Coffin-Lowry Syndrome: \textit{RPS6KA3} Gene Deletion/Duplication

\textbf{Test Code:} DPS6K  
\textbf{Turnaround time:} 2 weeks  
\textbf{CPT Codes:} 81228 x1

\section*{Condition Description}

Intellectual disability (ID) is a nonprogressive cognitive impairment affecting 1-3\% of the Western population. It is estimated that up to 50\% of moderate-severe cases have genetic causes and approximately 10\% are due to X-linked intellectual disability disorders (XLID). XLID can be syndromic or nonsyndromic and is observed in all ethnic groups. More than 100 XLID syndromes have been described in the literature to date. Fragile X is the most common XLID syndrome (~1 in 4000 males) while others can be quite rare with only a few patients reported in the literature. Males can have moderate to severe intellectual disability depending on the syndrome, and carrier females can also be affected, but typically have milder clinical symptoms.

Coffin-Lowry syndrome (CLS) is an X-linked condition characterized in males by mild to profound ID, dysmorphic facies and extremities. The facial features include prominent forehead, hypertelorism, large mouth, and prominent ears. The extremity features include fingers that taper, short, soft, fleshy hands with hyper-extensible fingers, and full, fleshy forearms. Females can range from asymptomatic carriers to fully affected.

Mutations in the \textit{RPS6KA3} gene (Xp22.2-p22.1), also known as \textit{RSK2}, cause CLS. It is the only gene known to be associated with CLS. 90-95\% of mutations can be identified in individuals clinically diagnosed with CLS. 70-80\% of individuals with CLS have no family history of CLS. Additionally, missense mutations in the \textit{RPS6KA2} gene have been demonstrated to cause XLMR 19.

For patients with suspected CLS, 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.

\section*{References:

- GeneReviews
- OMIM \#300075: \textit{RPS6KA3} gene
- OMIM \#303600: Coffin-Lowry syndrome
- OMIM \#300844: XLMR 19

\section*{Genes}

\textbf{RPS6KA3}

\section*{Indications}

This test is indicated for:

- Confirmation of a clinical diagnosis of Coffin-Lowry syndrome in an individual in whom sequence analysis was negative.
- Carrier testing in adults with a family history of Coffin-Lowry syndrome in whom sequence analysis was negative.

\section*{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.

\section*{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.

\section*{Specimen Requirements}

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

\section*{Type: DNA, Isolated}

\textbf{Specimen Requirements:}

- Microtainer
- 3\textmu g

Isolation using the Perkin Elmer™Chemagen™ 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/\mu L in TE buffer. Ship sample at room temperature with overnight delivery.

\section*{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 72 hours of collection. Do not freeze.

Special Instructions
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 *RPS6KA3* gene is available and is required before deletion/duplication analysis.
- 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.
- X-Linked Intellectual Disability panels are available for 30, 60, and 90 genes.