Stickler Syndrome: Sequencing Panel

<table>
<thead>
<tr>
<th>Test Code:</th>
<th>MM236</th>
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<tbody>
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<td>Turnaround time:</td>
<td>6 weeks</td>
</tr>
<tr>
<td>CPT Codes:</td>
<td>81479 x1</td>
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</tbody>
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### Condition Description

Stickler syndrome is a genetically heterogeneous connective tissue disorder that typically results in abnormalities of the ocular, auditory, and skeletal systems. Individuals can have a characteristic flat facial appearance that results from underdeveloped bones in the midface. Pierre Robin sequence, hearing impairment/loss and joint hypermobility are common. Eye manifestations include high myopia, cataract, retinal detachment, and vitreous abnormalities. While the disorder is completely penetrant, much phenotypic variability exists. Stickler syndrome can be inherited in an autosomal dominant (COL2A1, COL11A1 and COL11A2 genes) or autosomal recessive (COL9A1 and COL9A2 genes) manner.

References:
- OMIM
- GeneReviews

### Genes

COL11A1, COL11A2, COL2A1, COL9A1, COL9A2

### Indications

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

### 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
- Stickler Syndrome: Deletion/Duplication Panel