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# *Variant: NM_000350.3:c.4853G>A*

Version: 1.0

*CA341283237*

**Gene**: ABCA4 (HGNC:24)
**Condition**: ABCA4-related retinopathy (MONDO:0800406)
**Inheritance Mode**: Autosomal recessive inheritance
**UUID:** da047a0d-35cb-4d16-a931-acd33ee1fe53
**Approved on**: 2025/12/5
**Published on**: 2025/12/19

## *HGVS expressions*

**NM_000350.3:c.4853G>A**
NC_000001.11:g.94021405C>T
CM000663.2:g.94021405C>T
NC_000001.10:g.94486961C>T
CM000663.1:g.94486961C>T
NC_000001.9:g.94259549C>T
NG_009073.1:g.104745G>A
ENST00000370225.4:c.4853G>A
ENST00000370225.3:c.4853G>A
ENST00000460514.1:n.347G>A
ENST00000536513.5:c.1229G>A
NM_000350.2:c.4853G>A

**Pathogenic**

**Met criteria codes** 3

PM2_Supporting | PVS1 | PS4

Evidence Links 0

Expert Panel

ABCA4 VCEP

Criteria Specification Information

- **Criteria Specification:** *ClinGen ABCA4 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for ABCA4 Version 1.0.0*
- **Criteria Specification Approval History**
- **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

***ABCA4 VCEP***

**The NM_000350.3:c.4853G>A; p.Trp1618Ter variant in ABC4A is a nonsense variant predicted to cause a premature stop codon in biologically relevant exon 35/50 leading to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism (PVS1). This variant is absent from gnomAD v4.1.0 (PM2_Supporting). This variant was reported in individuals with ABCA4-related retinopathy (PMID: 31543898, 33301772). The prevalence of the variant in affected individuals is significantly increased compared with the prevalence in controls with an odds ratio at infinity and the confidence interval is from 2.24 to infinity, which is above the ABCA4 VCEP threshold of >5, where the CI does not contain 1 (PS4; PMID: 35120629). In summary, this variant meets the criteria to be classified**

**as pathogenic for ABCA4-related retinopathy based on the ACMG/AMP criteria applied, as specified by the ClinGen ABCA4 VCEP (Specification Version 1.0): PVS1, PS4, PM2_Supporting.**

**Met criteria codes**

| | | |
|---|---|---|
| **PM2_Supporting** | ✔ | This variant is absent from gnomAD v4.1.0 (PM2_Supporting). |
| **PVS1** | ✔ | This is a nonsense variant located in exon 35 out of 50, and introduces a premature stop codon between codons 1-2255 (PVS1). |
| **PS4** | ✔ | The prevalence of the variant in affected individuals is significantly increased compared with the prevalence in controls. The OR is infinity and the CI is 2.24 to infinity, which is above the ABCA4 VCEP threshold of >5, where the CI does not contain 1 (PS4; PMID: 35120629). |

Curation History

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