

Variant: NM_007294.4(BRCA1):c.5257A>G (p.Arg1753Gly)

Version: 1.0

CA10591040 [↗](#)

801086 (ClinVar) [↗](#)

Gene: BRCA1 ([HGNC:672](#))
Condition: BRCA1-related cancer predisposition ([MONDO:0700268](#))
Inheritance Mode: Autosomal dominant inheritance
UUID: c60f30dc-7369-4d49-9cea-6dab70fe4c4f
Approved on: 2025-05-23
Published on: 2025-05-23

HGVS expressions

NM_007294.4:c.5257A>G
NM_007294.4(BRCA1):c.5257A>G (p.Arg1753Gly)
NC_000017.11:g.43057072T>C
CM000679.2:g.43057072T>C
NC_000017.10:g.41209089T>C
CM000679.1:g.41209089T>C
NC_000017.9:g.38462615T>C
NG_005905.2:g.160912A>G
ENST00000461574.2:c.5254A>G
ENST00000470026.6:c.5257A>G
ENST00000473961.6:c.5131A>G
ENST00000476777.6:c.5251A>G
ENST00000477152.6:c.5179A>G
ENST00000478531.6:c.1945A>G
ENST00000489037.2:c.5179A>G
ENST00000493919.6:c.1807A>G
ENST00000494123.6:c.5257A>G
ENST00000497488.2:c.4369A>G
ENST00000618469.2:c.5257A>G
ENST00000634433.2:c.5134A>G
ENST00000644379.2:c.5323A>G
ENST00000644555.2:c.1807A>G
ENST00000652672.2:c.5116A>G
ENST00000484087.6:c.1819A>G
ENST00000357654.9:c.5257A>G
ENST00000471181.7:c.5320A>G
ENST00000644379.1:c.1644A>G
ENST00000352993.7:c.1831A>G
ENST00000357654.7:c.5257A>G
ENST00000461221.5:c.*5040A>G
ENST00000468300.5:c.1945A>G
ENST00000471181.6:c.5320A>G
ENST00000491747.6:c.1945A>G
ENST00000493795.5:c.5116A>G
ENST00000586385.5:c.187A>G
ENST00000591534.5:c.730A>G
ENST00000591849.5:c.-98-6882A>G

NM_007294.3:c.5257A>G
NM_007297.3:c.5116A>G
NM_007298.3:c.1945A>G
NM_007299.3:c.1945A>G
NM_007300.3:c.5320A>G
NR_027676.1:n.5393A>G
NM_007297.4:c.5116A>G
NM_007299.4:c.1945A>G
NM_007300.4:c.5320A>G
NR_027676.2:n.5434A>G

Likely Pathogenic

Met criteria codes 3

PS3 PP3 PM2_Supporting

Evidence Links 0

Expert Panel

ENIGMA BRCA1 and BRCA2 VCEP

Criteria Specification Information

Criteria Specifications for this VCEP

Evidence submitted by expert panel

ENIGMA BRCA1 and BRCA2 VCEP

The c.5257A>G variant in BRCA1 is a missense variant predicted to cause substitution of Arg by Gly at amino acid 1753 (p.(Arg1753Gly)). Reported by two calibrated studies to affect protein function similar to pathogenic control variants (PMIDs:30209399, 38709234) (PS3 met). This BRCA1 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.36, above the recommended threshold of 0.28 for prediction of impact on BRCA1 function via protein change. A SpliceAI score of 0.0 predicts no impact on splicing (score threshold ≤ 0.1) (PP3 met). 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). In summary, this variant meets the criteria to be classified as a Likely pathogenic variant for BRCA1-related cancer predisposition based on the ACMG/AMP criteria applied as specified by the ENIGMA BRCA1/2 VCEP (PS3, PP3, PM2_supporting).

Met criteria codes

PS3			Reported by two calibrated studies to affect protein function similar to pathogenic control variants (PMIDs:30209399, 38709234) (PS3 met).
PP3			This BRCA1 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.36, above the recommended threshold of 0.28 for prediction of impact on BRCA1 function via protein change. A SpliceAI score of 0.0 predicts no impact on splicing (score threshold ≤ 0.1) (PP3 met).
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).



 ▾

 ▾

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.