

## Overview

### Useful For

Follow up for abnormal biochemical results suggestive of a ketone disorder

Establishing a molecular diagnosis for patients with ketone disorders

Identifying variants within genes known to be associated with ketone disorders, allowing for predictive testing of at-risk family members

### Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
CULFB	Fibroblast Culture for Genetic Test	Yes	No

### Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in 9 genes associated with ketone disorders: *ACAA2*, *ACAT1*, *ACAT2*, *AKT2*, *BDH1*, *HMGCL*, *HMGCS2*, *OXCT1*, *SLC16A1*. See [Targeted Genes and Methodology Details for Ketone Disorders Gene Panel](#) in Special Instructions and Method Description for additional details.

Identification of a pathogenic variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for ketone disorders.

Additional first tier testing may be considered/recommended. For more information see Ordering Guidance.

### Testing Algorithm

For skin biopsy or cultured fibroblast specimens, fibroblast culture testing will be performed at an additional charge. If viable cells are not obtained, the client will be notified.

### Special Instructions

- [Molecular Genetics: Biochemical Disorders Patient Information](#)
- [Informed Consent for Genetic Testing](#)
- [Blood Spot Collection Card-Spanish Instructions](#)
- [Blood Spot Collection Card-Chinese Instructions](#)
- [Informed Consent for Genetic Testing \(Spanish\)](#)
- [Blood Spot Collection Instructions](#)
- [Targeted Genes and Methodology Details for Ketone Disorders Gene Panel](#)

### Method Name

Sequence Capture and Targeted Next-Generation Sequencing followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing.

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**NY State Available**

Yes

**Specimen****Specimen Type**

Varies

**Ordering Guidance**

The recommended first-tier biochemical testing for ketone disorders includes urine organic acids and plasma acylcarnitine profile. Order OAU / Organic Acids Screen, Random, Urine and ACRN / Acylcarnitines, Quantitative, Plasma.

Customization of this panel and single gene analysis for any gene present on this panel is available. For more information see CGPH / Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies

**Shipping Instructions**

Specimen preferred to arrive within 96 hours of collection.

**Specimen Required**

**Patient Preparation:** A previous bone marrow transplant from an allogenic donor 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:**

**Preferred:** Lavender top (EDTA) or yellow top (ACD)

**Acceptable:** Any anticoagulant

**Specimen Volume:** 3 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) 4 days/Refrigerated 14 days

**Specimen Type:** Skin biopsy

**Supplies:** Fibroblast Biopsy Transport Media (T115)

**Container/Tube:** Sterile container with any standard cell culture media (eg, minimal essential media, RPMI 1640). The solution should be supplemented with 1% penicillin and streptomycin.

**Specimen Volume:** 4-mm punch

**Specimen Stability Information:** Refrigerated (preferred)/Ambient

**Additional Information:** A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing. An additional 3 to 4 weeks is required to culture fibroblasts before genetic testing can occur.

**Specimen Type:** Cultured fibroblast

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**Container/Tube:** T-25 flask

**Specimen Volume:** 2 Flasks

**Collection Instructions:** Submit confluent cultured fibroblast cells from a skin biopsy from another laboratory. Cultured cells from a prenatal specimen will not be accepted.

**Specimen Stability Information:** Ambient (preferred)/Refrigerated (<24 hours)

**Additional Information:** A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing. An additional 3 to 4 weeks is required to culture fibroblasts before genetic testing can occur.

**Specimen Type:** Blood spot

**Supplies:** Card-Blood Spot Collection (Filter Paper) (T493)

**Container/Tube:**

**Preferred:** Collection card (Whatman Protein Saver 903 Paper)

**Acceptable:** PerkinElmer 226 (formerly Ahlstrom 226) filter paper or blood spot collection card

**Specimen Volume:** 5 Blood spots

**Collection Instructions:**

1. An alternative blood collection option for a patient 1 year of age or older is a fingerstick. For infants younger than 1 year, a heel stick should be used. See [How to Collect Dried Blood Spot Samples](#) via fingerstick.
2. Let blood dry on the filter paper at ambient temperature in a horizontal position for a minimum of 3 hours.
3. Do not expose specimen to heat or direct sunlight.
4. Do not stack wet specimens.
5. Keep specimen dry.

**Specimen Stability Information:** Ambient (preferred)/Refrigerated

**Additional Information:**

1. Due to lower concentration of DNA yielded from blood spot, it is possible that additional specimen may be required to complete testing.
2. For collection instructions, see [Blood Spot Collection Instructions](#)
3. For collection instructions in Spanish, see [Blood Spot Collection Card-Spanish Instructions](#) (T777)
4. For collection instructions in Chinese, see [Blood Spot Collection Card-Chinese Instructions](#) (T800)

**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)

**Specimen Volume:** 1 Swab

**Collection Instructions:** Collect and send specimen per kit instructions.

**Specimen Stability Information:** Ambient 30 days

**Additional Information:** Due to lower concentration of DNA yielded from saliva, it is possible that additional specimen may be required to complete testing.

## Forms

1. **New York Clients-Informed consent is required.** Document on the request form or electronic order that a copy is on file. The following documents are available in Special Instructions:

-[Informed Consent for Genetic Testing](#) (T576)

-[Informed Consent for Genetic Testing \(Spanish\)](#) (T826)

2. [Molecular Genetics: Biochemical Disorders Patient Information](#) (T527) in Special Instructions

## Specimen Minimum Volume

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See Specimen Required

**Reject Due To**

All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

**Specimen Stability Information**

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

**Clinical & Interpretive****Clinical Information**

Ketones are a chemical energy source used by tissues when glucose is low. Disorders of impaired ketone body metabolism include beta-ketothiolase (BKT) deficiency and succinyl-CoA:3-ketoacid CoA transferase (SCOT) deficiency. Disorders of ketogenesis are mitochondrial 3-hydroxy-3-methylglutaric acid CoA (HMG-CoA) synthase (mHS) and HMG-CoA lyase (HL) deficiencies.

BKT deficiency is caused by impaired activity of the enzyme acetoacetyl-CoA thiolase. Individuals with BKT deficiency are typically asymptomatic at birth, and symptoms are likely to develop from 6 to 18 months of age with illness or fasting, which appear as episodes of decompensation and severe ketoacidosis, vomiting, dehydration, and lethargy. Children are usually asymptomatic between episodes.

SCOT deficiency is a more severe ketone utilization disorder, as all experience recurrent ketoacidotic episodes, and most individuals have chronic ketosis. About 50% of infants with SCOT deficiency present in the first week of life, and the remaining 50% present between 6 to 24 months of age.

mHS deficiency is due to reduced activity of a mitochondrial enzyme mHS. Infants with mHS deficiency have episodes of hypoketotic hypoglycemia, which can progress to coma. In mHS deficiency, there is no diagnostic pattern of organic acids in urine. The only biochemical diagnostic test is enzyme assay of mHS in liver.

HL deficiency is due to reduced activity of mitochondrial and peroxisomal enzyme HL. Infants and children with HL deficiency also experience hypoketotic hypoglycemic episodes, and long-term impacts of these episodes can include epilepsy, intellectual disability, and white matter changes in the brain, usually due to hypoglycemia. Urine organic acids of individuals with HL are characteristic and demonstrate high levels of HMG and leucine metabolites.

All 4 of these ketone disorders are inherited in an autosomal recessive manner. BKT deficiency is caused by variants in *ACAT1*, and SCOT deficiency is caused by variants in the *OCT1*. HMG-CoA synthase deficiency is due to variants in *HMGCS2*, and HMG-CoA lyase deficiency is due to variants in *HMGCL*.

An additional disorder that impacts ketone metabolism and is included in this panel is monocarboxylate transporter 1 deficiency, due to 2 variants in *SLC16A1* and resulting in severe episodes of ketoacidosis with illness or fasting.

Treatment for these ketone disorders involves avoidance of fasting and provision of oral or intravenous carbohydrate to

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correct hypoglycemia and ketoacidosis. Long term neurologic sequelae occur in some individuals and are a consequence of hypoglycemia during ketoacidotic episodes.

Urine organic acids (OAU / Organic Acids Screen, Random, Urine) and plasma acylcarnitine profile (ACRN / Acylcarnitines, Quantitative, Plasma) are the recommended first-tier tests for assessment of ketone disorders. However, as these may be normal in all but severe BKT deficiency, molecular genetic testing is a rapid and effective tool to diagnose individuals with ketone disorder.

**Reference Values**

An interpretive report will be provided.

**Interpretation**

All detected alterations are evaluated according to American College of Medical Genetics and Genomics (ACMG) recommendations.<sup>(1)</sup> Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

**Cautions**

Clinical Correlations:

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 at least one 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 the Mayo Clinic Laboratory genetic counselors at 800-533-1710.

Technical Limitations:

Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some target regions; assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.

This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Insertions/deletions (indels) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller indels.

Deletion/Duplication Analysis:

This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural

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rearrangements (such as translocations and inversions) may not be detected.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.

Genes may be added or removed based on updated clinical relevance. Refer to the [Targeted Genes and Methodology Details for Ketone Disorders Gene Panel](#) in Special Instructions for the most up to date list of genes included in this test. For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent heterologous blood transfusion, results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who have received a bone marrow transplant.

#### Reclassification of Variants:

At this time, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages health care 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 is performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline. 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 should be interpreted with caution and professional clinical judgement.

#### Clinical Reference

1. Richards S, Aziz N, Bale S, et al: Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med.* 2015 May;17(5):405-424.
2. Mitchell GA, Fukao T: Inborn errors of ketone body metabolism. In: Valle D, Antonarakis S, Ballabio A, Beaudet A, Mitchell GA. eds. *The Online Metabolic and Molecular Bases of Inherited Disease* McGraw-Hill Education; 2019. Accessed January 07,2020. Available at <http://ommbid.mhmedical.com/content.aspx?bookid=2709&sectionid=225087757>
3. Hori T, Yamaguchi S, Shinkaku H, et al: Inborn errors of ketone body utilization. *Pediatr Int.* 2015;57(1):41-48
4. Fukao T, Mitchell G, Sass JO, Hori T, Orii K, Aoyama Y: Ketone body metabolism and its defects. *J Inherit Metab Dis.* 2014;37(4):541-551

## Performance

### Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing is performed to test for the presence of variants in coding regions and intron/exon boundaries of the genes analyzed, as well as some other regions that have known pathogenic variants. The human genome reference GRCh37/hg19 build was used for sequence read alignment. At least 99% of the bases are covered at a read depth over 30X. Sensitivity is estimated at above 99% for single nucleotide variants, above 94% for insertions/deletions (indels) less than 40 base pairs (bp), above 95% for deletions up to 75 bp and insertions up to 47 bp. NGS and/or a polymerase chain reaction (PCR)-based quantitative method is performed to test for the presence of deletions and duplications in the genes analyzed.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. See [Targeted Genes and Methodology Details for Ketone Disorders Gene Panel](#) for details regarding the targeted genes analyzed and the specific gene regions not routinely covered. (Unpublished Mayo method)

Genes analyzed: *ACAA2, ACAT1, ACAT2, AKT2, BDH1, HMGCL, HMGCS2, OXCT1, SLC16A1*.

### PDF Report

Supplemental

### Day(s) Performed

Varies

### Report Available

28 to 42 days

### Specimen Retention Time

Whole Blood: 2 weeks (if available); Extracted DNA: 3 months; Blood spots/Saliva: 1 month

### Performing Laboratory Location

Rochester

## Fees & Codes

### Fees

- Authorized users can sign in to [Test Prices](#) for detailed fee information.
- Clients without access to Test Prices can contact [Customer Service](#) 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact [Customer Service](#).

### Test Classification

This test was developed, and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the US Food and Drug Administration.

**CPT Code Information**

81479

88233-Tissue culture, skin, solid tissue biopsy (if appropriate)

88240-Cryopreservation (if appropriate)

**LOINC® Information**

Test ID	Test Order Name	Order LOINC® Value
KETGP	Ketone Disorders Gene Panel	In Process

Result ID	Test Result Name	Result LOINC® Value
608692	Test Description	62364-5
608693	Specimen	31208-2
608694	Source	31208-2
608695	Result Summary	50397-9
608696	Result	82939-0
608697	Interpretation	69047-9
608698	Resources	99622-3
608699	Additional Information	48767-8
608700	Method	85069-3
608701	Genes Analyzed	48018-6
608702	Disclaimer	62364-5
608703	Released By	18771-6