

Variant: *NM_000132.4:c.6028T>C*

Version: 1.1

CA414905047 [↗](#)

3358853 (ClinVar) [↗](#)

Gene: F8 ([HGNC:2157](#))

Condition: hemophilia A ([MONDO:0010602](#))

Inheritance Mode: X-linked inheritance

UUID: 1215dd51-794b-4904-8dc8-32938d93c1f4

Approved on: 2026/2/6

Published on: 2026/2/27

HGVS expressions

NM_000132.4:c.6028T>C

NC_000023.11:g.154902138A>G

CM000685.2:g.154902138A>G

NC_000023.10:g.154130413A>G

CM000685.1:g.154130413A>G

NC_000023.9:g.153783607A>G

NG_011403.1:g.125586T>C

NG_011403.2:g.125586T>C

ENST00000360256.9:c.6028T>C

ENST00000360256.8:c.6028T>C

NM_000132.3:c.6028T>C

Uncertain Significance

Met criteria codes **3**

BS2

PS4_Moderate

PM2_Supporting

Not Met criteria codes **1**

PP3

Evidence Links **0**

Expert Panel

Coagulation Factor Deficiency VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** ClinGen Coagulation Factor Deficiency Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for F8 Version 1.0.0

[↗](#) **Criteria Specification Approval History**

[↗](#) **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Coagulation Factor Deficiency VCEP

The F8 c.6028T>C (p.Ser2010Pro) variant is completely absent from population databases (gnomAD v2.1.1/gnomAD v3). This missense variant has a REVEL score of 0.599 (>0.6), which does not meet the cut off for PP3. At least three individuals with the p.Ser2010Pro variant and severe hemophilia A have been reported in the literature (PMID: 23306409). However, variant was also identified in an unaffected male with a factor VIII level of 90%. In summary, based on the evidence available at this time, the clinical significance of this variant is uncertain. ACMG/AMP criteria applied, as specified by the Coagulation Factor Deficiency Variant Curation Expert Panel for F8 Rule specification v1.0.0: PS4_Moderate, PM2_Supporting, BS2.

Met criteria codes

BS2			Proband with 90% factor VIII activity level from VCEP member submission.
PS4_Moderate			Three individuals reported with severe hemophilia A and inhibitors to factor replacement therapy.
PM2_Supporting			Variant is absent in males using gnomAD v2.1.

Not Met criteria codes

PP3			REVEL score is 0.599 (VCEP cutoff is 0.6). SpliceAI score is 0.1 (VCEP cutoff is 0.5).
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Curation History



 

 

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