

Variant: *NM_000552.5(VWF):c.4837T>C (p.Ser1613Pro)*

Version: 1.0

[CA114131](#)

[292 \(ClinVar\)](#)

Gene: VWF ([HGNC:7450](#))

Condition: von Willebrand disease type 2A ([MONDO:0015628](#))

Inheritance Mode: Autosomal dominant inheritance

UID: cf756b09-5a21-46f7-96ac-d8d1c3e2d497

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HGVS expressions

NM_000552.5:c.4837T>C

NM_000552.5(VWF):c.4837T>C (p.Ser1613Pro)

NC_000012.12:g.6018581A>G

CM000674.2:g.6018581A>G

NC_000012.11:g.6127747A>G

CM000674.1:g.6127747A>G

NC_000012.10:g.5998008A>G

NG_009072.1:g.111090T>C

NG_009072.2:g.111090T>C

ENST00000261405.10:c.4837T>C

ENST00000261405.9:c.4837T>C

ENST00000538635.5:n.421-24647T>C

NM_000552.3:c.4837T>C

NM_000552.4:c.4837T>C

Uncertain Significance

Met criteria codes **4**

PP3

PP4_Moderate

PM2_Supporting

PS4_Supporting

Not Met criteria codes **1**

PP1

Evidence Links **0**

Expert Panel

[von Willebrand Disease VCEP](#)

Criteria Specification Information

Criteria Specification: *ClinGen von Willebrand Disease Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for VWF Version 1.0.0*

Criteria Specification Approval History

Criteria Specifications for this VCEP









Evidence submitted by expert panel

von Willebrand Disease VCEP



The c.4837T>C variant in VWF is a missense variant predicted to cause substitution of Serine by Proline at amino acid 1613 (p.Ser1613Pro). At least 1 patient (Patient 14 from PMID: 38053262) with this variant displayed excessive mucocutaneous bleeding as well as laboratory phenotypes of very low VWF activity as indicated by a VWF activity-to-antigen ratio <0.7, and loss of high molecular weight multimers, which together are highly specific for VWD type 2A. Additional consistent phenotypes were also reported in the patient

including a FVIII activity consistent with VWF antigen (ratio >0.7) (PP4_Moderate). This variant has been reported in one additional proband (Zimmerman program) with activity/antigen ratio <0.37, abnormal multimers, and normal platelet binding (PS4_Supporting). The computational predictor REVEL gives a score of 0.7, which is above the ClinGen VWD VCEP threshold of >0.644 and predicts a damaging effect on VWF function (PP3). This variant is absent from gnomAD v4.1 (PM2_Supporting). In summary, this variant meets the criteria to be classified as VUS for autosomal recessive von Willebrand disease type 2A based on the ACMG/AMP criteria applied, as specified by the ClinGen VWD VCEP: PS4_Supporting, PP4_Moderate, PP3 and PM2_Supporting (VCEP specifications version 1.0.0; date of approval).

Met criteria codes

PP3			The computational predictor REVEL gives a score of 0.7, which is above the ClinGen VWD VCEP threshold of >0.644 and predicts a damaging effect on VWF function (PP3).
PP4_Moderate			At least 1 patient (Patient 14 from PMID: 38053262) with this variant displayed excessive mucocutaneous bleeding as well as laboratory phenotypes of very low VWF activity (VWF:RCo or VWF:GPIbM 12 IU/dL), a VWF activity-to-antigen ratio <0.7, and loss of high molecular weight multimers, which together are highly specific for VWD type 2A. Additional consistent phenotypes were also reported in the patient including a FVIII activity consistent with VWF antigen (ratio >0.7) (PP4_Moderate).
PM2_Supporting			This variant is absent from gnomAD v4.1 (PM2_Supporting).
PS4_Supporting			This variant has been reported in one additional proband (Zimmerman program) with activity/antigen ratio <0.37, abnormal multimers, and normal platelet binding (PS4_supoprtng).

Not Met criteria codes

PP1			At least one family has been reported (Zimmerman program) with the proband and daughter harboring this variant and a type 2A phenotype. This is insufficient segregations to meet the PP1 criterion.
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Curation History [↗](#)



Showing 1 to 1 of 1 rows



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