Noonan Syndrome: \textit{PTPN11} Gene Deletion/Duplication

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

### Condition Description

Noonan syndrome (NS) is an autosomal dominant dysmorphology syndrome characterized by short stature, congenital heart defect, and developmental delay of variable degree. Other findings can include broad or webbed neck, unusual chest shape with superior pectus carinatum and inferior pectus excavatum, cryptorchidism, varied coagulation defects, lymphatic dysplasias, ocular abnormalities, and deafness. Characteristic facies include hypertelorism (74%), downward sloping palpebral apertures (38%), epicanthal folds (39%), ptosis (48%), and low-set posteriorly rotated ears. Early feeding difficulties such as poor suck or gastrointestinal dysfunction are also common. Although birth length is usually normal, final adult height approaches the lower limit of normal. Up to one-third of affected individuals have mild intellectual disability.

Congenital heart disease occurs in 50%-80% of individuals with NS. Pulmonary valve stenosis, often with dysplasia, is the most common heart defect and is found in 20%-50% of individuals. Hypertrophic cardiomyopathy is found in 20%-30% of individuals, and may be congenital or develop in infancy or childhood. Other structural defects include atrial and ventricular septal defects, branch pulmonary artery stenosis, and tetralogy of Fallot.

NS is clinically diagnosed. Affected individuals have normal chromosome studies. Molecular genetic testing identifies mutations in \textit{PTPN11} in over 50% of affected individuals. (Other genes known to be involved include \textit{KRAS} in fewer than 5% of affected individuals, \textit{SOS1} in approximately 13%, and \textit{RAF1} in 3%-17%.) The \textit{PTPN11} gene (12q24.1) encodes a nontransmembrane protein-tyrosine phosphatase. One study showed that pulmonic stenosis was more prevalent among the group of individuals with NS who had \textit{PTPN11} mutations than it was in the group without them (70.6% vs 46.2%), while hypertrophic cardiomyopathy was less prevalent among those with \textit{PTPN11} mutations (5.9% vs 26.2%). The prevalence of other congenital heart malformations, short stature, pectus deformity, cryptorchidism, and developmental delay did not differ between the two groups.

Mutations in the \textit{NRAS}, \textit{BRAF}, and \textit{MAP2K1} genes have been reported in less than 1% of cases. Many affected individuals have de novo mutations; however, an affected parent is recognized in 30%-75% of families. When the parents are clinically unaffected, the risk to the sibs of a proband appears to be low (<1%). Noonan syndrome has an estimated incidence of 1 in 1,000 to 2,500 live births.

LEOPARD syndrome can also be caused by mutations in the \textit{PTPN11} gene. LEOPARD is an acronym for multiple lentigines, electrocardiographic conduction abnormalities, ocular hypertelorism, pulmonic stenosis, abnormal genitalia, retardation of growth, and sensorineural deafness. Sequence analysis of \textit{PTPN11} detects missense mutations in about 90% of individuals tested. Unlike the activating mutations found in NS, LEOPARD syndrome mutations are catalytically defective and act as dominant-negative mutations that interfere with growth factor/ERK-MAPK-mediated signaling.

### Genes

\textit{PTPN11}

### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of Noonan syndrome in individuals 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.

### Detection

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**

#### Type: Whole Blood (EDTA)

**Specimen Requirements:**

EDTA (Purple Top)  
Infants and Young Children (2 years of age to 10 years old): 3-5 ml  
Older Children & Adults: 5-10 ml  
Autopsy: 2-3 ml unclotted cord or cardiac blood

**Specimen Collection and Shipping:**  
Ship sample at room temperature for receipt at EGL within 24 hours of collection. Do not refrigerate or freeze.
Type: DNA, Isolated

Specimen Requirements:
Microtainer
3µg
Isolation using the Perkin Elmer™Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping:
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample 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 EGL Genetics, please submit a copy of the sequencing report with the test requisition.

Related Tests
- Sequence analysis of the PTPN11 gene is available and is required before deletion/duplication analysis.
- Sequence and deletion/duplication analysis for the NRAS, KRAS, RAF1 and SOS1 genes are also available.
- Prenatal testing is available to couples who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.