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_000018.4(ACADVL):c.1103A>C (p.Gln368Pro)

Version: 1.0

CA8337965

439360 (ClinVar)

Gene: ACADVL (HGNC:37)
Condition: very long chain acyl-CoA dehydrogenase deficiency (MONDO:0008723)
Inheritance Mode: Autosomal recessive inheritance
UUID: d71d6390-5664-4b34-bad8-622817b3c626
Approved on: 2024-09-10
Published on: 2024-12-18

HGVS expressions

NM_000018.4:c.1103A>C
NM_000018.4(ACADVL):c.1103A>C (p.Gln368Pro)
NC_000017.11:g.7223158A>C
CM000679.2:g.7223158A>C
NC_000017.10:g.7126477A>C
CM000679.1:g.7126477A>C
NC_000017.9:g.7067201A>C
NG_007975.1:g.8325A>C
NG_008391.2:g.1893T>G
ENST00000356839.10:c.1103A>C
ENST00000322910.9:c.*1058A>C
ENST00000350303.9:c.1037A>C
ENST00000356839.9:c.1103A>C
ENST00000543245.6:c.1172A>C
ENST00000578579.2:n.52A>C
ENST00000578824.5:n.519A>C
ENST00000579425.5:n.127A>C
ENST00000582379.1:n.754A>C
ENST00000583858.5:c.132A>C
ENST00000585203.6:n.311A>C
NM_000018.3:c.1103A>C
NM_001033859.2:c.1037A>C
NM_001270447.1:c.1172A>C
NM_001270448.1:c.875A>C
NM_001033859.3:c.1037A>C
NM_001270447.2:c.1172A>C
NM_001270448.2:c.875A>C

Uncertain Significance

Met criteria codes 2

PM2_Supporting PP3

Not Met criteria codes 1

PP4

Evidence Links 0

Expert Panel

ACADVL VCEP

Criteria Specification Information

Criteria Specifications for this VCEP

Evidence submitted by expert panel

ACADVL VCEP

The c.1103A>C (NM_000018.4) variant in ACADVL is a missense variant predicted to cause substitution of glutamine by proline at amino acid 368 (p.Gln368Pro). Several individuals with this variant were identified by newborn screen or were identified in individuals without additional laboratory data to support affected status, so this information is insufficient to use toward classification (PMID: 26385305, 31031081). This variant is only detected on one allele in gnomAD v2.1.1, which is lower than the ClinGen ACADVL Variant Curation Expert Panel threshold (<0.001) for PM2_Supporting, meeting this criterion (PM2_Supporting). The computational predictor REVEL gives a score of 0.98, which is above the threshold of 0.75, evidence that correlates with impact to ACADVL function (PP3). In summary, this variant meets the criteria to be classified as a variant of uncertain significance for autosomal recessive very long chain acyl-CoA dehydrogenase (VLCAD) deficiency based on the ACMG/AMP criteria applied, as specified by the ClinGen ACADVL Variant Curation Expert Panel: PM2_Supporting, PP3 (ACADVL VCEP specifications version 1; approved November 9, 2021).

Met criteria codes

PM2_Supporting	✔	This variant is only detected on one allele in gnomAD v2.1.1, which is lower than the ClinGen ACADVL Variant Curation Expert Panel threshold (<0.001) for PM2_Supporting, meeting this criterion (PM2_Supporting).
PP3	✔	The computational predictor REVEL gives a score of 0.98, which is above the threshold of 0.75, evidence that correlates with impact to ACADVL function (PP3).

Not Met criteria codes

PP4	✖	Several individuals with this variant were identified by newborn screen or were identified in individuals without additional laboratory data to support affected status, so this information is insufficient to use toward classification (PMID: 26385305, 31031081).

Curation History

Showing 1 to 1 of 1 rows