

Variant: NM_000314.6(PTEN):c.97_99delATT (p.Ile33del)

Version: 1.0

CA645559009 [↗](#)

449088 (ClinVar) [↗](#)

Gene: PTEN ([HGNC:5728](#))
Condition: PTEN hamartoma tumor syndrome ([MONDO:0017623](#))
Inheritance Mode: Autosomal dominant inheritance
UUID: 18b368f7-e2f3-4e09-a961-5f209be89228
Approved on: 2023/8/4
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HGVS expressions

NM_000314.6:c.97_99delATT
NM_000314.6(PTEN):c.97_99delATT (p.Ile33del)
NC_000010.11:g.87894042_87894044del
CM000672.2:g.87894042_87894044del
NC_000010.10:g.89653799_89653801del
CM000672.1:g.89653799_89653801del
NC_000010.9:g.89643779_89643781del
NG_007466.2:g.35604_35606del
ENST00000700029.2:c.97_99del
ENST00000710265.1:c.97_99del
ENST00000472832.3:c.97_99del
ENST00000688158.2:n.899+13604_899+13606del
ENST00000688922.2:c.97_99del
ENST00000700021.1:c.97_99del
ENST00000700022.1:c.97_99del
ENST00000706954.1:c.97_99del
ENST00000706955.1:c.*132_*134del
ENST00000686459.1:c.97_99del
ENST00000688158.1:c.*275+13604_*275+13606del
ENST00000688308.1:c.97_99del
ENST00000693560.1:c.616_618del
ENST00000371953.8:c.97_99del
ENST00000371953.7:c.97_99del
ENST00000462694.1:n.99_101del
ENST00000610634.1:c.-6_-4del
NM_000314.5:c.97_99del
NM_000314.6:c.97_99del
NM_001304717.2:c.616_618del
NM_001304718.1:c.-609_-607del
NM_000314.7:c.97_99del
NM_001304717.5:c.616_618del
NM_001304718.2:c.-609_-607del
NM_000314.8:c.97_99del

Likely Pathogenic

PM6_Strong PM2_Supporting
PS3_Moderate PP1

PTEN VCEP

Not Met criteria codes 22

BS2 PVS1 BS1 BS4 BS3
BP4 BP3 BP1 BP2 BP5 BP7
PS1 PS2 PS4 BA1 PP2 PP3
PP4 PM1 PM3 PM5 PM4

Evidence Links 0

Criteria Specification Information

- Criteria Specification: ClinGen PTEN Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for PTEN Version 3.0.0
- Criteria Specification Approval History
- Criteria Specifications for this VCEP

Evidence submitted by expert panel

PTEN VCEP

PTEN c.97_99delATT (c.94ATT[1]) (p.Ile33del) meets criteria to be classified as likely pathogenic for PTEN Hamartoma Tumor syndrome in an autosomal dominant manner using modified ACMG criteria (ACMG Classification Rules Specified for PTEN Variant Curation version 3.0.0). Please see a summary of the rules and criteria codes in the “PTEN ACMG Specifications Summary” document (assertion method column). PS3_Moderate: Phosphatase activity ≤ -1.11 per Mighell et al. 2018, PMID: 29706350. PM2_Supporting: Absent in large sequenced populations (PMID 27535533). PM6_Strong: An individual with a highly specific phenotype (Internal laboratory contributor SCV000616838.1). PP1: Co-segregation with disease in multiple affected family members, with 5 or 6 meioses observed. (PMID 10234502 , internal laboratory contributor SCV002559099.1)

Met criteria codes

PM6_Strong			Internal laboratory contributor SCV000616838.1; patient also earns PS4_P, criteria combined with PM6 to upgrade to strong with V3 rules.
PM2_Supporting			Not found in gnomAD
PS3_Moderate			Variant scored -4.13 on high throughput lipid phosphatase assay (PMID:29706350); values below -1.11 consistent with damaging/truncation-like range. PS3 drops to PS3_M with V3 rules
PP1			Individual N6 referenced in article is one of 3 females in the family with the variant. The article does not mention the relationship between the women. The table indicates that skin, thyroid, UG, LDD, macrocephaly are reported in these individuals. Minimum 2 meioses. Outside lab: one meiosis Will discuss with group, see if PP1 may be allowed.

Not Met criteria codes

BS2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PVS1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS1			

No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline			
BS4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP5			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP7			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS4			1 case with pediatric score = 6 from internal laboratory contributor SCV000616838.1. 1 phenotype specificity point = PS4_P. Criteria combined with PM6 to boost to PM6_S.
BA1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

PP4		✖	The table describing family N6 does not indicate ages, how many of the 3 females with the variant have thyroid, skin, UG, LDD or macrocephaly (the bar is half filled in for macrocephaly). It is unclear who has which combination of features. Cannot accurately calculate CC score.
PM1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM3		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM5		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM4		✖	Results in an in-frame deletion causing the loss of a single isoleucine residue within the phosphatase domain. This deletion is conserved across species.

Curation History 	
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