Congenital Disorders of Glycosylation: Sequencing Panel

**Test Code:** MCDG1  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81404 x1, 81405 x1, 81406 x1

### Condition Description

Congenital disorders of glycosylation (CDG) are a group of autosomal recessive genetic disorders caused by the alteration in synthesis and structure of protein and lipid glycosylation. In the past decade, over 30 genetic diseases have been identified that alter glycan synthesis, structure and ultimately the function of nearly all organ systems.

CDG type I (CDGI) disorders result from impaired synthesis of the incomplete lipid linked oligosaccharide (LLO) and/or its attachment to the growing polypeptide chain. CDG-Ia is the most common form reported, due to phosphomannomutase deficiency, an enzyme that converts mannose-6-phosphate to mannose-1-phosphate. CDG-Ib (phosphomannose isomerase, MPI deficiency) is the only known treatable form, by giving mannose orally. CDG type II (CDGII) includes defects in processing of N-glycans.

Phenotypes of this disorder are extremely variable. Manifestations range from severe developmental delay and hypotonia with multiple organ system involvement beginning in infancy, to hypoglycemia and protein-losing enteropathy with normal development. Most subtypes have been described in only a few individuals, however, thus understanding of the phenotypes is limited.

The current diagnostic test for CDG is analysis of serum transferrin glycoforms, also called "transferrin isoforms analysis," or "carbohydrate-deficient transferrin analysis." If positive, this testing can be followed by DNA testing to identify mutations in the gene involved. If a sample is not available for biochemical testing or if biochemical test results are inconclusive, this panel offers next generation sequence of CDG-associated genes.

**Note:** This test does not detect the retrotransposon insertion in the 3’ UTR of the *FKTN* gene common in some Asian populations. For patients with suspected Fukuyama congenital muscular dystrophy, testing for the *FKTN* insertion is recommended. Analysis for the *FKTN* insertion is available as a separate assay.

**References:**

### Genes

| ALG1, ALG11, ALG12, ALG13, ALG14, ALG2, ALG3, ALG6, ALG8, ALG9, ATP6V0A2, B3GAT3, B3GLCT, B4GA1T1, B4GA1T7, CHST14, CHST3, CHST6, CHSY1, COG1, COG4, COG5, COG6, COG7, COG8, DDOBT, DHDSS, DOLK, DPAGT1, DPM1, DPM3, EXT1, EXT2, FKRP, F KTN, GALT3, GFTT1, GNE, LARGE1, LFNG, MAN1B1, MGAT2, MOGS, MPDU1, MPI, NGLY1, PGMI, PIGA, PIGL, PIGM, PIGO, PMM2, POMGNT1, POMT1, POMT2, RFT1, SEC23B, SLC35A1, SLC35C1, SLC35D1, SRD5A3, ST3GAL3, ST3GAL5, TMEM165, TUSC3 |

### Indications

This test is indicated for:
- Confirmation of a clinical/biochemical diagnosis of a CDG, or when CDG is suspected and biochemical results are unavailable or inconclusive.
- Carrier testing in adults with a family history of a CDG.

### 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 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) or ACD (yellow 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: 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**

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 Emory Genetics Laboratory, please submit a copy of the sequencing report with the test requisition.

**Related Tests**

- Individual sequence analysis and deletion/duplication analysis is available for each of the genes in the panel.
- Biochemical testing for CDGs is available. See the test menu for details.
- 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 to adult couples who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.