# *Variant: NM_000018.2(ACADVL):c.343delG (p.Glu115Lysfs)*

Version: 1.1

*CA220206*

*1624 (ClinVar)*

**Gene**: ACADVL (HGNC:37)
**Condition**: very long chain acyl-CoA dehydrogenase deficiency (MONDO:0008723)
**Inheritance Mode**: Autosomal recessive inheritance
**UUID:** e1a7f305-d1e3-4e8b-9d38-0645f61fc98e
**Approved on**: 2021-11-09
**Published on**: 2022-04-06

## *HGVS expressions*

NM_000018.2(ACADVL):c.343delG (p.Glu115Lysfs)
NC_000017.11:g.7220924del
CM000679.2:g.7220924del
NC_000017.10:g.7124243del
CM000679.1:g.7124243del
NC_000017.9:g.7064967del
NG_007975.1:g.6091del
NG_008391.2:g.4128del
ENST00000356839.10:c.343del
ENST00000322910.9:c.*298del
ENST00000350303.9:c.277del
ENST00000356839.9:c.343del
ENST00000543245.6:c.412del
ENST00000577191.5:n.420del
ENST00000577433.5:n.551del
ENST00000577857.5:n.293+94del
ENST00000579286.5:n.524del
ENST00000579886.2:c.202-21del
ENST00000580365.1:n.74del
ENST00000581378.5:c.42del
ENST00000581562.5:n.390del
ENST00000582056.5:n.526del
ENST00000582166.1:n.324del
ENST00000583312.5:c.343del
ENST00000584103.5:c.376del
NM_000018.3:c.343del
NM_001033859.2:c.277del
NM_001270447.1:c.412del
NM_001270448.1:c.115del
NM_000018.4:c.343del
NM_001033859.3:c.277del
NM_001270447.2:c.412del
NM_001270448.2:c.115del

**Met criteria codes** 3

Expert Panel

**Pathogenic**

PVS1 PM2_Supporting PP4

**Not Met criteria codes** 1

PM3

Evidence Links 0

ACADVL VCEP

Criteria Specification Information

**Criteria Specifications for this VCEP**

Evidence submitted by expert panel

***ACADVL VCEP***

**The NM_000018.4(ACADVL): c.343del (p.Glu115Lysfs) variant in ACADVL is a frameshift predicted to cause a premature stop codon in biologically relevant exon 6/20 leading to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism (PVS1: PMIDs 9973285, 11590124). The highest population minor allele frequency in gnomAD v2.1.1 is 0.00004 in African population, which is lower than the ClinGen ACADVL Variant Curation Expert Panel threshold (<0.001) for PM2_Supporting, meeting this criterion (PM2_Supporting). To our knowledge, functional assays have not been reported for this variant, however it has been reported in the literature in at least four individuals with VLCADD (PP4: PMID: 7479827, 31031081, 32778825). In summary, this variant meets the criteria to be classified as pathogenic 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: PVS1, PM2_supporting, PP4.)**

**Met criteria codes**

| | | |
|---|---|---|
| **PVS1** | ✔ | Frameshift exon 6/20 |
| **PM2_Supporting** | ✔ | gnomAD frequency 0.001414% |
| **PP4** | ✔ | Assertion of VLCAD deficiency (PMID: 31031081 & 7479827) |

**Not Met criteria codes**

| | | |
|---|---|---|
| **PM3** | ✖ | One copy (p.R613W) confirmed inherited from the mother. Deletion not confirmed from father. PM3_supporting NOT applied, because (p.R613W) variant is not curated by VCEP yet. |

Curation History

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