Nemaline Myopathy, **TPM2-related**: **TPM2** Gene Deletion/Duplication

**Test Code**: DTPM2  
**Turnaround time**: 2 weeks  
**CPT Codes**: 81228 x1

### Condition Description

The term nemaline myopathy (NM) refers to a group of genetically distinct disorders linked by common morphologic features observed on muscle histology. NM is characterized by weakness, hypotonia, and depressed or absent deep tendon reflexes. Muscle weakness is usually most severe in the face, the neck flexors, and the proximal limb muscles. In some individuals with NM, the distal muscles are involved. There are six forms of NM, classified by onset and severity of motor and respiratory involvement: severe congenital (neonatal) form (16% of all individuals with NM); Amish NM, intermediate congenital form (20%); typical congenital form (46%); childhood-onset form (13%); and adult-onset (late-onset) form (4%). Considerable overlap occurs among the forms and there is variation in course and outcome even within families.

In congenital forms of NM, the face is often elongated and expressionless, with a tent-shaped mouth, high-arched palate, and retrognathia. Gross motor milestones are delayed, but most affected individuals are otherwise developmentally normal. Dysarthria and feeding difficulties are common. Respiratory problems secondary to involvement of the diaphragm and intercostal muscles are common. Many children with NM have hypermobility of joints in infancy and early childhood; contractures and deformities of the joints, including scoliosis, commonly develop with time. The extracocular muscles are usually spared. Cardiac contractility is usually normal.

Diagnosis is based on clinical findings and the observation of characteristic rod-shaped structures (nemaline bodies) on muscle biopsy stained with Gomori trichrome. Serum creatine kinase concentration is usually normal or minimally elevated. Disease-causing mutations have been identified in seven different genes, all of which encode protein components of the muscle thin filament: **ACTA1**, **NEB**, **TPM3**, **TPM2**, **TNNT1**, **CFL2**, and **KBTBD13**. Additional individuals with NM do not link to any of the seven identified loci, suggesting further genetic heterogeneity.

NM can be inherited in an autosomal dominant or autosomal recessive manner. In one study, approximately 20% of cases were autosomal recessive, approximately 30% autosomal dominant, and approximately 50% simplex (i.e., single occurrences in a family) representing heterozygosity for *de novo* dominant mutations or homozygosity for autosomal recessive mutations.

This testing is for mutations in the **TPM2** gene (9p13.2-p13.1) only.

Mutations in **TPM2** have also been associated with distal arthrogryposis multiplex congenita type I and with cap disease, a congenital myopathy with a nonspecific clinical phenotype defined by the finding on muscle biopsy of enlarged Z-discs and cap-like structures containing disorganized thin filaments at the periphery of muscle fibers.

For patients with suspected NM, sequence analysis is recommended as the first step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

### References

- GeneReviews: Nemaline Myopathy
- OMIM #609285 Nemaline Myopathy 4

### Genes

**TPM2**

### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of nemaline myopathy in individuals who have tested negative for sequence analysis
- Carrier testing in adults with a family history of autosomal recessive nemaline myopathy who have tested negative for sequence analysis

### Methodology

DNA isolated from peripheral blood is hybridized to a CGH array to detect deletions and duplications. The targeted CGH array has overlapping probes which cover the entire genomic region.

Please note that a “backbone” of probes across the entire genome are included on the array for analytical and quality control purposes. Rarely, off-target copy number variants causative of disease may be identified that may or may not be related to the patient’s phenotype. Only known pathogenic off-target copy number variants will be reported. Off-target copy number variants of unknown clinical significance will not be reported.
Detection is limited to duplications and deletions. The CGH array will not detect point or intronic mutations. Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

**Specimen Requirements**

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

**Type: Whole Blood**

Specimen Requirements:

In EDTA (purple top) or ACD (yellow top) tube:

- Infants (2 years): 3-5 ml
- Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Type: Saliva**

Specimen Requirements:

Oragene™ Saliva Collection kit (available through EGL) used according to manufacturer instructions.

Specimen Collection and Shipping: Store sample at room temperature. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Special Instructions**

Submit copies of diagnostic biochemical test results with the sample, if appropriate. Contact the laboratory if further information is needed.

Sequence analysis is required before deletion/duplication analysis by targeted CGH array. If sequencing is performed outside of Emory Genetics Laboratory, please submit a copy of the sequencing report with the test requisition.

**Related Tests**

- Sequence analysis of the **TPM2** gene is available and is required before deletion/duplication analysis.
- Sequence analysis and deletion/duplication analysis are also available for the **NEB**, **TNNT1**, **ACTA1**, and **TPM3** genes for nemaline myopathy.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.
- Prenatal testing is available for known familial mutations only. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.