Peters Plus Syndrome: \textit{B3GLCT} Gene Sequencing

\textbf{Test Code:} SB3GA  \\
\textbf{Turnaround time:} 4 weeks  \\
\textbf{CPT Codes:} 81479 x1

\section*{Condition Description}

Peters plus syndrome is characterized by developmental delay/intellectual disability, disproportionate short stature, cleft lip and/or palate, and anterior chamber eye anomalies with the most common being Peters' anomaly. Typical facial features include a cupid's bow-shaped upper lip, narrow palpebral fissures, a prominent forehead, and a long philtrum. Mutations in the \textit{B3GLCT} gene (13q12.3) cause the autosomal recessive Peters plus syndrome. Many individuals with Peters plus syndrome have the common c660+1G>A mutation in the \textit{B3GLCT} gene.

\section*{References:}
- GeneReviews
- OMIM \#610308: \textit{B3GLCT} gene
- OMIM \#261540: Peters plus syndrome

\section*{Genes}

\textit{B3GLCT}

\section*{Indications}

This test is indicated for:

- Confirmation of a clinical diagnosis of Peters plus syndrome.
- Carrier testing in adults with a family history of Peters plus syndrome.

\section*{Methodology}

\textbf{Next Generation Sequencing:} In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

\section*{Detection}

\textbf{Clinical Sensitivity:} Unknown. 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:} ~99%

\section*{Specimen Requirements}

\textit{Submit only 1 of the following specimen types}

\textbf{Type: DNA, Isolated}

\textbf{Specimen Requirements:}
- Microtainer
- 8µg
- Isolation using the Perkin Elmer™Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

\textbf{Specimen Collection and Shipping:}
- Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

\textbf{Type: Whole Blood (EDTA)}

\textbf{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 unclootted cord or cardiac blood

\textbf{Specimen Collection and Shipping:}
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

**Type: Saliva**

**Specimen Requirements:**
Oragene™ Saliva Collection Kit
Orangene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

**Specimen Collection and Shipping:**
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

**Related Tests**
- 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.