

Variant: NM_000022.4(ADA):c.937C>T (p.Arg313Trp)

Version: 1.0

CA9871463 [↗](#)

1195941 (ClinVar) [↗](#)

Gene: ADA ([HGNC:100](#))

Condition: adenosine deaminase deficiency ([MONDO:0007064](#))

Inheritance Mode: Autosomal recessive inheritance

UUID: 91eca944-2e6a-4f9c-ac73-6f66e12b9a9d

Approved on: 2024/4/23

Published on: 2024/4/23

HGVS expressions

NM_000022.4:c.937C>T

NM_000022.4(ADA):c.937C>T (p.Arg313Trp)

NC_000020.11:g.44621056G>A

CM000682.2:g.44621056G>A

NC_000020.10:g.43249697G>A

CM000682.1:g.43249697G>A

NC_000020.9:g.42683111G>A

NG_007385.1:g.35680C>T

ENST00000492931.6:n.1104C>T

ENST00000536076.2:c.784C>T

ENST00000536532.6:c.*80C>T

ENST00000537820.2:c.865C>T

ENST00000539235.6:c.*321C>T

ENST00000695889.1:c.412C>T

ENST00000695890.1:n.4432C>T

ENST00000695891.1:c.477C>T

ENST00000695927.1:c.1015C>T

ENST00000695949.1:c.862C>T

ENST00000695956.1:c.92C>T

ENST00000695957.1:c.*428C>T

ENST00000695991.1:c.475C>T

ENST00000695992.1:c.*80C>T

ENST00000695993.1:c.937C>T

ENST00000695994.1:c.*80C>T

ENST00000695995.1:c.547C>T

ENST00000695996.1:n.1019C>T

ENST00000696003.1:n.2721C>T

ENST00000696004.1:n.1105C>T

ENST00000696005.1:c.387C>T

ENST00000696006.1:c.*80C>T

ENST00000696007.1:c.864C>T

ENST00000696008.1:n.3291C>T

ENST00000696017.1:c.934C>T

ENST00000696034.1:c.*80C>T

ENST00000696035.1:n.1123C>T

ENST00000696036.1:n.1638C>T

ENST00000696037.1:n.2614C>T

	ENST00000696038.1:c.*694C>T ENST00000696039.1:n.1301C>T ENST00000696058.1:c.934C>T ENST00000696059.1:c.*882C>T ENST00000696060.1:c.1006C>T ENST00000696061.1:c.934C>T ENST00000696062.1:c.1000C>T ENST00000696063.1:c.1012C>T ENST00000696064.1:c.784C>T ENST00000696065.1:c.259C>T ENST00000696072.1:n.292C>T ENST00000696073.1:n.1248C>T ENST00000696074.1:n.488C>T ENST00000696075.1:c.*907C>T ENST00000696076.1:c.1006C>T ENST00000696077.1:c.931C>T ENST00000696078.1:c.934C>T ENST00000696079.1:c.934C>T ENST00000696080.1:c.937C>T ENST00000696081.1:n.1056C>T ENST00000696082.1:c.1012C>T ENST00000696083.1:n.1894C>T ENST00000696084.1:n.1114C>T ENST00000696104.1:c.*6C>T ENST00000372874.9:c.937C>T ENST00000372874.8:c.937C>T ENST00000372887.5:c.152-2877G>A ENST00000464097.5:n.687C>T ENST00000492931.5:n.1097C>T ENST00000536532.5:c.*80C>T ENST00000537820.1:c.865C>T ENST00000539235.5:c.*321C>T NM_000022.2:c.937C>T NM_000022.3:c.937C>T NM_001322050.1:c.532C>T NM_001322051.1:c.865C>T NR_136160.1:n.1023C>T NM_001322050.2:c.532C>T NM_001322051.2:c.865C>T NR_136160.2:n.964C>T
--	--

Uncertain Significance

Met criteria codes 1

PM2_Supporting

Not Met criteria codes 2

BS2

PM5

Evidence Links 0

Expert Panel

Severe Combined Immunodeficiency Disease VCEP

Criteria Specification Information

Criteria Specification: ClinGen Severe Combined Immunodeficiency Disease Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for ADA Version 1.0.0

Criteria Specification Approval History

Evidence submitted by expert panel

Severe Combined Immunodeficiency Disease VCEP

The c.937C>T (NM_000022.4) variant in ADA is a missense variant predicted to cause substitution of Arginine by Tryptophan at amino acid 313 (p.Arg313Trp). The filtering allele frequency (the upper threshold of the 95% CI of 25/1180022 alleles) of the c.937C>T variant in ADA is 0.00001454 for European (non-Finnish) chromosomes by gnomAD v4, which is lower than the ClinGen SCID VCEP threshold (<0.0001742) for PM2_Supporting, and therefore meets this criterion (PM2_Supporting). No homozygotes have been observed in gnomAD. Another missense variant [c.938G>A, p.Arg313Gln] in the same codon has been reported; however, the ClinGen SCID VCEP classified this variant as VUS (PM5 not met). To our knowledge, this variant has not been reported in the literature in individuals affected with ADA-related conditions or in functional studies. Due to insufficient evidence, this variant is classified as a variant of uncertain significance for autosomal recessive SCID based on ACMG/AMP criteria applied, as specified by the ClinGen SCID VCEP (specification version 1.0): PM2_Supporting.

Met criteria codes

PM2_Supporting			The filtering allele frequency (the upper threshold of the 95% CI of 25/1180022 alleles) of the c.937C>T variant in ADA is 0.00001454 for European (non-Finnish) chromosomes by gnomAD v4, which is lower than the ClinGen SCID VCEP threshold (<0.0001742) for PM2_Supporting, and therefore meets this criterion (PM2_Supporting). No homozygotes have been observed in gnomAD.
----------------	---	---	---

Not Met criteria codes

BS2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM5			Another missense variant [c.938G>A, p.Arg313Gln] in the same codon has been reported; However, this variant was classified as VUS by the ClinGen SCID VCEP (PM5 not met).

Curation History [↗](#)



 ▾

 ▾

Showing 1 to 1 of 1 rows

--

The information on this website is not intended for direct diagnostic use or medical decision-making without review by a genetics professional. Individuals should not change their health behavior solely on the basis of information contained on this website. If you have questions about the information contained on this website, please see a health care professional.

[ClinGen Terms of Use.](#)

[✕ Powered by BCM's Genboree.](#)