### Hyper IgE Syndromes: Sequencing Panel

**Test Code:** MM370  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81405 x1, 81479 x1

<table>
<thead>
<tr>
<th>Condition Description</th>
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<td>Hyper IgE syndromes (HIES) are characterized by highly elevated levels of IgE, eczema, and recurrent skin and respiratory tract infections. An autosomal dominant form of HIES is caused by pathogenic variants in <em>STAT3</em> and also involves connective tissue, vascular, and skeletal abnormalities. The autosomal recessive form is caused by pathogenic variants in <em>DOCK8</em> and causes an increased incidence of neurological abnormalities and viral infections of the skin. Other disorders with elevated IgE and similar symptoms include tyrosine kinase 2 deficiency caused by pathogenic variants in <em>TYK2</em> and Netherton syndrome caused by pathogenic variants in <em>SPINK5</em>.</td>
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### References:
- GeneReviews.
- OMIM.

### Genes
- *DOCK8*, *SPINK5*, *STAT3*, *TYK2*

### Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of Hyper IgE Syndromes.

### 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

**Next Generation Sequencing:** 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/duplications will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/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.

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Related Tests

- Hyper IgE Syndromes: Deletion/Duplication Panel