

Variant: *NM\_000033.4(ABCD1):c.1A>G (p.Met1Val)*

Version: 1.0

CA415097154 [↗](#)

851448 (ClinVar) [↗](#)

**Gene:** ABCD1 ([HGNC:215](#))

**Condition:** adrenoleukodystrophy ([MONDO:0018544](#))

**Inheritance Mode:** X-linked inheritance

**UUID:** c5c33107-d069-416c-ae57-e40dd95e3c99

**Approved on:** 2026/4/17

**Published on:** 2026/4/17

### HGVS expressions

**NM\_000033.4(ABCD1):c.1A>G (p.Met1Val)**

**NM\_000033.4:c.1A>G**

NC\_000023.11:g.153725267A>G

CM000685.2:g.153725267A>G

NC\_000023.10:g.152990722A>G

CM000685.1:g.152990722A>G

NC\_000023.9:g.152643916A>G

NG\_009022.2:g.5400A>G

NG\_023231.1:g.4480T>C

ENST00000218104.6:c.1A>G

ENST00000218104.5:c.1A>G

NM\_000033.3:c.1A>G

**Likely Pathogenic**

**Met criteria codes** **5**

PS4

PS3\_Supporting

PP4

PVS1\_Moderate

PM2\_Supporting

**Not Met criteria codes** **2**

PP3

BP4

**Evidence Links** **0**

### Expert Panel

**Peroxisomal Disorders VCEP** [↗](#)

### Criteria Specification Information

[↗](#) **Criteria Specification:** *ClinGen Peroxisomal Disorders Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for ABCD1 Version 1.0.0*

[↗](#) **Criteria Specification Approval History**

[↗](#) **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

#### ***Peroxisomal Disorders VCEP***

The c.1A>G (p.Met1Val) variant in ABCD1 may cause a truncated or absent protein by altering the start codon of the coding sequence (PVS1\_Moderate). At least one patient with this variant displayed a primary adrenal insufficiency and increased plasma VLCFAs, which is highly specific for X-linked adrenoleukodystrophy (PP4; PMID:22176151). This variant has been reported in six more male probands meeting with a primary adrenal insufficiency and increased VLCFA ratios (PS4; PMID:34946879). This variant is absent from gnomAD v2.1.1, v3.1.2 and v4.1.0 (PM2\_Supporting). Immunoblotting in transformed clonal cell lines showed severely reduced expression indicating that this variant impacts protein function. Beta-oxidation assay in transformed clonal cell lines showed the variant activity to be

about 19.6% of wild type activity indicating that this variant impacts protein function (PMID:27067449, PS3\_Supporting). In summary, this variant meets the criteria to be classified as likely pathogenic for X-linked adrenoleukodystrophy based on the ACMG/AMP criteria applied, as specified by the ClinGen Peroxisomal Disorders VCEP: PVS1\_Moderate, PS4, PP4, PM2\_Supporting, PS3\_Supporting (ClinGen Peroxisomal Disorders Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for ABCD1 Version 1.0.0)

Met criteria codes

|                |                                                                                   |                                                                                   |                                                                                                                                                                                                                                                                                                                                                            |
|----------------|-----------------------------------------------------------------------------------|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| PS4            |  |  | This variant has been reported in six more male probands meeting with a primary adrenal insufficiency and increased VLCFA ratios (PS4; PMID:34946879).                                                                                                                                                                                                     |
| PS3_Supporting |  |  | Immunoblotting in transformed clonal cell lines showed severely reduced expression indicating that this variant impacts protein function. Beta-oxidation assay in transformed clonal cell lines showed the variant activity to be about 19.6% of wild type activity indicating that this variant impacts protein function (PMID:27067449, PS3_Supporting). |
| PP4            |  |  | At least one patient with this variant displayed a primary adrenal insufficiency and increased plasma VLCFAs, which is highly specific for X-linked adrenoleukodystrophy (PP4; PMID:22176151).                                                                                                                                                             |
| PVS1_Moderate  |                                                                                   |  | The c.1A>G (p.Met1Val) variant in ABCD1 may cause a truncated or absent protein by altering the start codon of the coding sequence (PVS1_Moderate).                                                                                                                                                                                                        |
| PM2_Supporting |  |  | This variant is absent from gnomAD v2.1.1, v3.1.2 and v4.1.0 (PM2_Supporting).                                                                                                                                                                                                                                                                             |

Not Met criteria codes

|     |                                                                                     |                                                                                     |               |
|-----|-------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|---------------|
| PP3 |  |  | REVEL = 0.591 |
| BP4 |  |  | REVEL = 0.591 |

Curation History 



 

 

owing 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.](#)