

Variant: NM_000133.4(F9):c.1048T>G (p.Ser350Ala)

Version: 1.0

CA10529866 [↗](#)

1685803 (ClinVar) [↗](#)

Gene: F9 ([HGNC:2158](#))

Condition: hemophilia B ([MONDO:0010604](#))

Inheritance Mode: X-linked inheritance

UUID: 69e8c03b-45bb-450e-9a31-e5f2bc4bc746

Approved on: 2025/4/4

Published on: 2025/4/4

HGVS expressions

NM_000133.4(F9):c.1048T>G (p.Ser350Ala)

NM_000133.4:c.1048T>G

NC_000023.11:g.139561733T>G

CM000685.2:g.139561733T>G

NC_000023.10:g.138643892T>G

CM000685.1:g.138643892T>G

NC_000023.9:g.138471558T>G

NG_007994.1:g.35998T>G

ENST00000218099.7:c.1048T>G

ENST00000643157.1:n.1715T>G

ENST00000218099.6:c.1048T>G

ENST00000394090.2:c.934T>G

NM_000133.3:c.1048T>G

NM_001313913.1:c.934T>G

NM_001313913.2:c.934T>G

Benign

Met criteria codes **2**

BA1 **BP4**

Not Met criteria codes **1**

PS4

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 F9 Version 1.0.0

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

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

Evidence submitted by expert panel

Coagulation Factor Deficiency VCEP

The c.1048T>G variant in F9 is a missense variant predicted to cause substitution of Serine by Alanine at amino acid 350 (p.Ser350Ala). This variant has been reported in 1 proband meeting phenotypic criteria for mild Hemophilia B. However, PS4_Supporting cannot be applied because more than 3 males in gnomAD v2.1.1 are reported with this variant, as per CFD VCEP specifications (PMID: 23492913). The

highest population minor allele frequency in gnomAD v2.1.1 is 0.0006494 (9/13858 alleles) in the East Asian population, which is higher than the ClinGen Coagulation Factor Deficiency VCEP threshold (≥ 0.0000556) for BA1, and therefore meets this criterion (BA1). The computational predictor REVEL gives a score of 0.291, which is below the threshold (≤ 0.3) and the splice site predictor Splice AI indicated that the variant has no impact on splicing (score = 0,0,0,0), evidence that does not predict a damaging effect on F9 function (BP4). In summary, this variant meets the criteria to be classified as Benign for Hemophilia B based on the ACMG/AMP criteria applied, as specified by the ClinGen Coagulation Factor Deficiency VCEP (version 1.0.0, released 10/5/2023): BA1, BP4.

Met criteria codes

BA1			The highest population minor allele frequency in gnomAD v2.1.1 is 0.0006494 (9/13858 alleles) in the East Asian population, which is higher than the ClinGen Coagulation Factor Deficiency VCEP threshold (≥ 0.0000556) for BA1, and therefore meets this criterion (BA1). The highest MAF in gnomAD v4.1.0 is 0.0008 (27/33749) in the East Asian population.
BP4			The computational predictor REVEL gives a score of 0.291, which is below the threshold (≤ 0.3) and the splice site predictor Splice AI indicated that the variant has no impact on splicing (score = 0,0,0,0), evidence that does not predict a damaging effect on F9 function (BP4).

Not Met criteria codes

PS4			This variant has been reported in 1 proband meeting phenotypic criteria for mild Hemophilia B. However, PS4_Supporting cannot be applied because more than 3 males in gnomAD v2.1.1 are reported with this variant, as per CFD VCEP specifications (PMID: 23492913).
-----	---	---	--

Curation History



Showing 1 to 1 of 1 rows

--

The information on this website is not intended for direct diagnostic use or medical decision-making without review by a genetics professional. Individuals should not change their health behavior solely on the basis of information contained on this website. If you have questions about the information contained on this website, please see a health care professional.