Variant: NM_000051.4(ATM):c.5631_5635delinsA (p.Phe1877fs)

Version: 1.0

CA10579189

233573 (ClinVar)

Gene: ATM
Condition: ATM-related cancer predisposition (MONDO:0700270)
Inheritance Mode: Autosomal dominant inheritance
UUID: fd6e3003-802d-4057-8802-07351d5c8659
Approved on: 2025-11-11
Published on: 2026-04-10

HGVS expressions

NM_000051.4:c.5631_5635delinsA
NM_000051.4:c.5631_5635delCTCGCinsA
NM_000051.4(ATM):c.5631_5635delinsA (p.Phe1877fs)
NC_000011.10:g.108304809_108304813delinsA
CM000673.2:g.108304809_108304813delinsA
NC_000011.9:g.108175536_108175540delinsA
CM000673.1:g.108175536_108175540delinsA
NC_000011.8:g.107680746_107680750delinsA
NG_009830.1:g.86978_86982delinsA
ENST00000452508.7:c.5631_5635delinsA
ENST00000713593.1:c.*5102_*5106delinsA
ENST00000278616.9:c.5631_5635delinsA
ENST00000683174.1:n.7115_7119delinsA
ENST00000683524.1:n.855_859delinsA
ENST00000684152.1:n.1345_1349delinsA
ENST00000527805.6:c.*695_*699delinsA
ENST00000675595.1:c.*695_*699delinsA
ENST00000675843.1:c.5631_5635delinsA
ENST00000278616.8:c.5631_5635delinsA
ENST00000452508.6:c.5631_5635delinsA
ENST00000524792.5:n.1846_1850delinsA
ENST00000529588.5:c.143_147delinsA
ENST00000533690.5:n.1035_1039delinsA
NM_000051.3:c.5631_5635delinsA
NM_001351834.1:c.5631_5635delinsA
NM_001351834.2:c.5631_5635delinsA

Pathogenic

Met criteria codes 3

PVS1 PM5_Supporting PM3_Very Strong

Not Met criteria codes 1

PM2

Expert Panel

Hereditary Breast, Ovarian and Pancreatic Cancer VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Hereditary Breast, Ovarian and Pancreatic Cancer Expert Panel Specifications*

Evidence Links 0

to the ACMG/AMP Variant Interpretation Guidelines for ATM Version 1.4.0

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Hereditary Breast, Ovarian and Pancreatic Cancer VCEP

The c.5631_5635delinsA (p.Phe1877Leufs*39) variant in ATM is a frameshift variant predicted to cause a premature stop codon in a biologically-relevant-exon leading to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism. This alteration results in a termination codon upstream of the most C-terminus pathogenic alteration (ATM p.Arg3047*), as classified by the HBOP VCEP, and is expected to be more deleterious. This variant has been detected in at least four unrelated individuals with Ataxia-Telangiectasia (PMID: 15843990, 35260754, 2689183). The highest population minor allele frequency in gnomAD v4.1.0 is 0.0000064 in the South Asian population (PM2_Supporting, BS1, and BA1 are not met). 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. (PVS1, PM5_Supporting, PM3_VeryStrong)

Met criteria codes

PVS1	✔	The c.5631_5635delinsA (p.Phe1877LeufsTer?) variant in ATM is a frameshift variant in a biologically-relevant-exon predicted to cause a premature stop codon leading to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism.
PM5_Supporting	✔	Variant with premature termination codons upstream of p.Arg3047
PM3_Very Strong	✔	The variant has been documented in trans with a pathogenic variant in Ataxia-Telangiectasia patients.

Not Met criteria codes

PM2	✖	delTCGC=0.0000064 (9/1400754, GnomAD_exomes)

Curation History

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