

Variant: *NM_000018.4(ACADVL):c.693T>A (p.Ser231=)*

Version: 1.0

CA289257 [↗](#)

136261 (ClinVar) [↗](#)

Gene: ACADVL ([HGNC:37](#))

Condition: very long chain acyl-CoA dehydrogenase deficiency ([MONDO:0008723](#))

Inheritance Mode: Autosomal recessive inheritance

UUID: 5c47d0ce-9b49-4acb-8c42-f4302f28a649

Approved on: 2024/3/26

Published on: 2024/3/26

HGVS expressions

NM_000018.4:c.693T>A

NM_000018.4(ACADVL):c.693T>A (p.Ser231=)

NC_000017.11:g.7222022T>A

CM000679.2:g.7222022T>A

NC_000017.10:g.7125341T>A

CM000679.1:g.7125341T>A

NC_000017.9:g.7066065T>A

NG_007975.1:g.7189T>A

NG_008391.2:g.3029A>T

ENST00000356839.10:c.693T>A

ENST00000322910.9:c.*648T>A

ENST00000350303.9:c.627T>A

ENST00000356839.9:c.693T>A

ENST00000543245.6:c.762T>A

ENST00000577191.5:n.770T>A

ENST00000577857.5:n.509T>A

ENST00000579286.5:n.874T>A

ENST00000580365.1:n.424T>A

ENST00000581378.5:c.411T>A

ENST00000582379.1:n.77T>A

ENST00000583760.1:n.475T>A

NM_000018.3:c.693T>A

NM_001033859.2:c.627T>A

NM_001270447.1:c.762T>A

NM_001270448.1:c.465T>A

NM_001033859.3:c.627T>A

NM_001270447.2:c.762T>A

NM_001270448.2:c.465T>A

Benign

Met criteria codes **3**

BP7 BP4 BA1

Not Met criteria codes **3**

PM4 PVS1 BP3

Expert Panel

ACADVL VCEP [↗](#)

Criteria Specification Information **!**

[↗](#) Criteria Specifications for this VCEP

Evidence submitted by expert panel

ACADVL VCEP

The NM_000018.4(ACADVL):c.693T>A (p.Ser231=) variant is a synonymous (silent) variant that is not predicted by SpliceAI and NNSplice to impact splicing. In addition, it occurs at a nucleotide that is not conserved as shown by PhyloP and PhastCons (BP4, BP7). The highest population minor allele frequency in gnomAD v2.1.1 is 0.2061 in the African/African American population, which is higher than the ClinGen ACADVL Variant Curation Expert Panel threshold (≥ 0.007) for BA1, and therefore meets this criterion (BA1). In summary, this variant meets the criteria to be classified as benign 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: BA1, BP4 (ACADVL VCEP specifications version 1; approved November 9, 2021).

Met criteria codes

BP7			BP4 is met; variant is predicted to result in a synonymous substitution; 2 of 3 agree with no predicted abnormal splicing; SpliceAI predicts no impact on splicing (delta score = 0); potential loss of cryptic 3' acceptor 11 nucleotides downstream (MaxEntScn >15% reduction (WT=4.5, MUT=0), NNSplice no prediction of cryptic site); potential gain of 3' splice acceptor at variant position (MaxEntScn (WT=0, MUT=2.08)
BP4			Splice AI, NNSplice predict no change to splicing.
BA1			BA1 is met; highest continental population MAF = 2.061% (AFR) $\geq$ 0.7% max pop MAF established by ACADVL working group

Not Met criteria codes

PM4			PM4 is not met; variant is predicted to result in a synonymous substitution
PVS1			PVS1 is not met; variant is predicted to result in a synonymous substitution
BP3			BP3 is not met; variant is predicted to result in a synonymous substitution

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.