The ClinGen Evidence Repository is an **FDA-recognized human genetic variant database** containing expert-curated assertions regarding variants' pathogenicity and supporting evidence summaries. [Disclaimer]

Variant: NM_000132.3(F8):c.1804C>T (p.Arg602Ter)

Version: 1.0

CA255124

10232 (ClinVar)

Gene: F8 (HGNC:2157)
Condition: hemophilia A (MONDO:0010602)
Inheritance Mode: X-linked inheritance
UUID: 8d0f7cbb-2982-46ea-b526-c6afd4ec4be3
Approved on: 2024/2/2
Published on: 2024/7/11

HGVS expressions

NM_000132.3:c.1804C>T
NM_000132.3(F8):c.1804C>T (p.Arg602Ter)
NC_000023.11:g.154953991G>A
CM000685.2:g.154953991G>A
NC_000023.10:g.154182266G>A
CM000685.1:g.154182266G>A
NC_000023.9:g.153835460G>A
NG_011403.1:g.73733C>T
NG_011403.2:g.73733C>T
ENST00000360256.9:c.1804C>T
ENST00000647125.1:c.*1680C>T
ENST00000360256.8:c.1804C>T
NM_000132.4:c.1804C>T

Pathogenic

Met criteria codes 4

PS4 PP4_Moderate PVS1 PM2_Supporting

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 c.1804C>T (p.Arg602Ter) variant is a nonsense variant that is predicted to introduce a premature stop codon in exon 12 and expected to result in nonsense-mediated mRNA decay. This variant is absent from males in gnomAD v2.1.1 and v3.1.1, which meets criteria for PM2_Supporting. More than 25 patients with moderate-severe hemophilia A are reported in the literature and internal laboratory data, meeting criteria for PS4_Very Strong and PP4_Moderate (PMID: 29296726, 18387975, 18691168, 16769589, 8639447, 20331761). In

summary, this variant meets criteria to be classified as pathogenic. ACMG/AMP criteria applied, as specified by the Coagulation Factor Deficiency Variant Curation Expert Panel for F8/F9: PVS1, PS4_Very Strong, PP4_Moderate, PM2_Supporting.

Met criteria codes

PS4	✔	Numerous patients with moderate-severe hemophilia A are reported in the literature and internal laboratory data, meeting criteria for PS4_Very Strong (>8 probands).
PP4_Moderate	✔	Male with severe hemophilia A who had full F8 and F9 gene sequencing and deletion/duplication analysis through MLOF study.
PVS1	✔	The c.1804C>T (p.Arg602Ter) variant is a nonsense variant that is predicted to introduce a premature stop codon in exon 12 and expected to result in nonsense-mediated mRNA decay. Meets PVS1 criteria
PM2_Supporting	✔	The variant is absent from males in gnomAD v2.1.1 and v3.1.1

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.

ClinGen Terms of Use.
¤ Powered by BCM's Genboree.