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_000350.3(ABCA4):c.5371dup (p.Ala1791fs)

Version: 1.0

CA2573335086

2585325 (ClinVar)

Gene: ABCA4 (HGNC:24)
Condition: ABCA4-related retinopathy (MONDO:0800406)
Inheritance Mode: Autosomal recessive inheritance
UUID: 5d7bb5c5-8f11-4c04-a160-187990cf16ea
Approved on: 2025/12/5
Published on: 2025/12/19

HGVS expressions

NM_000350.3(ABCA4):c.5371dup (p.Ala1791fs)
NM_000350.3:c.5371dup
NC_000001.11:g.94014632dup
CM000663.2:g.94014632dup
NC_000001.10:g.94480188dup
CM000663.1:g.94480188dup
NC_000001.9:g.94252776dup
NG_009073.1:g.111518dup
ENST00000370225.4:c.5371dup
ENST00000370225.3:c.5371dup
ENST00000536513.5:c.1747dup
NM_000350.2:c.5371dup

Pathogenic

Met criteria codes 3

PM3_Supporting PVS1 PM2_Supporting

Not Met criteria codes 1

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.5371dup (p.Ala1791GlyfsTer9) variant in ABCA4 is a frameshift variant predicted to cause a premature stop codon in biologically-relevant exon 38/50 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 has been detected in at least one individual with ABCA4-related retinopathy. This individual was compound heterozygous for the variant and a pathogenic variant (c.5882G>A; p.Gly1961Glu) presumed to be in trans by NGS targeted gene panel testing (PM3_Supporting; PMID: 31816670). 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): PVS1, PM3_Supporting, PM2_Supporting.

Met criteria codes

PM3_Supporting	✔	Variant detected in proband with cone dystrophy who also harbors pathogenic variant ABCA4:c.5882G>A, p.G1961E. Testing involved NGS gene panel (200-7000 genes) associated with retinal phenotypes. Authors noted limitations on phase determination. Awarded 0.5 points towards criteria PM3_Supporting consideration.
PVS1	✔	This is a frameshift variant located in exon 38 out of 50, and introduces a premature stop codon between codons 1-2255 (PVS1).
PM2_Supporting	✔	This variant is absent from gnomAD v4.1.0 (PM2_Supporting).

Not Met criteria codes

PS4	✖	While odds ratio for this variant is above 5, the confidence interval contains 1 (PMID:35120629). Therefore, PS4 is not met.

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.

ClinGen Terms of Use.
¤ Powered by BCM's Genboree.