Comprehensive Muscular Dystrophy / Myopathy Panel

Test code: NE0701

The Blueprint Genetics Comprehensive Muscular Dystrophy / Myopathy Panel is a 51 gene test for genetic diagnostics of patients with clinical suspicion of distal myopathy or muscular dystrophy.

Different muscular dystrophies and myopathies can be inherited in an X-linked, autosomal dominant, or autosomal recessive manner. More than 50 loci have been associated to different forms of limb-girdle muscular dystrophy (LGMD) alone, making accurate diagnosis and genetic counseling a real challenge. This comprehensive panel is designed to achieve the highest clinical yield and enable the differential diagnostics of these highly variable and genetically heterogeneous neuromuscular diseases. This panel covers the smaller Nemaline Myopathy Panel, Limb Girdle Muscular Dystrophy Panel, Emery Dreifuss Muscular Dystrophy Panel and Collagen Type IV-Related Disorders Panel.

About Muscular Dystrophy and Myopathy

LGMD is a group of disorders with atrophy and weakness of proximal limb girdle muscles, typically sparing the heart and bulbar muscles. However, cardiac and respiratory impairment may be observed in certain forms of LGMD. In congenital muscular dystrophy (CMD), the muscle weakness typically presents from birth to early infancy. Clinical severity, age of onset, and disease progression are highly variable among the different forms of LGMD/CMD. Phenotypes overlap both within CMD subtypes and among the congenital muscular dystrophies, congenital myopathies, and LGMDs. EDMD is a condition that affects mainly skeletal muscle and heart. Usually it presents in early childhood with contractures, which restrict the movement of certain joints – most often elbows, ankles, and neck. Majority of the patients experience also slowly progressive muscle weakness and wasting, initiating from upper arm and lower leg muscles and progressing to shoulders and hips. Practically all patients with EDMD have cardiac involvement by adulthood. It presents clinically as cardiac conduction defects and/or arrhythmias. Cardiomyopathy phenotype is usually classified as dilated cardiomyopathy (DCM) but also ARVC and hypertrophic cardiomyopathies (HCM) have been described. A small proportion of patients with the autosomal dominant EDMD type experience cardiac manifestation without any skeletal muscle weakness or wasting. The dystrophinopathies include a spectrum of muscle diseases ranging from asymptomatic increase in serum concentration of creatine phosphokinase to the severe progressive muscle diseases that are classified as Duchenne or Becker muscular dystrophy when skeletal muscle is primarily affected and as DMD-associated DCM when the heart is primarily affected. Duchenne muscular dystrophy usually presents in early childhood with delayed milestones, including delays in sitting and standing independently. Duchenne is rapidly progressive, with affected children being wheelchair dependent by age 13 years and cardiomyopathy occurs soon after that. Becker muscular dystrophy is characterized by later onset skeletal muscle weakness; some individuals remain ambulatory until their 20s. However, heart failure from DCM is a common cause of death in the mid-40s. DMD-associated DCM is characterized by left ventricular dilation and congestive heart failure. Females heterozygous for a pathogenic variant in DMD are at increased risk for DCM. The collagen type VI-related disorders are nowadays considered to be a continuum of overlapping phenotypes with Bethlem myopathy at the mild end and Ullrich congenital muscular dystrophy (UCMD) at the severe end. In between these phenotypes there are collagen type VI-related limb-girdle muscular dystrophy and myosclerosis myopathy. Bethlem myopathy is characterized by proximal weakness and variable contractures. Elbows, ankles and fingers are most often affected. If the onset is in early childhood, delayed motor milestones, muscle weakness and contractures are evident. Adult onset patients require eventually ambulatory support. UCMD is characterized by congenital muscle weakness, proximal joint contractures, and striking hyperlaxity of distal joints. Affected children rarely gain the ability to walk independently and spinal rigidity and scoliosis develop. Respiratory failure is a common cause of death in the first and second decade of life. Intelligence is normal in both Bethlem myopathy and UCMD patients. Nemaline Myopathy is characterized by weakness, hypotonia, and depressed or absent deep tendon reflexes. Histopathologically, nemaline bodies are detected on muscle biopsy. The clinical classification defines six forms of Nemaline Myopathy, which are classified by onset and severity of motor and respiratory involvement. Considerable overlap occurs among the forms.

Availability

Results in 3-4 weeks. We do not offer a maternal cell contamination (MCC) test at the moment. We offer prenatal testing only for cases where the maternal cell contamination studies (MCC) are done by a local genetic laboratory. Read more: http://blueprintgenetics.com/faqs/#prenatal
## Gene set description

Genes in the Comprehensive Muscular Dystrophy / Myopathy Panel and their clinical significance

<table>
<thead>
<tr>
<th>Gene</th>
<th>Associated phenotypes</th>
<th>Inheritance</th>
<th>ClinVar</th>
<th>HGMD</th>
</tr>
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<tbody>
<tr>
<td>ACTA1</td>
<td>Myopathy</td>
<td>AD/AR</td>
<td>34</td>
<td>201</td>
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<tr>
<td>ANOS</td>
<td>Gnathodiaphysal dysplasia, LGMD2L and distal MMD3 muscular dystrophies</td>
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<td>106</td>
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<td>CAPN3</td>
<td>Muscular dystrophy, limb-girdle, Eosinophilic myositis</td>
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<td>CAV3</td>
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<td>CFL2</td>
<td>Nemaline myopathy</td>
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<td>COL4A1</td>
<td>Schizencephaly, Anterior segment dysgenesis with cerebral involvement, Retinal artery tortuosity, Porencephaly, Angiopathy, hereditary, with nephropathy, aneurysms, and muscle cramps, Brain small vessel disease</td>
<td>AD</td>
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<td>Hemorrhage, intracerebral</td>
<td>AD</td>
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<td>COL6A1</td>
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<td>COL12A1</td>
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<td>DES</td>
<td>Dilated cardiomyopathy (DCM), Myopathy, myofibrillar</td>
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<td>95</td>
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<td>DMD</td>
<td>Becker muscular dystrophy, Duchenne muscular dystrophy, Dilated cardiomyopathy (DCM)</td>
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<td>DNAJB6</td>
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<td>DYSF</td>
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<td>EMD</td>
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<td>FHL1*</td>
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<tr>
<td>FKRP</td>
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<td>FKTN</td>
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<td>AD/AR</td>
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<td>51</td>
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<td>GMPPB</td>
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<td>ISPD</td>
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<td>LAMA2</td>
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<td>Lims2</td>
<td>Muscular dystrophy, limb-girdle</td>
<td>AR</td>
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<td>3</td>
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<td>--------</td>
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<td>Lmna</td>
<td>Heart-hand syndrome, Slovenian, Limb-girdle muscular dystrophy, Muscular dystrophy, congenital, LMNA-related, Lipodystrophy (Dunnigan), Emery-Dreifuss muscular dystrophy, Malouf syndrome, Dilated cardiomyopathy (DCM), Mandibuloacral dysplasia type A, Progeria Hutchinson-Gilford type</td>
<td>AD/AR</td>
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<td>458</td>
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<td>Lmod3</td>
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<td>AR</td>
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<td>MtM1</td>
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<td>XL</td>
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<td>Myot</td>
<td>Myopathy, myofibrillar</td>
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<td>Neb*</td>
<td>Nemaline myopathy</td>
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<td>PnplA2</td>
<td>Neutral lipid storage disease with myopathy</td>
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<td>PomGnt1</td>
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<td>SGCA</td>
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<td>SMCHD1</td>
<td>Facioscapulohumeral muscular dystrophy</td>
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<td>TCAP</td>
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<td>Tmem43</td>
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<td>TNNT1</td>
<td>Nemaline myopathy</td>
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<td>Tnpo3</td>
<td>Muscular dystrophy, limb-girdle</td>
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<td>Tor1Aip1</td>
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<td>AD/AR</td>
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<td>TPM2</td>
<td>CAP myopathy, Nemaline myopathy, Arthrogryposis, distal</td>
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<td>37</td>
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<tr>
<td>TPM3*</td>
<td>CAP myopathy, Nemaline myopathy, Myopathy, congenital, with fiber-disproportion</td>
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<td>TRAPPc11</td>
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<td>Trim32</td>
<td>Bardet-Biedl syndrome, Muscular dystrophy, limb-girdle</td>
<td>AR</td>
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<td>15</td>
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<td>Ttn*</td>
<td>Dilated cardiomyopathy (DCM), Tibial muscular dystrophy, Limb-girdle muscular dystrophy</td>
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<td>437</td>
<td>226</td>
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</tbody>
</table>

*Some regions of the gene are duplicated in the genome leading to limited sensitivity within the regions. Thus, low-quality variants are filtered out from the duplicated regions and only high-quality variants confirmed by other methods are reported.*
Gene, refers to HGNC approved gene symbol; Inheritance to inheritance patterns such as autosomal dominant (AD), autosomal recessive (AR) and X-linked (XL); ClinVar, refers to a number of variants in the gene classified as pathogenic or likely pathogenic in ClinVar (http://www.ncbi.nlm.nih.gov/clinvar/); HGMD, refers to a number of variants with possible disease association in the gene listed in Human Gene Mutation Database (HGMD, http://www.hgmd.cf.ac.uk/ac/). The list of associated (gene specific) phenotypes are generated from CDG (http://research.nhgri.nih.gov/CGD/) or Orphanet (http://www.orpha.net/) databases.

Non-coding disease causing variants covered by the panel

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genomic location HG19</th>
<th>HGVS</th>
<th>RefSeq</th>
<th>RS-number</th>
<th>Comment</th>
<th>Reference</th>
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<td>COL6A1</td>
<td>Chr21:47409881</td>
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<td>DMD</td>
<td>ChrX:33192452</td>
<td>c.31+36947G&gt;A</td>
<td>NM_004006.2</td>
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<tr>
<td>DMD</td>
<td>ChrX:31983146</td>
<td>c.6614+3310G&gt;T</td>
<td>NM_004006.2</td>
<td>rs797045526</td>
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<td>DMD</td>
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<td>c.8217+18052A&gt;G</td>
<td>NM_004006.2</td>
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<td>DMD</td>
<td>ChrX:31279780</td>
<td>c.9225-647A&gt;G</td>
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<td>DMD</td>
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<td>c.9225-648A&gt;G</td>
<td>NM_004006.2</td>
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<td>DMD</td>
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<td>c.961-5831C&gt;T</td>
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<td>DYSF</td>
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<td>LMNA</td>
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Test performance

Blueprint Genetics offers a Comprehensive Muscular Dystrophy / Myopathy Panel that covers classical genes associated with autosomal recessive myosclerosis myopathy, Becker muscular dystrophy, Bethlem myopathy, collagen type VI-related autosomal dominant limb-girdle muscular dystrophy, congenital muscular dystrophy, distal myopathy, Duchenne muscular dystrophy, Emery-Dreifuss muscular dystrophy, Fukuyama congenital muscular dystrophy, limb-girdle muscular dystrophy, muscle-eye-brain disease, muscular dystrophy, nemaline myopathy, TMEM43-related myopathies, TTN-related myopathies, Ullrich congenital muscular dystrophy, walker-Warburg syndrome and x-linked myotubular myopathy. The genes are carefully selected based on the existing scientific evidence, our experience and most current mutation databases. Candidate genes are excluded from this first-line diagnostic test. The test does not recognise balanced translocations or complex inversions, and it may not detect low-level mosaicism. The test should not be used for analysis of sequence repeats or for diagnosis of disorders caused by mutations in the mitochondrial DNA.

Analytical validation is a continuous process at Blueprint Genetics. Our mission is to improve the quality of the sequencing process and each modification is followed by our standardized validation process. Average sensitivity and specificity in Blueprint NGS Panels is 99.3% and 99.9% for detecting SNPs. Sensitivity to for indels vary depending on the size of the alteration: 1-10bps (96.0%), 11-20 bps (88.4%) and 21-30 bps (66.7%). The longest detected indel was 46 bps by sequence analysis. Detection limit for Del/Dup (CNV) analysis varies through the genome depending on exon size, sequencing coverage and sequence content. The sensitivity is 71.5% for single exon deletions and duplications and 99% for three exons' deletions and duplications. We have validated the assays for different starting materials including EDTA-blood, isolated DNA (no FFPE) and saliva that all provide high-quality results. The diagnostic yield varies substantially depending on the used assay, referring healthcare professional, hospital and country. Blueprint Genetics’ Plus Analysis (Seq+Del/Dup) maximizes the chance to find molecular genetic diagnosis for your patient although Sequence Analysis or Del/Dup Analysis may be cost-effective first line test if your patient's phenotype is suggestive for a specific mutation profile.
Bioinformatics

The sequencing data generated in our laboratory is analyzed with our proprietary data analysis and annotation pipeline, integrating state-of-the-art algorithms and industry-standard software solutions. Incorporation of rigorous quality control steps throughout the workflow of the pipeline ensures the consistency, validity and accuracy of results. The highest relevance in the reported variants is achieved through elimination of false positive findings based on variability data for thousands of publicly available human reference sequences and validation against our in-house curated mutation database as well as the most current and relevant human mutation databases. Reference databases currently used are the 1000 Genomes Project (http://www.1000genomes.org), the NHLBI GO Exome Sequencing Project (ESP; http://evs.gs.washington.edu/EVS), the Exome Aggregation Consortium (ExAC; http://exac.broadinstitute.org), ClinVar database of genotype-phenotype associations (http://www.ncbi.nlm.nih.gov/clinvar) and the Human Gene Mutation Database (http://www.hgmd.cf.ac.uk). The consequence of variants in coding and splice regions are estimated using the following in silico variant prediction tools: SIFT (http://sift.jcvi.org), Polyphen (http://genetics.bwh.harvard.edu/pph2/), and Mutation Taster (http://www.mutationtaster.org).

Through our online ordering and statement reporting system, Nucleus, the customer can access specific details of the analysis of the patient. This includes coverage and quality specifications and other relevant information on the analysis. This represents our mission to build fully transparent diagnostics where the customer gains easy access to crucial details of the analysis process.

Clinical interpretation

In addition to our cutting-edge patented sequencing technology and proprietary bioinformatics pipeline, we also provide the customers with the best-informed clinical report on the market. Clinical interpretation requires fundamental clinical and genetic understanding. At Blueprint Genetics our geneticists and clinicians, who together evaluate the results from the sequence analysis pipeline in the context of phenotype information provided in the requisition form, prepare the clinical statement. Our goal is to provide clinically meaningful statements that are understandable for all medical professionals, even without training in genetics.

Variants reported in the statement are always classified using the Blueprint Genetics Variant Classification Scheme modified from the ACMG guidelines (Richards et al. 2015), which has been developed by evaluating existing literature, databases and with thousands of clinical cases analyzed in our laboratory. Variant classification forms the cornerstone of clinical interpretation and following patient management decisions. Our statement also includes allele frequencies in reference populations and in silico predictions. We also provide PubMed IDs to the articles or submission numbers to public databases that have been used in the interpretation of the detected variants. In our conclusion, we summarize all the existing information and provide our rationale for the classification of the variant.

A final component of the analysis is the Sanger confirmation of the variants classified as likely pathogenic or pathogenic. This does not only bring confidence to the results obtained by our NGS solution but establishes the mutation specific test for family members. Sanger sequencing is also used occasionally with other variants reported in the statement. In the case of variant of uncertain significance (VUS) we do not recommend risk stratification based on the genetic finding. Furthermore, in the case VUS we do not recommend use of genetic information in patient management or genetic counseling. For some cases Blueprint Genetics offers a special free of charge service to investigate the role of identified VUS.

We constantly follow genetic literature adapting new relevant information and findings to our diagnostics. Relevant novel discoveries can be rapidly translated and adopted into our diagnostics without delay. These processes ensure that our diagnostic panels and clinical statements remain the most up-to-date on the market.

CPT codes

SEQ 81479
DEL/DUP 81479

https://blueprintgenetics.com/
ICD codes

Commonly used ICD-10 codes when ordering the Comprehensive Muscular Dystrophy / Myopathy Panel

<table>
<thead>
<tr>
<th>ICD-10</th>
<th>Disease</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>G71.0 Muscular dystrophy</td>
</tr>
</tbody>
</table>

Accepted sample types

- EDTA blood, min. 1 ml
- Purified DNA, min. 5μg
- Saliva (Oragene DNA OG-500 kit)

Label the sample tube with your patient’s name, date of birth and the date of sample collection.

Note that we do not accept DNA samples isolated from formalin-fixed paraffin-embedded (FFPE) tissue.

Resources

- Muscular Dystrophy Association
- Muscular Dystrophy Campaign
- Muscular Dystrophy Family Foundation
- LGMD2I Research Fund
- LGMD-Info
- Cure CMD
- Duchenne Alliance
- Duchenne Foundation
- Fighting Duchenne Foundation
- Foundation Building Strength for Nemaline Myopathy
- Joshua Frase Foundation
- Myotubular Myopathy Resource Group
- Myotubular Trust
- NORD - Distal Myopathy
- NORD - Limb-Girdle Muscular Dystrophy
- NORD - Congenital Muscular Dystrophy
- NORD - Emery-Dreifuss Muscular Dystrophy
- NORD - Becker Muscular Dystrophy
- NORD - Duchenne Muscular Dystrophy
- NORD - Nemaline Myopathy
- NORD - Walker-Warburg Syndrome
- NORD - Fukuyama Congenital Muscular Dystrophy
- NORD - X-linked Myotubular Myopathy
- Gene Reviews - Limb-Girdle Muscular Dystrophy
- Gene Reviews - Congenital Muscular Dystrophy
- Gene Reviews - Emery-Dreifuss Muscular Dystrophy
- Gene Reviews - Becker/Duchenne Muscular Dystrophy
- Gene Reviews - Nemaline Myopathy
- Gene Reviews - Fukuyama Congenital Muscular Dystrophy
- Gene Reviews - X-linked Myotubular Myopathy