

Client: Example Client ABC123  
123 Test Drive  
Salt Lake City, UT 84108  
UNITED STATES

Physician: Doctor, Example

**Patient: Patient, Example**

**DOB:** 12/8/2003  
**Gender:** Male  
**Patient Identifiers:** 01234567890ABCD, 012345  
**Visit Number (FIN):** 01234567890ABCD  
**Collection Date:** 01/01/2017 12:34

**von Willebrand Disease, Type 2M (VWF) Sequencing**

ARUP test code 2005490

vWD Type 2M (VWF) Sequencing Specimen      whole Blood

vWD Type 2M (VWF) Sequencing Interp

Negative  
TEST PERFORMED - 2005490  
TEST DESCRIPTION - von Willebrand Disease Type 2M (VWF) Sequencing  
INDICATION FOR TEST - Confirm Diagnosis  
  
RESULT  
No pathogenic variants were detected in the VWF gene.  
  
INTERPRETATION  
No pathogenic variants were detected in the von Willebrand factor (VWF) gene using targeted sequencing of exons 28, 30, and 31. This decreases the risk for von Willebrand disease types 2A, 2B, and 2M by 80 percent.  
  
RECOMMENDATIONS  
Medical management should rely on clinical and phenotypic laboratory findings as well as family history. Genetic consultation is recommended.  
  
COMMENTS  
Reference sequence: GenBank # NM\_000552.3 (VWF)  
Nucleotide numbering begins at the "A" of the ATG initiation codon  
Likely benign and benign variants are not included in this report.  
  
This result has been reviewed and approved by [REDACTED]

**H=High, L=Low, \*=Abnormal, C=Critical**

Unless otherwise indicated, testing performed at:

BACKGROUND INFORMATION: von Willebrand Disease, Type 2M (VWF) Sequencing

CHARACTERISTICS: Mucocutaneous bleeding after brushing or flossing teeth, unexplained bruising, prolonged repeated nosebleeds, menorrhagia, and prolonged bleeding following childbirth, trauma or surgery.  
 INCIDENCE: Approximately 1 in 100 to 1 in 1000 individuals.  
 INHERITANCE: Autosomal dominant for type 2M.  
 PENETRANCE: Dominant mutations are incompletely penetrant when VWF:Ag and VWF:RCo levels are 25-50 IU/dL. Full penetrance is expected when VWF:Ag and VWF:RCo levels are less than 25 IU/dL.  
 CAUSE: Pathogenic VWF mutations in exons 28, 30, and 31.  
 CLINICAL SENSITIVITY: 80 percent for vWD types 2A, 2B, and 2M; unknown for other vWD subtypes.  
 METHODOLOGY: Bidirectional sequencing of VWF exons 28, 30, 31 and its intron-exon boundaries.  
 ANALYTICAL SENSITIVITY AND SPECIFICITY: 99 percent.  
 LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. Regulatory region mutations, deep intronic mutations, and large deletion/duplications will not be detected. Mutations lying outside of VWF exons 28, 30, and 31 will not be evaluated.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

VERIFIED/REPORTED DATES

| Procedure                             | Accession     | Collected             | Received               | Verified/Reported     |
|---------------------------------------|---------------|-----------------------|------------------------|-----------------------|
| vWD Type 2M (VWF) Sequencing Specimen | 19-297-401142 | 10/23/2019 2:40:00 PM | 10/24/2019 11:29:21 AM | 11/13/2019 5:16:00 PM |
| vWD Type 2M (VWF) Sequencing Interp   | 19-297-401142 | 10/23/2019 2:40:00 PM | 10/24/2019 11:29:21 AM | 11/13/2019 5:16:00 PM |

END OF CHART

H=High, L=Low, \*=Abnormal, C=Critical

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