Smith-Lemli-Opitz Syndrome: \textit{DHCR7} Gene Sequencing

\textbf{Test Code:} SDHCR  
\textbf{Turnaround time:} 6 weeks  
\textbf{CPT Codes:} 81405 x1

\section*{Condition Description}

Smith-Lemli-Opitz syndrome (SLOS) is a congenital multiple anomaly syndrome caused by an inherited disorder of cholesterol biosynthesis. The severity of the SLOS clinical phenotype can be highly variable ranging from individuals who have minor features and normal development to those with severe intellectual disability and congenital anomalies. These anomalies may include prenatal and postnatal growth retardation, microcephaly, characteristic facial features, cleft palate, cardiac anomalies, postaxial polydactyly, 2-3 syndactyly of the toes and males with underdeveloped genitalia.

Mutations of the \textit{DHCR7} (11q12-q13) gene cause SLOS. SLOS is inherited in an autosomal recessive manner.

For patients with suspected SLOS, 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.


\textbf{References:}
- GeneReviews
- OMIM \#602858: \textit{DHCR7} gene
- OMIM \#270400: SLOS

\section*{Genes}

\textit{DHCR7}

\section*{Indications}

This test is indicated for:
- Confirmation of a clinical diagnosis of Smith-Lemli-Opitz syndrome.
- Carrier testing in adults with a family history of Smith-Lemli-Opitz syndrome.

\section*{Methodology}

PCR amplification of 7 exons contained in the \textit{DHCR7} gene is performed on the patient's genomic DNA. Direct sequencing of amplification products is performed in both forward and reverse directions, using automated fluorescence dideoxy sequencing methods. The patient's gene sequences are then compared to a normal reference sequence. Sequence variations are classified as mutations, benign variants unrelated to disease, or variations of unknown clinical significance. Variants of unknown clinical significance may require further studies of the patient and/or family members. This assay does not interrogate the promoter region, deep intronic regions, or other regulatory elements, and does not detect large deletions.

\section*{Detection}

Sequence analysis of the \textit{DHCR7} gene detects approximately 96% of known mutations. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical and/or biochemical phenotype.

\textbf{Analytical Sensitivity:} \textasciitilde99%

\section*{Specimen Requirements}

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

\section*{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.

\section*{Type: Saliva}

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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.

Related Tests

- Deletion/duplication analysis of the DHCR7 gene by CGH array is available for those individuals in whom sequence analysis is negative.
- 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.