MAYO CLINIC LABORATORIES

NEW TEST

Notification Date: September 25, 2023
Effective Date: October 26, 2023

UDP-Glucuronosyltransferase 1A1 (UGT1A1), Full Gene Sequencing, Varies

Test ID: UGTFZ

Useful for:

- Establishing a diagnosis of Crigler-Najjar syndrome type I or type II and the trait of Gilbert syndrome
- Establishing carrier status for Crigler-Najjar syndrome type I or type II
- Identifying individuals who are at risk of hyperbilirubinemia or who have Gilbert syndrome
- Identifying individuals who are at increased risk of adverse drug reactions or hyperbilirubinemia when taking drugs that are metabolized by *UGT1A1*, including atazanavir, belinostat, irinotecan, nilotinib, pazopanib, and sacituzumab govitecan
- Identifying individuals who may have increased drug levels when taking dolutegravir or raltegravir
- Follow-up testing for individuals with a suspected *UGT1A1* variant, who had negative TA repeat region testing

Genetics Information:

This is a full gene sequencing test for *UGT1A1* that includes the TA repeat region of the promoter and all intron/exon boundaries. Results are interpreted for the purposes of UGT1A1 drug metabolism and hereditary hyperbilirubinemia syndromes (Gilbert syndrome and Crigler-Najjar syndrome). This test does not include deletion/duplication analysis of the *UGT1A1* gene.

Testing Algorithm:

For information see *UGT1A1* Test-Ordering Algorithm.

Methods:

Polymerase Chain Reaction (PCR) followed by DNA Sequence Analysis

Reference Values:

An interpretive report will be provided.

Specimen Requirements:

Patient Preparation: A previous liver transplant, bone marrow transplant from an allogenic donor, or a recent (ie, <6 weeks from time of sample collection) heterologous blood transfusion will interfere with testing. Call 800-533-1710 for instructions for testing patients who have received a bone marrow transplant.

Submit only 1 of the following specimens:

Specimen Type:	**Whole blood**
Container/Tube:	Adults: Lavender top (EDTA) Pediatrics: Purple microtube
Specimen Volume:	Adults: 3 mL Pediatrics: 1 mL
Collection Instructions:	1. Invert several times to mix blood 2. Send whole blood specimen in original tube. **Do not aliquot.**
Specimen Stability Information:	Ambient (preferred) 9 days/Refrigerated 30 days
Minimum Volume:	0.45 mL

Specimen Type:	**Saliva**
Patient Preparation:	Patient should not eat, drink, smoke, or chew gum 30 minutes prior to collection.
Supplies:	Saliva Swab Collection Kit (T786)
Container/Tube:	Saliva Swab Collection Kit
Specimen Volume:	One Swab
Collection Instructions:	Collect and send specimen per kit instructions.
Specimen Stability Information:	Ambient 30 days

Shipping Instructions:

If submitting microtube, place inside a larger tube or vial for transport.

Specimen Stability Information:

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

Ordering Guidance:

If analysis of only the UGT1A1 promoter TA repeat region (*28, *36, *37 alleles) is desired, see U1A1Q / UDP-Glucuronosyltransferase 1A1 TA Repeat Genotype, *UGT1A1*, Varies.

Interpretation:

- An interpretive report will be provided that includes assessment of risk for UGT1A1-associated adverse drug reactions as well as interpretation for hyperbilirubinemia syndromes.

- All detected variants are evaluated according to American College of Medical Genetics and Genomics (ACMG) recommendations.(9) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.
- For additional information regarding pharmacogenomic genes and their associated drugs, see Pharmacogenomic Associations Tables. This resource includes information regarding enzyme inhibitors and inducers, as well as potential alternate drug choices

Cautions:

Clinical Correlations:

- If the patient has had an allogeneic hematopoietic stem cell transplant (bone marrow transplant) or a recent non-leukocyte reduced blood transfusion, results may be inaccurate due to the presence of donor DNA. For individuals who have received allogeneic hematopoietic stem cell transplantation, a pretransplant DNA specimen is recommended for testing. *UGT1A1* genetic test results in patients who have undergone liver transplantation may not accurately reflect the patient's *UGT1A1* status. Contact Mayo Clinic Laboratories for information and guidance when testing patients who have received a transplant. Absence of a detectable gene variant does not rule out the possibility that the patient may have a genetic cause for increased unconjugated bilirubin.
- Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
- If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Detection of a reportable variant in an affected family member would allow for more informative testing of at-risk individuals.
- To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact Mayo Clinic Laboratories genetic counselors at 800-533-1710.

Technical Limitations:

- Rare variants exist that could lead to false-negative or false-positive results. If results obtained do not match the clinical findings, additional testing should be considered.

Reclassification of Variants:

- Currently, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare providers to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time.

Variant Evaluation:

- Evaluation and categorization of variants are performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.(9) Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.
- Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools are interpreted with caution and professional clinical judgment.

CPT Code:

81404

Day(s) Performed: Monday through Friday **Report Available:** 7 to 14 days

Questions

Contact Michelle Raths, Laboratory Resource Coordinator at 800-533-1710.