Hypophosphatasia: \textit{ALPL} Gene Sequencing

\textbf{Test Code: MSALP}
\textbf{Turnaround time: 6 weeks}
\textbf{CPT Codes: 81479 x1}

\section*{Condition Description}

Hypophosphatasia is a rare disorder characterized by impaired mineralization in bones and/or teeth due to deficiency in serum and bone alkaline phosphatase. At least six clinical forms are currently recognized based on age at diagnosis and severity of features. The highly variable clinical presentation ranges from a severe perinatal form to a mild odonto-hypophosphatasia form in which only teeth are affected. Clinical features may include prenatal long-bone bowing, infantile rickets with growth failure, craniosynostosis, scoliosis, costochondral enlargements, hypotonia, hypercalcemia and hypercalciuria, bone pain, and premature loss of deciduous teeth.

Hypophosphatasia is caused by pathogenic variants in the \textit{ALPL} gene. The \textit{ALPL} gene provides instructions for making the enzyme alkaline phosphatase, which is essential in the formation of strong bones and teeth.

Hypophosphatasia is caused by pathogenic variants in the \textit{ALPL} gene. The \textit{ALPL} gene provides instructions for making the enzyme alkaline phosphatase, which is essential in the formation of strong bones and teeth. Perinatal and infantile forms are inherited in an autosomal recessive manner, while milder forms, such as adult hypophosphatasia and odontohypophosphatasia, may be inherited in an autosomal recessive or autosomal dominant fashion. Severe forms of hypophosphatasia affect an estimated 1 in 100,000 newborns and appears most commonly in a Mennonite population in Manitoba, Canada.

\textbf{References:}


\section*{Genes}

\textit{ALPL}

\section*{Indications}

This test is indicated for:

- Individuals with a clinical diagnosis of hypophosphatasia.

\section*{Methodology}

PCR amplification of 11 exons contained in the \textit{ALPL} 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 pathogenic variants, 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}

\textbf{Clinical Sensitivity:} Unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element pathogenic variants 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 biochemical phenotype.

\textbf{Analytical Sensitivity:} \textasciitilde 99\%.

\section*{Specimen Requirements}

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: Ship sample at room temperature with overnight delivery.

**Type: Isolated DNA**

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping: Refrigerate until time of shipment in 100 ng/ul of TE buffer. Ship sample at room temperature with overnight delivery.

**Related Tests**

Hypophosphatasia: ALPL Deletion/Duplication