XLMR 91: ZDHHC15 Gene Sequencing

<table>
<thead>
<tr>
<th>Test Code: SZDHH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Turnaround time: 4 weeks</td>
</tr>
<tr>
<td>CPT Codes: 81479 x1</td>
</tr>
</tbody>
</table>

**Condition Description**

A female with a translocation resulting in the loss of ZDHHC15 (Xq13.3) expression has been described in the literature. This individual had severe muscular hypotonia in infancy, early childhood obesity, small hands and feet, facial changes and delayed psychomotor development. As an adult, she was reported to be of average height and weight but had severe psychomotor delays. Additionally, she had seizures, dysmorphic facies, and no speech. The t(X;15)(q13.3;cen) balanced translocation in this individual resulted in the ZDHHC15 transcript being absent from lymphocytes. Methylation studies revealed 100% skewed X inactivation with the normal X chromosome inactive.

For patients with suspected XLMR 91, 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.

References:

**Genes**

ZDHHC15

**Indications**

This test is indicated for:
- Confirmation of a clinical diagnosis of XLMR 91.
- Carrier testing in adults with a family history of XLMR 91.

**Methodology**

PCR amplification of 11 exons contained in the ZDHHC15 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 mutations, 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.

**Detection**

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 will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's biochemical phenotype.

Analytical Sensitivity: ~99%

**Specimen Requirements**

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

**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: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Type: Saliva**

Specimen Requirements:

Oragene™ Saliva Collection kit (available through EGL) used according to manufacturer instructions.
Specimen Collection and Shipping: Store sample at room temperature. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Special Instructions**

Submit copies of diagnostic biochemical test results with the sample, if appropriate. Contact the laboratory if further information is needed.

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**

- Deletion/duplication analysis of the *ZDHHC15* gene by CGH array is available for those individuals in whom sequence analysis is negative.
- 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.