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_000314.8(PTEN):c.959T>C (p.Leu320Ser)

Version: 1.0

CA377485996

1043063 (ClinVar)

Gene: PTEN (HGNC:5728)
Condition: PTEN hamartoma tumor syndrome (MONDO:0017623)
Inheritance Mode: Autosomal dominant inheritance
UUID: aa83475e-8914-404e-906e-44d8564409c8
Approved on: 2025/12/5
Published on: 2025/12/17

HGVS expressions

NM_000314.8:c.959T>C
NM_000314.8(PTEN):c.959T>C (p.Leu320Ser)
NC_000010.11:g.87961051T>C
CM000672.2:g.87961051T>C
NC_000010.10:g.89720808T>C
CM000672.1:g.89720808T>C
NC_000010.9:g.89710788T>C
NG_007466.2:g.102613T>C
ENST00000700029.2:c.1052T>C
ENST00000710265.1:c.959T>C
ENST00000472832.3:c.959T>C
ENST00000688158.2:n.1694T>C
ENST00000688922.2:c.*789T>C
ENST00000700021.1:c.914T>C
ENST00000700022.1:c.*298T>C
ENST00000700023.1:n.2117T>C
ENST00000700024.1:n.2351T>C
ENST00000700025.1:n.1728T>C
ENST00000700026.1:n.596T>C
ENST00000706954.1:c.959T>C
ENST00000706955.1:c.*994T>C
ENST00000686459.1:c.*545T>C
ENST00000688158.1:c.*1070T>C
ENST00000688308.1:c.959T>C
ENST00000688922.1:c.880T>C
ENST00000693560.1:c.1478T>C
ENST00000371953.8:c.959T>C
ENST00000371953.7:c.959T>C
ENST00000472832.2:c.386T>C
NM_000314.5:c.959T>C
NM_000314.6:c.959T>C
NM_001304717.2:c.1478T>C
NM_001304718.1:c.368T>C
NM_000314.7:c.959T>C
NM_001304717.5:c.1478T>C
NM_001304718.2:c.368T>C

Likely Pathogenic

Met criteria codes 5

PP2 PP3 PM6_Strong PS3_Moderate PM2_Supporting

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.959T>C (p.Leu320Ser) 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 3.1.0). Please see a summary of the rules and criteria codes in the "PTEN ACMG Specifications Summary" document (assertion method column). PM6_S: One proband with presumed de novo occurrence (maternity/paternity not confirmed) for a patient with highly specific phenotype (PMID 31149344). PS3_M: Functional studies supportive of a damaging effect on the gene or gene product. Score of this variant = -2.07 (≤ -1.11) on a high throughput phosphatase assay (PMID 29706350). 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. PP3: REVEL score > 0.7 (score of this variant = 0.913). PM2_Supporting: Absent in large sequenced populations (PMID 27535533).

Met criteria codes

PP2	✔	Missense alteration
PP3	✔	REVEL score of 0.913
PM6_Strong	✔	see Ueno et al 2019. Second article by Furukawa et al 2025 appears to publish on the same patient
PS3_Moderate	✔	score of -3.35 in mighell.
PM2_Supporting	✔	Variant absent from gnomAD

Curation History

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