

Variant: *NM_000059.4(BRCA2):c.9302T>C (p.Leu3101Pro)*

Version: 1.0

[CA337754](#)

[216263 \(ClinVar\)](#)

Gene: BRCA2 ([HGNC:675](#))

Condition: BRCA2-related cancer predisposition ([MONDO:0700269](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: bc482469-58f8-4a75-a829-75bff9a8140f

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HGVS expressions

NM_000059.4:c.9302T>C

NM_000059.4(BRCA2):c.9302T>C (p.Leu3101Pro)

NC_000013.11:g.32394734T>C

CM000675.2:g.32394734T>C

NC_000013.10:g.32968871T>C

CM000675.1:g.32968871T>C

NC_000013.9:g.31866871T>C

NG_012772.3:g.84255T>C

ENST00000470094.2:c.9302T>C

ENST00000528762.2:c.*669T>C

ENST00000530893.7:c.8933T>C

ENST00000665585.2:c.*864T>C

ENST00000666593.2:c.*147T>C

ENST00000700202.2:c.9251T>C

ENST00000700202.1:c.1718T>C

ENST00000700203.1:n.1429T>C

ENST00000380152.8:c.9302T>C

ENST00000544455.6:c.9302T>C

ENST00000614259.2:c.9310T>C

ENST00000665585.1:c.2180T>C

ENST00000666593.1:c.324T>C

ENST00000680887.1:c.9302T>C

ENST00000380152.7:c.9302T>C

ENST00000470094.1:c.259T>C

ENST00000544455.5:c.9302T>C

NM_000059.3:c.9302T>C

Likely Pathogenic

Met criteria codes **4**

PP3 **PP4** **PM2_Supporting** **PS3**

Evidence Links **0**

Expert Panel

[ENIGMA BRCA1 and BRCA2 VCEP](#)

Criteria Specification Information









Criteria Specification: *ClinGen ENIGMA BRCA1 and BRCA2 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for BRCA2 Version 1.2.0*

Evidence submitted by expert panel

ENIGMA BRCA1 and BRCA2 VCEP

The c.9302T>C variant in BRCA2 is a missense variant predicted to cause substitution of Leucine by Proline at amino acid 3101 (p. (Leu3101Pro)). This variant is absent from gnomAD v2.1 (exomes only, non-cancer subset, read depth ≥ 25) and gnomAD v3.1 (non-cancer subset, read depth ≥ 25) (PM2_Supporting met). Reported by three calibrated studies to exhibit protein function similar to pathogenic control variants (PMIDs: 38417439, 32444794, 39779857) (PS3 met). This BRCA2 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.32, above the recommended threshold of 0.30 for prediction of impact on BRCA2 function via protein change. A SpliceAI score of 0 predicts no impact on splicing (score threshold < 0.10) (PP3 met). Multifactorial likelihood ratio analysis using clinically calibrated data produced a combined LR for this variant of 2.19 (based on Family History LR=2.19), within the thresholds for supporting evidence towards pathogenicity (LR > 2.08 & ≤ 4.3) (PP4 met; PMID: 31853058). In summary, this variant meets the criteria to be classified as a Likely pathogenic variant for BRCA2-related cancer predisposition based on the ACMG/AMP criteria applied as specified by the ENIGMA BRCA1/2 VCEP (PM2_Supporting, PS3, PP3, PP4).

Met criteria codes

PP3	 	This BRCA2 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.32, above the recommended threshold of 0.30 for prediction of impact on BRCA2 function via protein change. A SpliceAI score of 0 predicts no impact on splicing (score threshold < 0.10) (PP3 met).
PP4	 	Multifactorial likelihood ratio analysis using clinically calibrated data produced a combined LR for this variant of 2.19 (based on Family History LR=2.19), within the thresholds for supporting evidence towards pathogenicity (LR > 2.08 & ≤ 4.3) (PP4 met; PMID: 31853058).
PM2_Supporting	 	This variant is absent from gnomAD v2.1 (exomes only, non-cancer subset, read depth ≥ 25) and gnomAD v3.1 (non-cancer subset, read depth ≥ 25) (PM2_Supporting met).
PS3	 	Reported by three calibrated studies to exhibit protein function similar to pathogenic control variants (PMIDs: 38417439, 32444794, 39779857) (PS3 met).

Curation History [↗](#)

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