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Variant: NM_000020.3(ACVRL1):c.698C>T (p.Ser233Leu)

Version: 1.0

CA6572972

439385 (ClinVar)

Gene: ACVRL1 (HGNC:94)
Condition: telangiectasia, hereditary hemorrhagic, type 2 (MONDO:0010880)
Inheritance Mode: Autosomal dominant inheritance
UUID: 3fbd6b7d-fddd-4fda-a30c-cf0b0143132a
Approved on: 2026/2/13
Published on: 2026/8/28

HGVS expressions

NM_000020.3:c.698C>T
NM_000020.3(ACVRL1):c.698C>T (p.Ser233Leu)
NC_000012.12:g.51914511C>T
CM000674.2:g.51914511C>T
NC_000012.11:g.52308295C>T
CM000674.1:g.52308295C>T
NC_000012.10:g.50594562C>T
NG_009549.1:g.12094C>T
ENST00000547400.6:c.428C>T
ENST00000551576.6:c.698C>T
ENST00000552678.2:c.698C>T
ENST00000388922.9:c.698C>T
ENST00000388922.8:c.698C>T
ENST00000419526.6:c.176C>T
ENST00000547400.5:c.428C>T
ENST00000550683.5:c.740C>T
NM_000020.2:c.698C>T
NM_001077401.1:c.698C>T
NM_001077401.2:c.698C>T

Likely Pathogenic

Met criteria codes 3

PP4_Moderate PM2_Supporting PS4

Evidence Links 0

Expert Panel

Hereditary Hemorrhagic Telangiectasia VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Hereditary Hemorrhagic Telangiectasia Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for ACVRL1 Version 1.1.0*
Criteria Specification Approval History
Criteria Specifications for this VCEP

Evidence submitted by expert panel

Hereditary Hemorrhagic Telangiectasia VCEP

The NM_000020.3: c.698C>T variant in ACVRL1 is a missense variant predicted to cause substitution of serine by leucine at amino acid 233 (p.Ser233Leu). The variant is observed in 1 allele in gnomAD v2.1.1 (PM2_Supporting). The computational predictor REVEL gives a score of 0.626, which is neither above nor below the thresholds predicting a damaging or benign impact on ACVRL1 function. This variant has been reported in 4 probands with a phenotype consistent with HHT (PS4). At least one patient's phenotype meets Curacao Criteria for HHT, and sequencing and large deletion/duplication analysis was performed for ENG and ACVRL1, which is highly specific for HHT (PP4_Moderate; PMID: 19767588). In summary, this variant meets the criteria to be classified as Likely Pathogenic for autosomal dominant hereditary hemorrhagic telangiectasia based on the ACMG/amp criteria applied, as specified by the ClinGen Hereditary Hemorrhagic Telangiectasia Variant Curation Expert Panel: PM2_Supporting, PP4_Moderate, PS4 (specification version 1.1.0; 02/13/2026).

Met criteria codes

PP4_Moderate	✔	At least one patient's phenotype meets Curacao Criteria for HHT, and sequencing and large deletion/duplication analysis was performed for ENG and ACVRL1, which is highly specific for HHT (PP4_Moderate; PMID: 19767588).
PM2_Supporting	✔	The variant is observed in 1 allele in gnomAD v2.1.1 (PM2 _Supporting).
PS4	✔	The computational predictor REVEL gives a score of 0.626, which is neither above nor below the thresholds predicting a damaging or benign impact on ACVRL1 function. This variant has been reported in 4 probands with a phenotype consistent with HHT (PS4_Strong).

Curation History

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