Fucosidosis: **FUCA1 Gene Sequencing**

**Test Code:** SFUCA  
**Turnaround time:** 4 weeks  
**CPT Codes:** 81479 x1

### Condition Description

Fucosidosis is an autosomal recessive lysosomal storage disorder due to deficient activity of the alpha-1-fucosidase enzyme. When this enzyme is deficient, a build-up of fucosyl-glycolipids, glycopeptides, and oligosaccharides occurs in various tissues. Major features of fucosidosis include neurodegeneration with progressive motor and mental deterioration. Additional features include muscle wasting and dystrophy, growth retardation, spasticity, contractures, recurrent infections, seizures, coarse features, dysostosis multiplex, angiokeratoma corporis diffusum, ocular abnormalities, visceromegaly, and hearing loss. Fucosidosis has a wide continuous clinical spectrum; however, all of the features are progressive and ultimately lead to an early death. The disease may take a rapid course with death occurring in infancy or it may be more mild, with death occurring in adulthood.

Mutations in the **FUCA1** gene (1p36.11) cause fucosidosis. Missense, nonsense, and splice-site mutations have been reported as well as small deletions, large deletions, insertions, and duplications. Willems et al. (1999) report 79 out of 80 mutations in 40 patients.

For patients with suspected fucosidosis, 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:**
- OMIM #612280: FUCA1 gene
- OMIM #230000: Fucosidosis

### Genes

**FUCA1**

### Indications

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

### Methodology

PCR amplification of 8 exons contained in the **FUCA1** 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: Willems et al. (1999) report 79 out of 80 mutations in 40 patients. 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 clinical and/or 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.

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
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.

Related Tests

- Deletion/duplication analysis of the FUCAT 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.