MAYO CLINIC LABORATORIES

Test Definition: PHCGD

Phagocytic Disorders and Chronic Granulomatous Disease Gene Panel, Varies

Overview

Useful For

Providing a comprehensive genetic evaluation for patients with a personal or family history of chronic granulomatous disease, Papillon-Lefevre syndrome, specific granule deficiency, leukocyte adhesion deficiency, or other phagocytic disorder

Establishing a diagnosis of chronic granulomatous disease or other phagocytic disorder, allowing for appropriate management and surveillance of disease features based on the gene or variant involved

Identifying variants within genes known to be associated with chronic granulomatous disease and other phagocytic disorders, allowing for predictive testing of at-risk family members

Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
CULAF	Amniotic Fluid Culture/Genetic Test	Yes	No
_STR1	Comp Analysis using STR (Bill only)	No, (Bill only)	No
_STR2	Add'l comp analysis w/STR (Bill Only)	No, (Bill only)	No
CULFB	Fibroblast Culture for Genetic Test	Yes	No
MATCC	Maternal Cell Contamination, B	Yes	No

Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in 20 genes associated with phagocytic disorders and chronic granulomatous disease (CGD): *CEBPE, CFTR, CSF2RA, CSF2RB, CTSC, CYBA, CYBB, CYBC1, FERMT3, G6PD, ITGB2, MRTFA, NCF1, NCF2, NCF4, RAC2, SLC35C1, SLC7A7, SMARCD2,* and *WDR1*. See Targeted Genes and Methodology Details for Phagocytic Disorders and Chronic Granulomatous Disease Gene Panel and Method Description for additional details.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, recurrence risk assessment, familial screening, and genetic counseling for chronic granulomatous disease, Papillon-Lefevre syndrome, specific granule deficiency, leukocyte adhesion deficiency, and other phagocytic disorders.

Testing Algorithm

Skin biopsy:

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

Cord blood:
For cord blood specimens that have an accompanying maternal blood specimen, maternal cell contamination studies will be performed at an additional charge.

Special Instructions

- 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
- Inborn Errors of Immunity, Autoimmunity, and Autoinflammatory Disease Patient Information
- Targeted Genes and Methodology Details for Phagocytic Disorders and Chronic Granulomatous Disease Gene Panel

Method Name

Sequence Capture and Amplicon-Based Next-Generation Sequencing (NGS), followed Droplet Digital Polymerase Chain Reaction (ddPCR)/Quantitative Real-Time Polymerase Chain Reaction (qPCR) and Sanger Sequencing as needed

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

Patients who have had a previous bone marrow transplant from an allogenic donor should not have blood, bone marrow, or saliva submitted for testing, as results generated will reflect the genome of the donor rather than the recipient. Testing on patients who have an active hematologic malignancy or hematologic disorder with clonal proliferation may identify both somatic mutations and germline variants, which may result in test failure or necessitate follow-up testing to determine whether the detected variant is germline or somatic. For these patients, testing a skin biopsy or cultured fibroblasts is recommended. For instructions for testing patients who have received a bone marrow transplant or have an active hematologic disorder, call 800-533-1710. For more information see Cautions.

Customization of this panel and single gene analysis for any gene present on this panel are available. For more information see CGPH / Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies. To modify this panel via CGPH, use the Inborn Errors of Immunity/Bone Marrow Failure/Telomeropathy/Pulmonary Fibrosis/Very Early Onset IBD/Pancreatitis disease state for step 1 on the Custom Gene Ordering Tool.

Targeted testing for familial variants (also called site-specific or known variants testing) is available for the genes on this panel. See FMTT / Familial Variant, Targeted Testing, Varies. To obtain more information about this testing option, call

800-533-1710.

Specimen Required

Patient Preparation: A previous hematopoietic stem cell transplant from an allogenic donor will interfere with testing. For information about testing patients who have received a hematopoietic stem cell transplant, call 800-533-1710.

Submit only 1 of the following specimens:

Specimen Type: Whole blood
Container/Tube:
Preferred: Lavender top (EDTA) or yellow top (ACD)
Acceptable: Green top (sodium heparin)
Specimen Volume: 3 mL
Collection Instructions:
1. Invert several times to mix blood.
2. Send whole blood specimen in original tube. **Do not aliquot.**
3. Whole blood collected postnatal from an umbilical cord is also acceptable. See Additional Information
Specimen Stability Information: Ambient 4 days/Refrigerated 4 days/Frozen 4 days
Additional Information:
1. Specimens are preferred to be received within 4 days of collection. Extraction will be attempted for specimens received after 4 days, and DNA yield will be evaluated to determine if testing may proceed.
2. To ensure minimum volume and concentration of DNA are met, the requested volume must be submitted. Testing may be canceled if DNA requirements are inadequate.
3. For postnatal umbilical cord whole blood specimens, maternal cell contamination studies are recommended to ensure test results reflect that of the patient tested. A maternal blood specimen is required to complete maternal cell contamination studies. Order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on both the cord blood and maternal blood specimens under separate order numbers.

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: Ambient (preferred) <24 hours/Refrigerated <24 hours
Additional Information:
1. Specimens are preferred to be received within 24 hours of collection. Culture and extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.
2. A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical and Molecular Testing, Tissue. An additional 3 to 4 weeks are required to culture fibroblasts before genetic testing can occur.

Specimen Type: Cultured fibroblasts
Source: Skin or tissue
Container/Tube: T-25 flask
Specimen Volume: 2 Flasks

Collection Instructions: Submit confluent cultured fibroblast cells from a skin or tissue. Cultured cells from a prenatal specimen **will not be accepted**.
Specimen Stability Information: Ambient (preferred) <24 hours/Refrigerated <24 hours
Additional Information:
1. Specimens are preferred to be received within 24 hours of collection. Culture and extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.
2. A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical and Molecular Testing, Tissue. An additional 3 to 4 weeks are required to culture fibroblasts before genetic testing can occur.

Specimen Type: Bone marrow aspirate
Container/Tube:
Preferred: Lavender top (EDTA)
Acceptable: Yellow top (ACD)
Specimen Volume: 2 mL
Collection Instructions:
1. Invert several times to mix bone marrow.
2. Label specimen as bone marrow.
3. Send bone marrow specimen in original tube. **Do not aliquot.**
Specimen Stability Information: Ambient (preferred) 4 days/Refrigerate 4 days/Frozen 4 days
Additional Information:
1. Specimens are preferred to be received within 4 days of collection. Extraction will be attempted for specimens received after 4 days, and DNA yield will be evaluated to determine if testing may proceed.
2. To ensure minimum volume and concentration of DNA are met, the requested volume must be submitted. Testing may be canceled if DNA requirements are inadequate.

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 filter paper or blood spot collection card
Specimen Volume: 2 to 5 Blood spots
Collection Instructions:
1. An alternative blood collection option for a patient older than 1 year is a fingerstick. For detailed instructions, see How to Collect a Dried Blood Spot Sample.
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. Blood spot specimens are acceptable but not recommended. Multiple extractions will be required to obtain sufficient yield for supplemental analysis, and there is significant risk for test failure due to insufficient DNA.
2. Due to lower concentration of DNA yielded from blood spot, some aspects of the test may not perform as well as DNA extracted from a whole blood sample. When applicable, specific gene regions that were unable to be interrogated will

be noted in the report. Alternatively, additional specimen may be required to complete testing.
3. For collection instructions, see Blood Spot Collection Instructions.
4. For collection instructions in Spanish, see Blood Spot Collection Card-Spanish Instructions (T777).
5. 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:
DNA Saliva Kit High Yield (T1007)
Saliva Swab Collection Kit (T786)
Container/Tube:
Preferred: High-yield DNA saliva kit
Acceptable: Saliva swab
Specimen Volume: 1 Tube if using T1007 or 2 swabs if using T786
Collection Instructions: Collect and send specimen per kit instructions.
Specimen Stability Information: Ambient (preferred) 30 days/Refrigerated 30 days
Additional Information: Saliva specimens are acceptable but not recommended. Due to lower quantity/quality of DNA yielded from saliva, some aspects of the test may not perform as well as DNA extracted from a whole blood sample. When applicable, specific gene regions that were unable to be interrogated will be noted in the report. Alternatively, additional specimen may be required to complete testing.

Specimen Type: Extracted DNA
Container/Tube:
Preferred: Screw Cap Micro Tube, 2 mL with skirted conical base
Acceptable: Matrix tube, 1 mL
Collection Instructions:
1. The preferred volume is at least 100 mcL at a concentration of 75 ng/mcL.
2. Include concentration and volume on tube.
Specimen Stability Information: Frozen (preferred) 1 year/Ambient/Refrigerated
Additional Information: DNA must be extracted in a CLIA-certified laboratory, or equivalent, and must be extracted from a specimen type listed as acceptable for this test (including applicable anticoagulants). Our laboratory has experience with Chemagic, Puregene, Autopure, MagnaPure, and EZ1 extraction platforms and cannot guarantee that all extraction methods are compatible with this test. If testing fails, one repeat will be attempted, and if unsuccessful, the test will be reported as failed and a charge will be applied. If applicable, specific gene regions that were unable to be interrogated due to DNA quality will be noted in the report.

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:
-Informed Consent for Genetic Testing (T576)
-Informed Consent for Genetic Testing (Spanish) (T826)
2. Inborn Errors of Immunity, Autoimmunity and Autoinflammatory Disease Patient Information

Specimen Minimum Volume

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

Inborn errors of immunity that affect the function of phagocytes (neutrophils, monocytes, macrophages, and eosinophils) predispose patients to specific infections as a result of impaired killing of bacteria and fungi.

Chronic granulomatous disease (CGD) due to impaired production of reactive oxygen intermediates is characterized by infections (eg, *Staphylococcus aureus, Burkholderia cepacia complex, Serratia marcescens, Nocardia,* and *Aspergillus* sp.) that involve the skin, lungs, lymph nodes, liver, and bones, although any organ or tissue can be affected. Patients may also experience immune dysregulation, resulting in granuloma formation, colitis, and other inflammatory disorders. While most affected individuals are diagnosed prior to age 5 years, patients may present into late adulthood. Tests that measure neutrophil superoxide production by nicotinamide adenine dinucleotide phosphate (NADPH) oxidase, usually the dihydrorhodamine (DHR) test, may be used in establishing a diagnosis. X-linked CGD, the most common form, is caused by disease-causing variants in *CYBB*. In some cases, a contiguous gene deletion may result in CGD along with McLeod neuroacanthocytosis syndrome. In cases of a large contiguous gene deletion, patients may also inherit *RPGR*-related retinitis pigmentosa, Duchenne muscular dystrophy, and ornithine transcarbamylase deficiency. A chromosomal microarray may be indicated if a contiguous gene deletion is suspected. In addition to the X-linked form, CGD may also be inherited in an autosomal recessive pattern, due to biallelic disease-causing variants in the other genes that encode the remainder of the subunits of phagocyte NADPH, including *CYBA, NCF1, NCF2,* and *NCF4.* Similarly to CGD, complete glucose 6-phosphate dehydrogenase (G6PD) deficiency can result in an increased susceptibility to infection due to impaired neutrophil respiratory burst. G6PD deficiency is also inherited in an X-linked pattern due to disease-causing variants in *G6PD.* Chronic nonspherocytic hemolytic anemia occurs in severe deficiency, while acute hemolytic episodes (typically triggered by some medications, ingestion of fava beans, viral or bacterial infections, etc) are observed in less severe G6PD deficiency.

Neutrophils contain azurophilic (or primary) granules, specific (or secondary) granules, and tertiary granules that contain antimicrobial substances. Azurophilic granules contain myeloperoxidase, bactericidal/permeability-increasing protein, defensins, neutrophil elastase, and cathepsin G. Specific granules contain lactoferrin, lysozyme, NADPH oxidase, alkaline phosphatase, collagenase, histaminase, and cathelicidin. Tertiary granules contain cathepsin, gelatinase, and collagenase. Papillon-Lefevre syndrome (PALS) is an autosomal recessive disorder due to disease-causing variants in *CTSC* (lysosomal cysteine protease cathepsin C, also known as dipeptidyl peptidase I [DPPI]). DPPI is necessary for posttranslational modification of the serine proteases in the neutrophil azurophilic granules, activation of granzymes A

and B of cytotoxic lymphocytes, and activation of mast cell chymases. PALS typically presents with severe periodontal disease and keratosis palmoplantaris, along with mild immunodeficiency. In specific granule deficiency (SGD), neutrophils lack expression of secondary and tertiary granule proteins, have an atypical bilobed nuclear morphology, and demonstrate defects in chemotaxis and bactericidal activity. SGD is due to disease-causing variants in *CEBPE*, which is a myeloid-specific transcription factor, or *SMARCD2*, which interacts with the CCAAT-enhancer-binding protein epsilon transcription factor.

Leukocyte adhesion deficiencies (LAD) are characterized by recurrent bacterial infections due to reduced ability of neutrophils to adhere to various substances and migrate to sites of infection, as well as defective phagocytic and respiratory burst response to bacteria and yeast. Patients often are first noticed due to omphalitis, but later gingivitis/periodontitis, pneumonia, peritonitis, and deep abscesses may develop. LAD can be caused by disease-causing variants in *ITGB2*, which encodes for the CD18 antigen (LAD1); and *SLC35C1*, which encodes for a guanosine diphosphate fucose transporter (LAD2) or *FERMT3* (LAD3). Although the neutrophil functional studies are similar between LAD1 and LAD2, the clinical course in LAD2 is milder, though patients may also present with other features (ie, developmental delay, intellectual disability, and short stature) and show the rare Bombay (hh) blood type due to abnormal fucose metabolism. LAD3 presents similarly to LAD1, but platelets are also affected resulting in clotting defects.

Granulocyte-macrophage colony-stimulating factor (GM-CSF) stimulates the formation of colonies of neutrophils and macrophages from bone marrow precursors but is also required for proper neutrophil function. Recessive inheritance of disease-causing variants in *CSF2RA* and *CSF2RB*, which encode for the alpha and beta chains of the GM-CSF receptor, disrupts GM-CSF signaling and results in defects in neutrophil adhesion, phagocytosis, superoxide formation, and microbial killing. Clinically, this manifests as pulmonary alveolar proteinosis and increased susceptibility to infections (pulmonary and extrapulmonary).

Reference Values

An interpretive report will be provided.

Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(1) 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 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:

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. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

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

Deletion/duplication events that extend past the genes included on the panel may occur. In these instances, genes included in the ordered test are provided on the report and interpreted, and genomic breakpoints are reported if they are confirmed. However, copy number variants for genes not listed in the Method Description are typically not reported or interpreted for haploinsufficiency/triplosensitivity. CMACB / Chromosomal Microarray, Congenital, Blood; WESPR / Panel to Whole Exome Sequencing Reflex Test, Varies; or WGSDX / Whole Genome Sequencing for Hereditary Disorders, Varies is recommended for a full interpretation of deletions/duplications predicted to extend past the genes included on the panel.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic mutations 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. For the most up to date list of genes included in this test and 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 non-leukocyte-reduced blood transfusion, results of tests performed on blood, bone marrow, or saliva specimens may be clinically inaccurate due to the presence of donor DNA. Test orders for blood, bone marrow, or saliva will be canceled by the laboratory if there is a history of an allogeneic hematopoietic stem cell transplant. Similarly, blood, bone marrow, and saliva results may be impacted by presence of active hematologic malignancy or hematologic disorder with clonal proliferation. Call Mayo Clinic Laboratories for instructions for testing a skin biopsy or fibroblast culture for patients who have received a bone marrow transplant or have an active hematologic disorder.

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 professionals to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time. Due to broadening genetic knowledge, it is possible that the laboratory may discover new information of relevance to the patient. Should that occur, the laboratory may issue an amended report.

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.(1) 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 judgment.

Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. These findings will be carefully reviewed to determine whether they will be reported.

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;17(5):405-424
2. Tangye SG, Al-Herz W, Bousfiha A, et al. Human inborn errors of immunity: 2022 update on the classification from the International Union of Immunological Societies Expert Committee. J Cllin Immunol. 2022;42(7):1473-1507
3. Yang AH, Sullivan B, Zerbe CS, et al. Gastrointestinal and hepatic manifestations of chronic granulomatous disease. J Allergy Clin Immunol Pract. 2023;11(5):1401-1416
4. Leiding JW, Holland SM. Chronic Granulomatous Disease. In: Adam MP, Bick S, Mirzaa GM, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 2012. Updated January 22, 2026. Accessed June 1, 2026. Available at www.ncbi.nlm.nih.gov/books/NBK99496/
5. Silva LM, Brenchley L, Moutsopoulos NM. Primary immunodeficiencies reveal the essential role of tissue neutrophils in periodontitis. Immunol Rev. 2019;287(1):226-235
6. Das J, Sharma A, Jindal A, Aggarwal V, Rawat A. Leukocyte adhesion defect: Where do we stand circa 2019? Genes Dis. 2019;7(1):107-114.
7. Trapnell BC, Nakata K, Bonella F, et al. Pulmonary alveolar proteinosis. Nat Rev Dis Primers. 2019;5(1):16
8. Schim van der Loeff I, Sprenkeler EGG, Tool ATJ, et al. Defective neutrophil development and specific granule deficiency caused by a homozygous splice-site mutation in SMARCD2. J Allergy Clin Immunol. 2021;147(6):2381-2385.

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 disease-causing 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 deletions/insertions (delins) 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. A supplemental droplet digital PCR method is used to detect the c.75_76del; p.Tyr26Hisfs*26 (delta GT) disease-causing variant in *NCF1*.

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 Phagocytic Disorders and Chronic Granulomatous Disease Gene Panel for details regarding the targeted genes analyzed for each test and specific gene regions not routinely covered.(Unpublished Mayo method)

Genes analyzed: *CEBPE, CFTR, CSF2RA, CSF2RB, CTSC, CYBA, CYBB, CYBC1, FERMT3, G6PD, ITGB2, MRTFA, NCF1*, *NCF2, NCF4, RAC2, SLC35C1, SLC7A7, SMARCD2,* and *WDR1*

PDF Report
No

Day(s) Performed
Varies

Report Available
28 to 42 days

Specimen Retention Time
Whole blood: 25 days (if available); Saliva: 30 days (if available); Hair root bulb (if available)/Extracted DNA: 3 months; Blood spots: 1 year (if available)

Performing Laboratory Location
Mayo Clinic Laboratories - Rochester Main Campus

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. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information

81223
81249
81479
81479 (if appropriate for government payers)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
PHCGD	CGD and PhagocyteDisorder GenePanel	112331-4

Result ID	Test Result Name	Result LOINC® Value
621576	Test Description	62364-5
621577	Specimen	31208-2
621578	Source	31208-2
621579	Result Summary	50397-9
621580	Result	82939-0
621581	Interpretation	69047-9
621582	Additional Results	82939-0
621583	Resources	99622-3
621584	Additional Information	48767-8
621585	Method	85069-3
621586	Genes Analyzed	82939-0
621587	Disclaimer	62364-5
621588	Released By	18771-6
MG155	Is this Bone Marrow	31208-2