

Variant: *NM_000314.8(PTEN):c.408T>G (p.Cys136Trp)*

Version: 1.0

CA357779 [↗](#)

224543 (ClinVar) [↗](#)

Gene: PTEN ([HGNC:5728](#))

Condition: PTEN hamartoma tumor syndrome ([MONDO:0017623](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: a8ec82c1-a3b5-4e8c-ad81-ac59b2b541ef

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Published on: 2025/6/5

HGVS expressions

NM_000314.8(PTEN):c.408T>G (p.Cys136Trp)

NM_000314.8:c.408T>G

NC_000010.11:g.87933167T>G

CM000672.2:g.87933167T>G

NC_000010.10:g.89692924T>G

CM000672.1:g.89692924T>G

NC_000010.9:g.89682904T>G

NG_007466.2:g.74729T>G

ENST00000700029.2:c.408T>G

ENST00000710265.1:c.408T>G

ENST00000472832.3:c.408T>G

ENST00000688158.2:n.1143T>G

ENST00000688922.2:c.*238T>G

ENST00000700021.1:c.363T>G

ENST00000700022.1:c.408T>G

ENST00000700029.1:c.242T>G

ENST00000706954.1:c.408T>G

ENST00000706955.1:c.*443T>G

ENST00000686459.1:c.408T>G

ENST00000688158.1:c.*519T>G

ENST00000688308.1:c.408T>G

ENST00000688922.1:c.329T>G

ENST00000693560.1:c.927T>G

ENST00000371953.8:c.408T>G

ENST00000371953.7:c.408T>G

ENST00000498703.1:n.234T>G

ENST00000610634.1:c.306T>G

NM_000314.5:c.408T>G

NM_000314.6:c.408T>G

NM_001304717.2:c.927T>G

NM_001304718.1:c.-343T>G

NM_000314.7:c.408T>G

NM_001304717.5:c.927T>G

NM_001304718.2:c.-343T>G

Pathogenic

Met criteria codes 6

- PM2_Supporting
- PM6_Strong
- PP2
- PP3
- PM5
- PS3_Moderate

Not Met criteria codes 1

PS4

Evidence Links 0

Expert Panel

PTEN VCEP

Criteria Specification Information

[Criteria Specification:](#) *ClinGen PTEN Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for PTEN Version 3.1.0*

[Criteria Specification Approval History](#)

[Criteria Specifications for this VCEP](#)

Evidence submitted by expert panel

PTEN VCEP

PTEN c.408T>G (p.Cys136Trp) meets criteria to be classified as pathogenic for PTEN Hamartoma Tumor syndrome in an autosomal dominant manner using modified ACMG criteria (PMID 30311380). Please see a summary of the rules and criteria codes in the “PTEN ACMG Specifications Summary” document (assertion method column). PM6_S: Assumed de novo, but without confirmation of paternity and maternity in a patient with the disease and no family history (internal laboratory contributor(s) SCV003926429.1). PM5: Missense change at an amino acid residue where a different missense change determined to be pathogenic or likely pathogenic and with equal or lesser BLOSUM62 score has been seen before (ClinVar Variation ID 189406, SCV000840468.3). PS3_M: Functional studies supportive of a damaging effect on the gene or gene product. Score of this variant = -3.54 ($\leq$ -1.11) on a high throughput phosphatase assay (PMID 29706350). PP3: REVEL score > 0.7 (score of this variant = 0.954). PP2: PTEN is defined by the PTEN Expert Panel as a gene that has a low rate of benign missense variation and where missense variants are a common mechanism of disease. PM2_P: Absent in large sequenced populations (PMID 27535533).

Met criteria codes

PM2_Supporting			Absent in gnomAD v2 and v4
PM6_Strong			GeneDx proband (ped score = 7)
PP2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP3			REVEL score (0.954) > 0.7
PM5			BLOSUM score for focal variant (-2) is the same as one candidate classified as P y the VCEP (c.407G>A p.Cys136Tyr)
PS3_Moderate			Mighell et al 2018 (PMID 29706350)

Not Met criteria codes

PS4			Ambry proband: 0.5 proband points
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Curation History



 

 

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