MAYO CLINIC LABORATORIES

Test Definition: GNHMA

Hemophilia A, F8 Gene, Next-Generation Sequencing, Varies

Overview

Useful For

Confirming a clinical diagnosis of hemophilia A in affected male patients with the identification of a disease-causing variant in the *F8* gene

Determining the disease-causing alteration within the *F8* gene to delineate the underlying molecular defect in a male patient with a laboratory diagnosis of hemophilia A

Identifying the causative alteration for prognostic and genetic counseling purposes

Assessing hemophilia A carrier status for female patients with a family history of hemophilia A

Prenatal testing for hemophilia A when a familial *F8* variant has been previously identified in a family member

Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
_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
CULAF	Amniotic Fluid Culture/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 the *F8* gene associated with hemophilia A (also known as factor VIII deficiency). See 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 hemophilia A.

Testing Algorithm

The clinical workup for hemophilia A in symptomatic male patients should begin with special coagulation testing for factor VIII (FVIII) activity. Genetic testing is indicated if FVIII activity is less than 40% of normal (Note: reference range may vary depending on the locally established reference range) and von Willebrand factor antigen testing is normal. For more information see Hemophilia Testing Algorithm.

FVIII clotting activity does not correlate as well with bleeding severity in female patients and therefore, is unreliable in the detection of female carriers of hemophilia A. Carrier status is determined by identification of a heterozygous disease-causing variant in *F8* by molecular genetic testing. For female patients with a suspected or confirmed diagnosis of hemophilia A in a family member, carrier testing is recommended as specified by the Hemophilia Carrier Testing Algorithm.(1-3)

Acquired (nongenetic) causes of hemophilia A that should be excluded before genetic testing include heparin use, disorders associated with antibodies to clotting factors such as systemic lupus erythematosus or antiphospholipid syndrome, pregnancy/postpartum period, rheumatic disease, solid or hematologic malignancies, and use of certain drugs such as penicillin, sulfamides, phenytoin, interferon, fludarabine.

Prenatal genetic testing for hemophilia A is not routinely performed without the prior identification of a familial *F8* variant in an affected male relative or a carrier female relative. Requests for prenatal testing for hemophilia A without a known familial *F8* variant are performed at the discretion of a Molecular Hematopathology Laboratory Director.

If an amniotic fluid specimen is received, an amniotic fluid culture will be performed at an additional charge.
If a chorionic villi specimen or cultured chorionic villi are received, a fibroblast culture will be performed at an additional charge.
For any prenatal specimen that is received, maternal cell contamination testing will be performed at an additional charge.

Special Instructions

- Informed Consent for Genetic Testing
- Hemophilia Carrier Testing Algorithm
- Hemophilia Testing Algorithm
- Hemophilia A Patient Information
- Informed Consent for Genetic Testing (Spanish)

Method Name

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

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

For male patients, this test should only be considered if clinical and family history, initial coagulation screens, and/or

initial activity tests indicate a diagnosis of hemophilia A. For female patients, this test should only be considered if there is a confirmed diagnosis of hemophilia A in a family member or the patient has abnormally low factor VIII (FVIII) activity.

This test does not measure FVIII activity levels. For assessment of FVIII activity, order F8A / Coagulation Factor VIII Activity Assay, Plasma.

For individuals with bleeding symptoms and no known personal or family history of hemophilia A, consider ALBLD / Bleeding Diathesis Profile, Limited, Plasma or the specific factor assays.

This test does not evaluate for the presence of inversions in the *F8* gene that can cause hemophilia A. If testing for possible inversions in the *F8* gene is desired, order F8INV / Hemophilia A *F8* Gene, Intron 1 and 22 Inversion Mutation Analysis, Whole Blood.

If genetic testing for hereditary bleeding disorders using a larger panel is desired, both a 6-gene focused bleeding panel and a 25-gene comprehensive bleeding panel are available. For more information see GNBLF / Bleeding Disorders, Focused Gene Panel, Next-Generation Sequencing, Varies or GNBLC / Bleeding Disorders, Comprehensive Gene Panel, Next-Generation Sequencing, Varies

Targeted testing for familial variants (also called site-specific or known variants testing) is available for the *F8* gene. See FMTT / Familial Variant, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.

Additional Testing Requirements

All prenatal specimens must be accompanied by a maternal blood specimen; order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on both the prenatal specimen and the maternal specimen as separate order numbers.

Necessary Information

Hemophilia A Patient Information **is required.** Testing may proceed without the patient information, however, the information aids in providing a more thorough interpretation. Ordering healthcare professionals are strongly encouraged to fill out the form and send with the specimen.

Specimen Required

Patient Preparation: A previous bone marrow transplant from an allogenic donor will interfere with whole blood testing. For information about testing patients who have received a bone marrow transplant, call 800-533-1710.
Submit only 1 of the following specimens:

Specimen Type: Whole blood
Container/Tube:
Preferred: Lavender top (EDTA)
Acceptable: Yellow top (ACD)
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 4 days
Additional Information: 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.

Prenatal Specimens
Due to its complexity, consultation with the laboratory is required for all prenatal testing; call 800-533-1710 to speak to a genetic counselor.

Specimen Type: Amniotic fluid
Container/Tube: Amniotic fluid container
Specimen Volume: 20 mL
Specimen Stability Information: Refrigerated (preferred) 24 hours/Ambient 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 CULAF / Culture for Genetic Testing, Amniotic Fluid. An additional 2 to 3 weeks are required to culture amniotic fluid before genetic testing can occur.

3. **All prenatal specimens must be accompanied by a maternal blood specimen;** order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on the maternal specimen.

Specimen Type: Chorionic villi
Container/Tube: 15-mL Tube containing 15 mL of transport media
Specimen Volume: 20 mg
Specimen Stability Information: 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 or Molecular Testing. An additional 2 to 3 weeks are required to culture amniotic fluid before genetic testing can occur.

3. **All prenatal specimens must be accompanied by a maternal blood specimen;** order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on the maternal specimen.

Specimen Type: Confluent cultured cells
Container/Tube: T-25 flask
Specimen Volume: 2 Full flasks
Collection Instructions: Submit confluent cultured cells from another laboratory.
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 or Molecular Testing.
3. **All prenatal specimens must be accompanied by a maternal blood specimen;** order MATCC / Maternal Cell

Contamination, Molecular Analysis, Varies on the maternal specimen.

Forms

1. Hemophilia A Patient Information **(T712) is required.**

2. 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)

3. If not ordering electronically, complete, print, and send an Coagulation Test Request (T753) with the specimen.

Specimen Minimum Volume

Blood: 1 mL; Amniotic fluid: 10 mL; Other specimen types: 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

Hemophilia A is a hereditary bleeding disorder associated with germline variants in the *F8* gene. It is inherited in an X-linked recessive manner with variable expressivity and is estimated to affect 1 in 4000-5000 live male births.(2)

Hemophilia A is characterized by a deficiency in clotting factor VIII (FVIII), an essential blood coagulation protein. Symptomatic male patients may experience mild to severe bleeding problems, including excessive bruising, prolonged epistaxis, post-operative bleeding, hemarthrosis, deep-muscle hematomas, and/or intracranial or gastrointestinal tract bleeding.(2,3) Female carriers are not typically affected but some may experience increased bleeding tendencies especially after medical procedures and surgery. Note that FVIII activity may not correlate with the severity of symptoms in females.(4-6)

Several causes of acquired (nongenetic) hemophilia A should be excluded prior to genetic testing, including heparin use, disorders associated with antibodies to clotting factors such as systemic lupus erythematosus or antiphospholipid syndrome, pregnancy and the postpartum period, rheumatic disease, solid and hematologic malignancies, and use of certain drugs (eg, penicillin, sulfamides, phenytoin, interferon, fludarabine).(7)

The World Federation of Hemophilia provides guidelines regarding diagnosis, management, and laboratory testing for individuals with hemophilia A.(8)

Reference Values

An interpretive report will be provided.

Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(9) 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 the 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 gene tested may occur. In these instances, only the gene included in the ordered test is provided on the report and interpreted, and genomic breakpoints are reported if they are confirmed. Genes not on this ordered test 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 tested gene.

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.

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 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:
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.(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 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. Pruthi RK. Hemophilia: A practical approach to genetic testing. Mayo Clin Proc. 2005;80(11):1485-1499
2. Berntorp E, Fischer K, Hart DP, et al. Haemophilia. Nat Rev Dis Primers. 2021;7(1):45
3. Konkle BA, Fletcher SN: Hemophilia A. In: Adam MP, Everman DB, Mirzaa GM, et al. GeneReviews [Internet]. University of Washington, Seattle; 2000. Updated August 7, 2025. Accessed March 2, 2026. Available at www.ncbi.nlm.nih.gov/books/NBK1404/
4. Plug I, Mauser-Bunschoten EP, Brocker-Vriends AHJT, et al. Bleeding in carriers of hemophilia. Blood. 2006;108(1):52-56
5. Miesbach W, Alesci S, Geisen C, Oldenburg J. Association between phenotype and genotype in carriers of haemophilia A. Haemophilia. 2011;17(2):246-251
6. Paroskie A, Gailani D, DeBaun MR, Sidonio RF Jr: A cross-sectional study of bleeding phenotype in haemophilia A

carriers. Br J Haematol. 2015;170(2):223-228
7. Haider MZ: Acquired hemophilia. In: Anwer F, ed. StatPearls [Internet]. StatPearls Publishing; 2021. Updated December 13, 2022. Accessed March 2, 2026. Available at www.statpearls.com/articlelibrary/viewarticle/114240
8. Srivastava A, Santagostino E, Dougall A, et al. WFH Guidelines for the Management of Hemophilia, 3rd edition. Haemophilia. 2020 Aug;26 Suppl 6:1-158
9. Richards S, Aziz N, Bale S, et al; ACMG Laboratory Quality Assurance Committee: Standards and guidelines for the interpretation of sequence variants: a joint c

Performance

Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing are performed to test for the presence of variants in coding regions and intron/exon boundaries of the *F8* gene, 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-based quantitative method is performed to test for the presence of deletions and duplications in the *F8* gene.

There may be regions of the *F8* gene 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.(Unpublished Mayo method)

The reference transcript for *F8* gene is NM_000132.3. Reference transcript numbers may be updated due to transcript re-versioning. Always refer to the final patient report for gene transcript information referenced at the time of testing. Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

PDF Report

No

Day(s) Performed

Varies

Report Available

28 to 42 days

Specimen Retention Time

Whole blood: 2 weeks (if available); Amniotic fluid, cultured amniocytes, chorionic villi, cultured chorionic villi: 1 month; Extracted DNA: 3 months

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

81407
88233-Tissue culture, skin, solid tissue biopsy (if appropriate)
88240-Cryopreservation (if appropriate)
88235-Amniotic fluid culture (if appropriate)
81265-Maternal cell contamination (if appropriate)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
GNHMA	F8 Gene, Full Gene NGS	94234-2

Result ID	Test Result Name	Result LOINC® Value
619104	Test Description	62364-5
619105	Specimen	31208-2
619106	Source	31208-2
619107	Result Summary	50397-9
619108	Result	82939-0
619109	Interpretation	69047-9
619110	Additional Results	82939-0
619111	Resources	99622-3
619112	Additional Information	48767-8
619113	Method	85069-3
619114	Genes Analyzed	82939-0
619115	Disclaimer	62364-5
619116	Released By	18771-6