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_000051.4(ATM):c.8495G>T (p.Arg2832Leu)

Version: 1.0

CA382518109

430406 (ClinVar)

Gene: ATM (HGNC:472)
Condition: ATM-related cancer predisposition (MONDO:0700270)
Inheritance Mode: Autosomal dominant inheritance
UUID: ed8e3ae5-6f75-435c-b2b5-a739fa22815c
Approved on: 2026/8/4
Published on: 2026/8/5

HGVS expressions

NM_000051.4:c.8495G>T
NM_000051.4(ATM):c.8495G>T (p.Arg2832Leu)
NC_000011.10:g.108345819G>T
CM000673.2:g.108345819G>T
NC_000011.9:g.108216546G>T
CM000673.1:g.108216546G>T
NC_000011.8:g.107721756G>T
NG_009830.1:g.127988G>T
NG_054724.1:g.129014C>A
ENST00000452508.7:c.8495G>T
ENST00000713593.1:c.*7966G>T
ENST00000278616.9:c.8495G>T
ENST00000638786.2:n.1193G>T
ENST00000682286.1:n.3252G>T
ENST00000682302.1:n.2913G>T
ENST00000683174.1:n.9979G>T
ENST00000683524.1:n.3719G>T
ENST00000684152.1:n.3911G>T
ENST00000684180.1:n.969G>T
ENST00000684447.1:n.4988G>T
ENST00000527805.6:c.*3559G>T
ENST00000675595.1:c.*3630G>T
ENST00000675843.1:c.8495G>T
ENST00000278616.8:c.8495G>T
ENST00000452508.6:c.8495G>T
ENST00000524755.5:c.227-10527C>A
ENST00000524792.5:n.4710G>T
ENST00000525729.5:c.641-36748C>A
ENST00000526725.1:n.272-5455C>A
ENST00000527531.5:c.*1196+9096C>A
ENST00000615746.4:c.*1196+9096C>A
NM_000051.3:c.8495G>T
NM_001330368.1:c.641-36748C>A
NM_001351110.1:c.695-10527C>A
NM_001351834.1:c.8495G>T
NR_147053.2:n.2301+9096C>A
NM_001330368.2:c.641-36748C>A

NM_001351110.2:c.695-10527C>A
NM_001351834.2:c.8495G>T
NR_147053.3:n.2299+9096C>A

Pathogenic

Met criteria codes 4

PM3_Very Strong | PM2_Supporting | PP1 | PP3

Evidence Links 0

Expert Panel

Hereditary Breast, Ovarian and Pancreatic Cancer VCEP

Criteria Specification Information

- **Criteria Specification:** *ClinGen Hereditary Breast, Ovarian and Pancreatic Cancer Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for ATM Version 1.5*
- **Criteria Specification Approval History**
- **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Hereditary Breast, Ovarian and Pancreatic Cancer VCEP

The c.8495G>T variant in ATM is a missense variant predicted to cause substitution of arginine by leucine at amino acid 2832 (p.Arg2832Leu). This variant has been detected in individual(s) with Ataxia-Telangiectasia (personal communication; PMID: 37438524). This variant has been reported to segregate with Ataxia-Telangiectasia in two affected individuals from one family (personal communication). This variant is absent from gnomAD v4.1.1. The computational predictor REVEL gives a score of 0.822, which is above the threshold of 0.733, evidence that correlates with impact to ATM function. In summary, this variant meets the criteria to be classified as pathogenic for autosomal dominant ATM-related cancer predisposition and autosomal recessive Ataxia-Telangiectasia based on the ACMG/AMP criteria applied as specified by the HBOP VCEP. (PM3_Very_Strong, PP1, PP3, PM2_Supporting)

Met criteria codes

PM3_Very Strong	✔	This variant has been detected in at least 3 individuals with Ataxia-Telangiectasia (PMID: 37438524, personal communication) (PM3_VeryStrong)
PM2_Supporting	✔	Variant is absent from gnomAD V4.1.1 (PM2_Supporting)
PP1	✔	This variant has been reported to segregate with Ataxia-Telangiectasia in two affected family members from one family (personal communication) (PP1).
PP3	✔	The computational predictor REVEL gives a score of 0.822, which is above the threshold of 0.733, evidence that correlates with impact to ATM function (PP3). SpliceAI does not predict any aberrant splicing associated with this variant.

Curation History

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