
**Test Code:** DPEX2  
**Turnaround time:** 2 weeks  
**CPT Codes:** 81228 x1

## Condition Description

Peroxisome biogenesis disorders, Zellweger syndrome spectrum (PBD, ZSS) is a continuum that encompasses three distinct phenotypes; Zellweger syndrome (ZS), neonatal adrenoleukodystrophy (NALD), and infantile Refsum disease (IRD). Individuals with PBD, ZSS usually present during the newborn period or later in childhood. Features during the newborn period include hypotonia, poor feeding, distinctive facial features, seizures, and liver cysts with hepatic dysfunction. Infants with ZS, the most severe phenotype on the spectrum, are significantly impaired and usually do not survive past the first year of life. Those that do survive past the first year have developmental delay with hypotonia, liver dysfunction, sensorineural hearing loss, and retinal dystrophy. Features of NALD and IRD (the least severe phenotype on the spectrum) are variable. They include developmental delays, liver dysfunction, episodes of intracranial bleeding, hearing loss, and vision impairments. PBD, ZSS can be slowly progressive.

PBD, ZSS is inherited in an autosomal recessive manner. Biochemical assays can definitively diagnose PBD, ZSS. Mutations in twelve different PEX genes have been identified to cause PBD, ZSS. They are the *PEX1, PEX2, PEX3, PEX5, PEX6, PEX10, PEX12, PEX13, PEX14, PEX16, PEX19,* and *PEX26* genes. About 68% of individuals with PBD, ZSS have mutations in the *PEX1* gene. Mutations in the *PEX6, PEX10, PEX12,* and *PEX26* genes account for an additional 26% of mutations in individuals with PBD, ZSS.

Please note that this test is for the *PEX2* gene (8q21.1) only.

For patients with suspected PBD, ZSS, 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
- OMIM #170993: *PEX2* gene
- OMIM #214100: ZS

## Genes

**PEX2**

## Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of peroxisome biogenesis disorders, Zellweger syndrome in an individual in whom sequence analysis was negative.
- Carrier testing in adults with a family history of peroxisome biogenesis disorders, Zellweger syndrome in whom sequence analysis was negative.

## 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

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\textsuperscript{TM} 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 \textit{PEX2} gene is available and is required before deletion/duplication analysis.
- Sequence and deletion/duplication analysis for the \textit{PEX1, PEX3, PEX5, PEX6, PEX12, PEX14} and \textit{PEX26} genes are also available.
- 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 only for known familial mutations to individuals who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.