The ClinGen Evidence Repository is an **FDA-recognized human genetic variant database** containing expert-curated assertions regarding variants' pathogenicity and supporting evidence summaries. [Disclaimer]

Variant: NM_007294.4(BRCA1):c.70T>A (p.Cys24Ser)

Version: 1.0

CA10602017

638952 (ClinVar)

Gene: BRCA1 (HGNC:672)
Condition: BRCA1-related cancer predisposition (MONDO:0700268)
Inheritance Mode: Autosomal dominant inheritance
UUID: d31081e6-bce5-4959-a064-c4e916b0115d
Approved on: 2026/7/15
Published on: 2026/7/15

HGVS expressions

NM_007294.4(BRCA1):c.70T>A (p.Cys24Ser)
NM_007294.4:c.70T>A
NC_000017.11:g.43124027A>T
CM000679.2:g.43124027A>T
NC_000017.10:g.41276044A>T
CM000679.1:g.41276044A>T
NC_000017.9:g.38529570A>T
NG_005905.2:g.93957T>A
ENST00000354071.8:n.134T>A
ENST00000461574.2:c.70T>A
ENST00000470026.6:c.70T>A
ENST00000473961.6:c.70T>A
ENST00000476777.6:c.70T>A
ENST00000477152.6:c.70T>A
ENST00000478531.6:c.70T>A
ENST00000489037.2:c.70T>A
ENST00000493919.6:c.-18T>A
ENST00000494123.6:c.70T>A
ENST00000497488.2:c.-219+1244T>A
ENST00000618469.2:c.70T>A
ENST00000634433.2:c.70T>A
ENST00000644379.2:c.70T>A
ENST00000644555.2:c.-217T>A
ENST00000652672.2:c.-191T>A
ENST00000484087.6:c.70T>A
ENST00000700182.1:c.70T>A
ENST00000700183.1:c.70T>A
ENST00000700184.1:n.313T>A
ENST00000700185.1:n.189T>A
ENST00000700186.1:n.189T>A
ENST00000357654.9:c.70T>A
ENST00000471181.7:c.70T>A
ENST00000642945.1:c.70T>A
ENST00000644555.1:c.-217T>A
ENST00000652672.1:c.-191T>A
ENST00000352993.7:c.70T>A
ENST00000354071.7:c.70T>A

ENST00000357654.7:c.70T>A
ENST00000461221.5:c.70T>A
ENST00000461798.5:c.70T>A
ENST00000468300.5:c.70T>A
ENST00000470026.5:c.70T>A
ENST00000471181.6:c.70T>A
ENST00000476777.5:c.70T>A
ENST00000477152.5:c.70T>A
ENST00000478531.5:c.70T>A
ENST00000489037.1:c.70T>A
ENST00000491747.6:c.70T>A
ENST00000492859.5:c.70T>A
ENST00000493795.5:c.-18T>A
ENST00000493919.5:c.-18T>A
ENST00000494123.5:c.70T>A
ENST00000497488.1:c.-219+1244T>A
ENST00000586385.5:c.4+1155T>A
ENST00000591534.5:c.-44+1244T>A
ENST00000591849.5:c.-99+1244T>A
ENST00000618469.1:c.70T>A
ENST00000634433.1:c.70T>A
NM_007294.3:c.70T>A
NM_007297.3:c.-18T>A
NM_007298.3:c.70T>A
NM_007299.3:c.70T>A
NM_007300.3:c.70T>A
NR_027676.1:n.231T>A
NM_007297.4:c.-18T>A
NM_007299.4:c.70T>A
NM_007300.4:c.70T>A
NR_027676.2:n.272T>A

Likely Pathogenic

Met criteria codes 3

PP3 PS3 PM2_Supporting

Evidence Links 1

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 1.1.0*

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

ENIGMA BRCA1 and BRCA2 VCEP

The variant c.70T>A in BRCA1 is a missense variant predicted to cause substitution of Cysteine by Serine at amino acid 24 (p.Cys24Ser). This variant is absent from gnomAD v4.1 (read depth ≥25x in >90% samples, PM2_Supporting met). This BRCA1 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.56, above the recommended threshold of 0.28

for prediction of impact on BRCA1 function via protein change. A SpliceAI score of 0.02 predicts no impact on splicing (score threshold <0.10) (PP3 met). This variant is reported by one calibrated study to exhibit protein function similar to pathogenic control variants (PMID: 30209399) (PS3 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, PM2_Supporting, PP3).

Met criteria codes

PP3	✔	This BRCA1 missense variant is within a key functional domain and the computational predictor BayesDel (noAF) gives a score of 0.56, above the recommended threshold of 0.28 for prediction of impact on BRCA1 function via protein change. A SpliceAI score of 0.02 predicts no impact on splicing (score threshold <0.10) (PP3 met).
PS3	✔	Reported by one calibrated study to affect protein function similar to pathogenic control variants (PMID:30209399). Variant classified as non-functional based on a saturation genome editing (SGE) assay measuring survival in a haploid cell line. PubMed:30209399
PM2_Supporting	✔	This variant is absent from gnomAD v4.1 (read depth ≥25x in >90% samples, PM2_Supporting met).

Curation History

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.

ClinGen Terms of Use.
¤ Powered by BCM's Genboree.