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, spinal cord atrophy, recurrent infections, seizures, coarse features, dysostosis multiplex, angioedema, 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**

**Type: Whole Blood (EDTA)**

**Specimen Requirements:**

EDTA (Purple Top)

- Infants and Young Children (2 years of age to 10 years old): 3-5 ml
- Older Children & Adults: 5-10 ml

Autopsy: 2-3 ml unclotted cord or cardiac blood

**Specimen Collection and Shipping:**

Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

**Type: DNA, Isolated**
Specimen Requirements:
Microtainer
8µg
Isolation using the Perkin Elmer™Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping:
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

Type: Saliva

Specimen Requirements:
Oragene™ Saliva Collection Kit
Oragene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

Specimen Collection and Shipping:
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

Related Tests

- Deletion/duplication analysis of the FUCA1 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.