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Variant: NM_001754.5(RUNX1):c.1417G>T (p.Glu473Ter)

Version: 1.1

CA410146662

2028205 (ClinVar)

Gene: RUNX1 (HGNC:861)
Condition: hereditary thrombocytopenia and hematologic cancer predisposition syndrome (MONDO:0011071)
Inheritance Mode: Autosomal dominant inheritance
UUID: 9f6519c6-b96e-4e07-ac25-857af6fcdd65
Approved on: Mon, 05 Oct 2026 00:00:00 +0000
Published on: Mon, 05 Oct 2026 00:00:00 +0000

HGVS expressions

NM_001754.5(RUNX1):c.1417G>T (p.Glu473Ter)
NM_001754.5:c.1417G>T
NC_000021.9:g.34792161C>A
CM000683.2:g.34792161C>A
NC_000021.8:g.36164458C>A
CM000683.1:g.36164458C>A
NC_000021.7:g.35086328C>A
NG_011402.2:g.1197551G>T
ENST00000675419.1:c.1417G>T
ENST00000300305.7:c.1417G>T
ENST00000344691.8:c.1336G>T
ENST00000399240.5:c.1144G>T
ENST00000437180.5:c.1417G>T
ENST00000482318.5:c.*1007G>T
NM_001001890.2:c.1336G>T
NM_001754.4:c.1417G>T
NM_001001890.3:c.1336G>T

Likely Pathogenic

Met criteria codes 3

PVS1_Strong PM2_Supporting PM5_Supporting

Not Met criteria codes 23

PP1 PP2 PP3 PP4 PM1 PM3 BA1 PM4 PM6 BS2 BS1 BS4 BS3 PS1 PS2 PS3 PS4 BP4 BP3 BP1 BP2 BP5 BP7

Evidence Links 0

Expert Panel

Myeloid Malignancy VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Myeloid Malignancy Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for RUNX1 Version 3.1*
Criteria Specification Approval History
Criteria Specifications for this VCEP

Evidence submitted by expert panel

Myeloid Malignancy VCEP

NM_001754.5(RUNX1):c.1417G>T (p.Glu473Ter) is a nonsense variant which is not predicted to undergo NMD (PVS1_Strong). This variant is downstream of c.98 (PM5_Supporting) and is completely absent from all population databases with at least 20x coverage for RUNX1 (PM2_Supporting). In summary, this variant meets criteria to be classified as likely pathogenic. ACMG/AMP criteria applied, as specified by the ClinGen Myeloid Malignancy Variant Curation Expert Panel for RUNX1: PVS1_Strong, PM5_Supporting, PM2_Supporting.

Met criteria codes

PVS1_Strong	✔	This variant is not predicted to undergo NMD, and the truncated/altered region is critical for protein function (nonsense c.917-c.1440 as per VCEP specifications) (PVS1_Strong).
PM2_Supporting	✔	This variant is completely absent from all population databases with at least 20x coverage for RUNX1 (PM2_Supporting).
PM5_Supporting	✔	This variant is a nonsense/frameshift variants that is downstream of c.98 (PM5_Supporting).

Not Met criteria codes

PP1	✖	Segregation data for this variant has not been reported in literature.
PP2	✖	This rule is not applicable for MM-VCEP.
PP3	✖	This variant is not a missense, synonymous, or frameshift variant.
PP4	✖	This rule is not applicable for MM-VCEP.
PM1	✖	This variant does not affect any of the following amino acid residues, nor is it located within the RHD: R107, K110, A134, R162, R166, S167, R169, G170, K194, T196, D198, R201, R204 OR within residues 89-204.
PM3	✖	This rule is not applicable for MM-VCEP.
BA1	✖	This variant does not have a MAF ≥ 0.0015 (0.15%) in any general continental population dataset.
PM4	✖	This variant is not an in-frame deletion/insertion.
PM6	✖	De novo data for this variant has not been reported in literature.
BS2	✖	This rule is not applicable for MM-VCEP.
BS1	✖	This variant does not have a MAF between 0.00015 (0.015%) and 0.0015 (0.15%) in any general continental dataset.

BS4	ℹ	✖	Segregation data for this variant has not been reported in literature.
BS3	ℹ	✖	In vitro or in vivo functional data has not been reported for this variant in the literature.
PS1	ℹ	✖	This variant is not a missense, synonymous, or frameshift variant.
PS2		✖	De novo data for this variant has not been reported in literature.
PS3	ℹ	✖	In vitro or in vivo functional data has not been reported for this variant in the literature.
PS4	ℹ	✖	Proband data for this variant has not been reported in literature.
BP4	ℹ	✖	This variant is not a missense, synonymous, or frameshift variant.
BP3		✖	This rule is not applicable for MM-VCEP.
BP1		✖	This rule is not applicable for MM-VCEP.
BP2	ℹ	✖	This variant has not been observed in trans with a pathogenic variant for a fully penetrant dominant gene/disorder or observed in cis with a pathogenic variant in any inheritance pattern.
BP5		✖	This rule is not applicable for MM-VCEP.
BP7	ℹ	✖	This variant is not a synonymous or intronic variant.

Curation History

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