

Variant: *NM_001754.5(RUNX1):c.910C>T (p.Pro304Ser)*

Version: 1.0

CA410149674 [↗](#)

1010346 (ClinVar) [↗](#)

Gene: RUNX1 ([HGNC:861](#))

Condition: hereditary thrombocytopenia and hematologic cancer predisposition syndrome ([MONDO:0011071](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: 5fd9325f-9198-42aa-b000-5c8811ca747a

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HGVS expressions

NM_001754.5(RUNX1):c.910C>T (p.Pro304Ser)

NM_001754.5:c.910C>T

NC_000021.9:g.34799358G>A

CM000683.2:g.34799358G>A

NC_000021.8:g.36171655G>A

CM000683.1:g.36171655G>A

NC_000021.7:g.35093525G>A

NG_011402.2:g.1190354C>T

ENST00000675419.1:c.910C>T

ENST00000300305.7:c.910C>T

ENST00000344691.8:c.829C>T

ENST00000399240.5:c.637C>T

ENST00000437180.5:c.910C>T

ENST00000482318.5:c.*500C>T

NM_001001890.2:c.829C>T

NM_001754.4:c.910C>T

NM_001001890.3:c.829C>T

Uncertain Significance

Met criteria codes **2**

BP4

PM2_Supporting

Not Met criteria codes **15**

PM1

PM5

PM4

PM6

BS1

BS3

PVS1

PS1

PS2

PS3

PS4

BP2

BP7

BA1

PP3

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 Version 2

[↗](#) PDF

[↗](#) Criteria Specification Approval History

[↗](#) Criteria Specifications for this VCEP

Evidence submitted by expert panel

Myeloid Malignancy VCEP

NM_001754.5(RUNX1):c.910C>T (p.Pro304Ser) is a missense variant which is completely absent from population databases which provide at least 20x coverage for RUNX1 (PM2_supporting). This variant has a REVEL score of 0.167, which is less than 0.50 and a spliceAI score >0.2 (0.0) (BP4). In summary, the clinical significance of this variant is uncertain. ACMG/AMP criteria applied, as specified by the Myeloid Malignancy Variant Curation Expert Panel for RUNX1: PM2_supporting, BP4.

Met criteria codes			
BP4			This rule cannot be applied since this missense variant has not a REVEL score <0.50 (0.167).
PM2_Supporting			This variant is completely absent from all population databases (gnomAD v2.1.1) with at least 20x coverage for RUNX1 (PM2_supporting).
Not Met criteria codes			
PM1			This rule cannot be applied since this missense variant affects amino acid residue 304, which is out of RHD or residues 89-204.
PM5			This rule cannot be applied because, to our knowledge, this missense variant does not impact an amino acid residue where a different pathogenic missense change has previously been observed.
PM4			This rule cannot be applied since this is a missense variant.
PM6			This rule cannot be applied since, to our knowledge, this variant has not been reported in any study.
BS1			This rule cannot be applied since the variant is completely absent from all population databases.
BS3			To our knowledge, no in vitro or in vivo functional studies are available for this variant.
PVS1			This rule cannot be applied since this is a missense variant.
PS1			This rule cannot be applied because, to our knowledge, this missense variant does not generate the same amino acid change as a previously identified pathogenic variant regardless of nucleotide change.
PS2			This rule cannot be applied since, to our knowledge, this variant has not been reported in any study.
PS3			To our knowledge, no in vitro or in vivo functional studies are available for this variant.
PS4			This rule cannot be applied since, to our knowledge, this variant has not been reported in any study.
BP2			This rule cannot be applied since, to our knowledge, this variant has not been reported in any study.
BP7			This rule cannot be applied since this is a missense variant.

