

Variant: NM_000546.5(TP53):c.1096T>G (p.Ser366Ala)

Version: 2.0

CA000036 [↗](#)

135360 (ClinVar) [↗](#)

Gene: TP53 ([HGNC:7157](#))

Condition: Li-Fraumeni syndrome ([MONDO:0018875](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: 31191c76-8849-45a1-8fdf-bfb7d0098021

Approved on: 2024/8/5

Published on: 2024/8/5

HGVS expressions

NM_000546.5(TP53):c.1096T>G (p.Ser366Ala)

NM_000546.5:c.1096T>G

NC_000017.11:g.7670613A>C

CM000679.2:g.7670613A>C

NC_000017.10:g.7573931A>C

CM000679.1:g.7573931A>C

NC_000017.9:g.7514656A>C

NG_017013.2:g.21938T>G

ENST00000503591.2:c.1096T>G

ENST00000508793.6:c.1096T>G

ENST00000509690.6:c.700T>G

ENST00000514944.6:c.817T>G

ENST00000604348.6:c.1075T>G

ENST00000269305.9:c.1096T>G

ENST00000269305.8:c.1096T>G

ENST00000359597.8:c.993+2922T>G

ENST00000413465.6:c.782+3568T>G

ENST00000420246.6:c.*203T>G

ENST00000445888.6:c.1096T>G

ENST00000455263.6:c.*115T>G

ENST00000504290.5:c.*115T>G

ENST00000504937.5:c.700T>G

ENST00000510385.5:c.*203T>G

ENST00000576024.1:c.54-923T>G

ENST00000610292.4:c.979T>G

ENST00000610538.4:c.*115T>G

ENST00000610623.4:c.*115T>G

ENST00000615910.4:c.1063T>G

ENST00000617185.4:c.*203T>G

ENST00000618944.4:c.*203T>G

ENST00000619186.4:c.619T>G

ENST00000619485.4:c.979T>G

ENST00000620739.4:c.979T>G

ENST00000622645.4:c.*203T>G

ENST00000635293.1:c.979T>G

NM_001126112.2:c.1096T>G

NM_001126113.2:c.*115T>G

	NM_001126114.2:c.*203T>G NM_001126115.1:c.700T>G NM_001126116.1:c.*203T>G NM_001126117.1:c.*115T>G NM_001126118.1:c.979T>G NM_001276695.1:c.*115T>G NM_001276696.1:c.*203T>G NM_001276697.1:c.619T>G NM_001276698.1:c.*203T>G NM_001276699.1:c.*115T>G NM_001276760.1:c.979T>G NM_001276761.1:c.979T>G NM_001276695.2:c.*115T>G NM_001276696.2:c.*203T>G NM_001276697.2:c.619T>G NM_001276698.2:c.*203T>G NM_001276699.2:c.*115T>G NM_001276760.2:c.979T>G NM_001276761.2:c.979T>G NM_000546.6:c.1096T>G NM_001126112.3:c.1096T>G NM_001126113.3:c.*115T>G NM_001126114.3:c.*203T>G NM_001126115.2:c.700T>G NM_001126116.2:c.*203T>G NM_001126117.2:c.*115T>G NM_001126118.2:c.979T>G NM_001276695.3:c.*115T>G NM_001276696.3:c.*203T>G NM_001276697.3:c.619T>G NM_001276698.3:c.*203T>G NM_001276699.3:c.*115T>G NM_001276760.3:c.979T>G NM_001276761.3:c.979T>G
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Benign

Met criteria codes 3

BS3BS2BP4

Not Met criteria codes 13

PVS1BS1BS4PS2PS3
PS4BA1PP1PP3PP4
PM2PM1PM5

Evidence Links 0

Expert Panel

TP53 VCEP

Criteria Specification Information

Criteria Specification: ClinGen TP53 Expert Panel
Specifications to the ACMG/AMP Variant Interpretation
Guidelines for TP53 Version 2.0.0

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

TP53 VCEP

The NM_000546.6: c.1096T>G variant in TP53 is a missense variant predicted to cause substitution of serine by alanine at amino acid 366 (p.Ser366Ala). This variant has been observed in at least 8 heterozygous unrelated females from the same data source with no personal history of cancer prior to age 60 years and no personal history of sarcoma at any age (BS2, Internal lab contributors: SCV000214696.6). In vitro assays performed in yeast and/or human cell lines showed functional transactivation and retained growth suppression activity indicating that this variant does not impact protein function (BS3; PMIDs: 12826609, 29979965, 30224644). Computational predictor scores (BayesDel = 0.1186; Align GVGD Class C0) are below the recommended thresholds (BayesDel < 0.16 and an Align GVGD Class ≤ 55), evidence that does not predict a damaging effect on TP53 via protein change. SpliceAI predicts that the variant has no impact on splicing (BP4). In summary, this variant meets the criteria to be classified as Benign for Li Fraumeni Syndrome based on the ACMG/AMP criteria applied, as specified by the ClinGen TP53 VCEP: BS2, BS3, BP4. (Bayesian Points: -9; VCEP specifications version 2.0; 7/24/2024)

Met criteria codes

BS3			In vitro assays performed in yeast and/or human cell lines showed functional transactivation and retained growth suppression activity indicating that this variant does not impact protein function (BS3; PMIDs: 12826609, 29979965, 30224644)
BS2			This variant has been observed in at least 8 heterozygous unrelated females from the same data source with no personal history of cancer prior to age 60 years and no personal history of sarcoma at any age (Internal lab contributors: SCV000214696.6).
BP4			Computational predictor scores (BayesDel = 0.1186; Align GVGD Class C0) are below the recommended thresholds (BayesDel < 0.16 and an Align GVGD Class ≤ 55), evidence that does not predict a damaging effect on TP53 via protein change. SpliceAI predicts that the variant has no impact on splicing (BP4).

Not Met criteria codes

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
PS2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BA1			

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

PP1			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			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM2			The highest population minor allele frequency in gnomAD v41.0 is 0.0001836 (11/59898 alleles) in th Admixed American population (PM2, BS1, and BA1 are not met).
PM1			This variant does not reside within a region of TP53 that is defined as a mutational hotspot by the ClinGen TP53 VCEP (PM1 not met).
PM5			4 different missense variants (p.Ser366Phe, p.Ser366Cys, p.Ser366Thr, p.Ser366Pro) in the same codon have been reported. However, these variants have not yet been curated to determine if they would be classified as pathogenic or likely pathogenic by the ClinGen TP53 VCEP’s specifications (PM5 not evaluated).

Curation History



 

 

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