Leber Congenital Amaurosis: Sequencing Panel

<table>
<thead>
<tr>
<th>Test Code: MM137</th>
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<td>Turnaround time: 6 weeks</td>
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<tr>
<td>CPT Codes: 81404 x1, 81406 x1, 81408 x1</td>
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### Condition Description

Leber congenital amaurosis (LCA) is characterized by poor vision beginning between birth or early childhood, nystagmus, an initially normal fundus exam and a nonrecordable electroretinogram (ERG). In addition, other typical findings include defective pupillary responses, photophobia, and the characteristic Franceschetti's oculo-digital sign. Over time, macular coloboma and pigmented retinopathy may develop. Due to the early manifestation of LCA, other syndromic or nonsyndromic conditions may be incorrectly diagnosed as LCA. LCA is most commonly inherited in an autosomal recessive manner. Please note, the \textit{NMNAT1} gene is not included in the NGS panel at this time due to presence of at least four pseudogenes. For clinicians that would like \textit{NMNAT1} analysis in the event that all other genes test negative, we request that you contact EGL directly.

### References
- OMIM
- GeneReviews

### Genes

\begin{verbatim}
AIPL1, CABP4, CEP290, CNGA3, CNGB3, CRB1, CRX, GNAT2, GUCY2D, IMPDH1, IQCB1, KCNJ13, LCA5, LRAT, OTX2, PDE6C, PDE6H, RD3, RDH12, RPE65, RPGRIP1, SPATA7, TULP1
\end{verbatim}

### Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of Leber congenital amaurosis.
- Carrier testing in adults with a family history of Leber congenital amaurosis.

### Methodology

**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.

### Detection

**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 clinical and/or biochemical phenotype.

**Analytical Sensitivity:** ~99%.

### Specimen Requirements

Submit only 1 of the following specimen types

#### 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.

Special Instructions

Please include fundus photographs, electroretinogram (ERG) findings, visual field findings, and visual acuity, if available, for expert review and clinical correlation with test results.

Related Tests

- Eye Disorders: Comprehensive Sequencing and Deletion/Duplication Panels.