

Variant: NM_000314.7(PTEN):c.367C>G (p.His123Asp)

Version: 1.0

CA377482278 [↗](#)

428277 (ClinVar) [↗](#)

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

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

Inheritance Mode: Autosomal dominant inheritance

UUID: 363d5223-feca-47e8-a3b8-115e05778f7f

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HGVS expressions

NM_000314.7:c.367C>G

NM_000314.7(PTEN):c.367C>G (p.His123Asp)

NC_000010.11:g.87933126C>G

CM000672.2:g.87933126C>G

NC_000010.10:g.89692883C>G

CM000672.1:g.89692883C>G

NC_000010.9:g.89682863C>G

NG_007466.2:g.74688C>G

ENST00000700029.2:c.367C>G

ENST00000710265.1:c.367C>G

ENST00000472832.3:c.367C>G

ENST00000688158.2:n.1102C>G

ENST00000688922.2:c.*197C>G

ENST00000700021.1:c.322C>G

ENST00000700022.1:c.367C>G

ENST00000700029.1:c.201C>G

ENST00000706954.1:c.367C>G

ENST00000706955.1:c.*402C>G

ENST00000686459.1:c.367C>G

ENST00000688158.1:c.*478C>G

ENST00000688308.1:c.367C>G

ENST00000688922.1:c.288C>G

ENST00000693560.1:c.886C>G

ENST00000371953.8:c.367C>G

ENST00000371953.7:c.367C>G

ENST00000498703.1:n.193C>G

ENST00000610634.1:c.265C>G

NM_000314.5:c.367C>G

NM_000314.6:c.367C>G

NM_001304717.2:c.886C>G

NM_001304718.1:c.-384C>G

NM_001304717.5:c.886C>G

NM_001304718.2:c.-384C>G

NM_000314.8:c.367C>G

Pathogenic

Met criteria codes **5**

PM2 PM1 PS4_Supporting PS3

PP2

Not Met criteria codes **1**

PP4

Evidence Links **3**

Expert Panel

PTEN VCEP [↗](#)

Criteria Specification Information **!**

[↗](#) Criteria Specifications for this VCEP

Evidence submitted by expert panel

PTEN VCEP

PTEN c.367C>G (p.His123Asp) 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). PS3: Phosphatase activity <50% of wild type OR RNA, mini-gene, or other assay shows impact on splicing. (PMID 29706350, 21828076) PM1: Located at a residue within a catalytic motif as defined by the ClinGen PTEN Expert Panel. PM2: Absent in large sequenced populations (PMID 27535533). 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. PS4_P: Proband(s) with phenotype specificity score of 1-1.5. (internal laboratory contributor SCV000580072.3)

Met criteria codes

PM2	✓	Not present in gnomAD (coverage >90X).
PM1	✓	This amino acid position, 123, is in a catalytic motif.
PS4_Supporting	✓	Teenager with fundic gland polyps diagnosed as a child with hamartomatous features, multiple lipomas, Hashimoto thyroiditis, right thigh hamartoma, macrocephaly, penile freckling. Pediatric CC score of 11 (1 point) (Ambry Genetics).
PS3	✓	Comprehensive in vivo functional analysis of human PTEN using a heterologous yeast reconstitution system. Phosphatase activity was fully inactive (Rodríguez-Escudero I et al2011). Comprehensive in vivo functional analysis of human PTEN using a heterologous yeast reconstitution system. Phosphatase activity was fully inactive. PubMed:21828076 ↗ High-throughput functional assay testing PTEN lipid phosphatase activity score of -4.345802175 so this variant had truncation-like function and was 'TRUE'. PubMed:29706350 ↗
PP2	✓	Missense

Not Met criteria codes

PP4	✗	Teenager with fundic gland polyps diagnosed as a child with hamartomatous features, multiple lipomas, Hashimoto thyroiditis, right thigh hamartoma, macrocephaly, penile freckling. Pediatric CC score of 11 (1 point) (Ambry Genetics).
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PubMed:11918710 

Curation History



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