

Variant: NM_000022.4(ADA):c.938G>A (p.Arg313Gln)

Version: 1.0

CA9871461 [↗](#)

1038658 (ClinVar) [↗](#)

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

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

Inheritance Mode: Autosomal recessive inheritance

UUID: 4fb2c181-8222-4334-9881-43100da106d7

Approved on: 2024/4/23

Published on: 2024/4/23

HGVS expressions

NM_000022.4(ADA):c.938G>A (p.Arg313Gln)

NM_000022.4:c.938G>A

NC_000020.11:g.44621055C>T

CM000682.2:g.44621055C>T

NC_000020.10:g.43249696C>T

CM000682.1:g.43249696C>T

NC_000020.9:g.42683110C>T

NG_007385.1:g.35681G>A

ENST00000492931.6:n.1105G>A

ENST00000536076.2:c.785G>A

ENST00000536532.6:c.*81G>A

ENST00000537820.2:c.866G>A

ENST00000539235.6:c.*322G>A

ENST00000695889.1:c.413G>A

ENST00000695890.1:n.4433G>A

ENST00000695891.1:c.478G>A

ENST00000695927.1:c.1016G>A

ENST00000695949.1:c.863G>A

ENST00000695956.1:c.93G>A

ENST00000695957.1:c.*429G>A

ENST00000695991.1:c.476G>A

ENST00000695992.1:c.*81G>A

ENST00000695993.1:c.938G>A

ENST00000695994.1:c.*81G>A

ENST00000695995.1:c.548G>A

ENST00000695996.1:n.1020G>A

ENST00000696003.1:n.2722G>A

ENST00000696004.1:n.1106G>A

ENST00000696005.1:c.388G>A

ENST00000696006.1:c.*81G>A

ENST00000696007.1:c.865G>A

ENST00000696008.1:n.3292G>A

ENST00000696017.1:c.935G>A

ENST00000696034.1:c.*81G>A

ENST00000696035.1:n.1124G>A

ENST00000696036.1:n.1639G>A

ENST00000696037.1:n.2615G>A

	ENST00000696038.1:c.*695G>A ENST00000696039.1:n.1302G>A ENST00000696058.1:c.935G>A ENST00000696059.1:c.*883G>A ENST00000696060.1:c.1007G>A ENST00000696061.1:c.935G>A ENST00000696062.1:c.1001G>A ENST00000696063.1:c.1013G>A ENST00000696064.1:c.785G>A ENST00000696065.1:c.260G>A ENST00000696072.1:n.293G>A ENST00000696073.1:n.1249G>A ENST00000696074.1:n.489G>A ENST00000696075.1:c.*908G>A ENST00000696076.1:c.1007G>A ENST00000696077.1:c.932G>A ENST00000696078.1:c.935G>A ENST00000696079.1:c.935G>A ENST00000696080.1:c.938G>A ENST00000696081.1:n.1057G>A ENST00000696082.1:c.1013G>A ENST00000696083.1:n.1895G>A ENST00000696084.1:n.1115G>A ENST00000696104.1:c.*7G>A ENST00000372874.9:c.938G>A ENST00000372874.8:c.938G>A ENST00000372887.5:c.152-2878C>T ENST00000464097.5:n.688G>A ENST00000492931.5:n.1098G>A ENST00000536532.5:c.*81G>A ENST00000537820.1:c.866G>A ENST00000539235.5:c.*322G>A NM_000022.2:c.938G>A NM_000022.3:c.938G>A NM_001322050.1:c.533G>A NM_001322051.1:c.866G>A NR_136160.1:n.1024G>A NM_001322050.2:c.533G>A NM_001322051.2:c.866G>A NR_136160.2:n.965G>A
--	--

Uncertain Significance

Met criteria codes 1

PM2_Supporting

Not Met criteria codes 1

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.938G>A (NM_000022.4) variant in ADA is a missense variant predicted to cause substitution of Arginine by Glutamine at amino acid 313 (p.Arg313Gln). The filtering allele frequency (the upper threshold of the 95% CI of 2/91080 alleles) of the c.938G>A variant in ADA is 0.000003650 for South Asian 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. No homozygotes have been observed in gnomAD. Another missense variant [c.937C>T, p.Arg313Trp] 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 2/91080 alleles) of the c.938G>A variant in ADA is 0.000003650 for South Asian 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. No homozygotes have been observed in gnomAD.
-----------------------	---	---	---

Not Met criteria codes

PM5			Another missense variant [c.937C>T, p.Arg313Trp] 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

--

