Type**: Saliva
**Patient Preparation:** Patient should not eat, drink, smoke, or chew gum 30 minutes prior to collection.
**Supplies:**
DNA Saliva Kit High Yield (T1007)
Saliva Swab Collection Kit (T786)
**Container/Tube:**
**Preferred**: High-yield DNA saliva kit
**Acceptable**: Saliva swab
**Specimen Volume**: 1 Tube if using T1007 or 2 swabs if using T786
**Collection Instructions:** Collect and send specimen per kit instructions.

**Specimen Stability Information:** Ambient (preferred) 30 days/Refrigerated 30 days
**Additional Information:** Saliva specimens are acceptable but not recommended. Due to lower quantity/quality of DNA yielded from saliva, some aspects of the test may not perform as well as DNA extracted from a whole blood sample. When applicable, specific gene regions that were unable to be interrogated will be noted in the report. Alternatively, additional specimen may be required to complete testing.

**Specimen Type**: Extracted DNA
**Container/Tube**:
**Preferred**: Screw Cap Micro Tube, 2mL with skirted conical base
**Acceptable**: Matrix tube, 1mL
**Collection Instructions**:
1. The preferred volume is at least 100 mcL at a concentration of 75 ng/mcL.
2. Include concentration and volume on tube.
**Specimen Stability Information**: Frozen (preferred) 1 year/Ambient/Refrigerated
**Additional Information**: DNA must be extracted in a CLIA-certified laboratory or equivalent and must be extracted from a specimen type listed as acceptable for this test (including applicable anticoagulants). Our laboratory has experience with Chemagic, Puregene, Autopure, MagnaPure, and EZ1 extraction platforms and cannot guarantee that all extraction methods are compatible with this test. If testing fails, one repeat will be attempted, and if unsuccessful, the test will be reported as failed and a charge will be applied. If applicable, specific gene regions that were unable to be interrogated due to DNA quality will be noted in the report.

### Forms

1. **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. Molecular Genetics: Neurology Patient Information
3. If not ordering electronically, complete, print, and send a Neurology Specialty Testing Client Test Request (T732) 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 | Varies | | |

## Clinical & Interpretive

### Clinical Information

Muscular dystrophies are a heterogeneous group of neuromuscular conditions characterized by skeletal muscle wasting due to muscle dysfunction. The muscular dystrophies can be subdivided into the dystrophinopathies: Emery-Dreifuss muscular dystrophy, limb-girdle muscular dystrophies, distal myopathies, and congenital muscular dystrophies. A clinical diagnosis is typically based on distribution and severity of muscular involvement, mode of inheritance, and other associated symptoms.

The dystrophinopathies include Duchenne muscular dystrophy and Becker muscular dystrophy. These 2 forms are inherited in an X-linked manner and typically present with variable degrees of a limb-girdle pattern of weakness and can develop dilated cardiomyopathy. Emery-Dreifuss muscular dystrophy is characterized by the triad of joint contractures, slowly progressive muscle weakness and wasting, and cardiac involvement. Limb-girdle muscular dystrophy is characterized by weakness and wasting predominately of the hips, shoulders, and proximal extremity muscles. Distal myopathies are disorders with weakness and atrophy predominantly in the distal muscles. Congenital muscular dystrophies are progressive early-onset muscle disorders that often have brain and other organ involvement. They are characterized by hypotonia, delayed motor development, and progressive weakness.

Given the clinical overlap of muscular dystrophies, multigene panels can be an efficient and cost-effective way to establish a molecular diagnosis for individuals who are symptomatic.

## Reference Values

An interpretive report will be provided.

## Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(1) 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.

Deletion/duplication events that extend past the genes included on the panel may occur. In these instances, genes included in the ordered test are provided on the report and interpreted, and genomic breakpoints are reported if they are confirmed. However, copy number variants for genes not listed in the Method Description are typically not reported or interpreted for haploinsufficiency/triplosensitivity. CMACB / Chromosomal Microarray, Congenital, Blood; WESPR / Panel to Whole Exome Sequencing Reflex Test, Varies; or WGSDX / Whole Genome Sequencing for Hereditary Disorders, Varies is recommended for a full interpretation of deletions/duplications predicted to extend past the genes included on the panel.

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. 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:
Currently, 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. Due to broadening genetic knowledge, it is possible that the laboratory may discover new information of relevance to the patient. Should that occur, the laboratory may issue an amended report.

Variant Evaluation:
Evaluation and categorization of variants are performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.(1) 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. These findings will be carefully reviewed to determine whether they will be reported.

### Clinical Reference

1. 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;17(5):405-424
2. Hermans MC, Pinto YM, Merkies IS, et al. Hereditary muscular dystrophies of the heart. Neuromuscul Disord. 2010;20(8):479-492
3. Wicklund MP, Kissel JT. The limb-girdle muscular dystrophies. Neurol Clin. 2014;32(3):729-749
4. Flanigan KM. The muscular dystrophies. Semin Neurol. 2012;32(3):255-263
5. Iannaccone ST, Castro D. Congenital muscular dystrophies and congenital myopathies. Continuum (Minneap Minn). 2013;19(6 Muscle Disease):1509-1534

## Performance

### Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing are 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 deletions-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 (GC) content, and repetitive sequences. See Targeted Genes and Methodology Details for Inherited Muscular Dystrophy 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: *ACTA1, ANO5, B3GALNT2, B4GAT1, BAG3, BIN1, BVES, CAPN3, CAV3, CAVIN1, CHKB, COL12A1, COL6A1, COL6A2, COL6A3, CRPPA, CRYAB, DAG1, DES, DMD, DNAJB6, DNM2, DPM1, DPM2, DPM3, DYSF, EMD, FHL1, FKRP, FKTN,*

*FLNC, GAA, GMPPB, GNE, GOSR2, HNRNPA1, HNRNPA2B1, HNRNPDL, INPP5K, ITGA7, JAG2, LAMA2, LARGE1, LDB3, LMNA, MATR3, MSTO1, MYH7, MYOT, PLEC, POGLUT1, POMGNT1, POMGNT2, POMK, POMT1, POMT2, RXYLT1, SELENON, SGCA, SGCB, SGCD, SGCG, SQSTM1, SUN1, SUN2, SYNE1, TCAP, TIA1, TMEM43, TNPO3, TOR1AIP1, TRAPPC11, TRIM32, TTN*, and *VCP*.

### PDF Report
No

### Day(s) Performed
Varies

### Report Available
21 to 35 days

### Specimen Retention Time
Whole blood: 30 days (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
81443

### LOINC® Information

| Test ID | Test Order Name | Order LOINC® Value |
|---|---|---|
| MDYSP | Muscular Dystrophy Gene Panel | 103952-8 |

| Result ID | Test Result Name | Result LOINC® Value |
|---|---|---|
| 617637 | Test Description | 62364-5 |
| 617638 | Specimen | 31208-2 |
| 617639 | Source | 31208-2 |

| | | |
|---|---|---|
| 617640 | Result Summary | 50397-9 |
| 617641 | Result | 82939-0 |
| 617642 | Interpretation | 69047-9 |
| 618185 | Additional Results | 82939-0 |
| 617643 | Resources | 99622-3 |
| 617644 | Additional Information | 48767-8 |
| 617645 | Method | 85069-3 |
| 617646 | Genes Analyzed | 48018-6 |
| 617647 | Disclaimer | 62364-5 |
| 617648 | Released By | 18771-6 |