Peters Plus Syndrome: \textit{B3GLCT} Gene Sequencing

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

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\textbf{Condition Description} \\
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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.  \\
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References:
- GeneReviews
  - OMIM \#610308: \textit{B3GLCT} gene
  - OMIM \#261540: Peters plus syndrome

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\textbf{Genes} \\
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\textit{B3GLCT} \\
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\textbf{Indications} \\
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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.  \\
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\textbf{Methodology} \\
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\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.  \\
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\textbf{Detection} \\
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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.  \\
Analytical Sensitivity: \textsim 99\%  \\
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\textbf{Specimen Requirements} \\
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Submit only 1 of the following specimen types  \\
* Preferred specimen type: Whole Blood  \\

\textbf{Type: Whole Blood}  \\
Specimen Requirements:  \\
- In EDTA (purple 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.  \\

\textbf{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.

\textbf{Disclaimer:} This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
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.