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Variant: NM_001034853.2:c.28+2T>C

Version: 1.0

CA412746845

Gene: RPGR (HGNC:6103)
Condition: RPGR-related retinopathy (MONDO:0100437)
Inheritance Mode: X-linked inheritance
UUID: d7141b55-3ee4-4e0a-a1c9-6d464eb14293
Approved on: Sat, 26 Sep 2026 00:00:00 +0000
Published on: Sat, 26 Sep 2026 00:00:00 +0000

HGVS expressions

NM_001034853.2:c.28+2T>C
NC_000023.11:g.38327338A>G
CM000685.2:g.38327338A>G
NC_000023.10:g.38186591A>G
CM000685.1:g.38186591A>G
NC_000023.9:g.38071535A>G
NG_009553.1:g.5198T>C
ENST00000642373.1:c.28+2T>C
ENST00000642395.2:c.28+2T>C
ENST00000642558.1:c.28+2T>C
ENST00000642739.1:c.28+2T>C
ENST00000644238.1:c.28+2T>C
ENST00000644337.1:c.28+2T>C
ENST00000645032.1:c.28+2T>C
ENST00000645124.1:c.28+2T>C
ENST00000646020.1:c.28+2T>C
ENST00000647261.1:c.28+2T>C
ENST00000318842.11:c.28+2T>C
ENST00000339363.7:c.28+2T>C
ENST00000378505.6:c.28+2T>C
ENST00000465127.1:c.172-338783A>G
ENST00000474584.5:c.28+2T>C
ENST00000482855.5:c.28+2T>C
NM_000328.2:c.28+2T>C
NM_001034853.1:c.28+2T>C
NM_001367245.1:c.28+2T>C
NM_001367246.1:c.28+2T>C
NM_001367247.1:c.28+2T>C
NM_001367249.1:c.28+2T>C
NM_001367250.1:c.28+2T>C
NM_001367251.1:c.28+2T>C
NR_159803.1:n.170+2T>C
NR_159804.1:n.170+2T>C
NR_159805.1:n.170+2T>C
NR_159806.1:n.170+2T>C
NR_159807.1:n.170+2T>C
NM_000328.3:c.28+2T>C

Pathogenic

Met criteria codes 3

PS1_Supporting PM2_Supporting PVS1

Not Met criteria codes 2

PP4 PS4

Evidence Links 0

Expert Panel

X-linked Inherited Retinal Disease VCEP

Criteria Specification Information

- **Criteria Specification:** *ClinGen X-linked Inherited Retinal Disease Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for RPGR Version 1.0*
- **Criteria Specification Approval History**
- **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

X-linked Inherited Retinal Disease VCEP

The NM_001034853.2(RPGR):c.28+2T>C variant is a canonical splice site variant in intron 1, located 2 nucleotides before exon 1. This variant occurs at a canonical splice site in intron 1 and is predicted to disrupt splicing and induce skipping of exon 1, which is expected to introduce a premature stop codon in RPGR (PVS1). This variant is found in the +/- 1,2 dinucleotide and meets PVS1 (met) and another variant, c.28+1G>A, was previously classified as pathogenic in the same donor/acceptor +/-1,2 dinucleotide for the RPGR-related retinopathy by ClinGen X-linked IRD VCEP (PS1_supporting). This variant is absent from hemizygous individuals in gnomAD v4.1.0 (PM2_Supporting). This variant has been reported in at least 2 apparently unrelated probands (PMID: 30105367, 36819107). However, the number of individuals meeting the PS4 requirement of being a male with some functional vision impairment by age 30 and/or decreased or absent ERG responses, or a female with functional visual abnormality and documentation of a male relative affected with retinitis pigmentosa was fewer than the requirement of at least 2 unrelated probands, so PS4_Supporting was not met. In summary, this variant is classified as pathogenic for RPGR-related retinopathy based on the ClinGen X-linked Inherited Retinal Disease Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for RPGR Version 1.0.0: PVS1, PS1_Supporting, and PM2_Supporting.

Met criteria codes

PS1_Supporting	✔	This variant is found in the +/- 1,2 dinucleotide and meets PVS1 (met) and another variant, c.28+1G>A, was previously classified as pathogenic in the same donor/acceptor +/-1,2 dinucleotide for the RPGR-related retinopathy by ClinGen X-linked IRD VCEP (PS1_supporting).
PM2_Supporting	✔	This variant is absent from hemizygous individuals in gnomAD v4.1.0 (PM2_Supporting).
PVS1	✔	This variant occurs at a canonical splice site in intron 1 and is predicted to disrupt splicing and induce skipping of exon 1, which is expected to introduce a premature stop codon in RPGR (PVS1).

Not Met criteria codes

PP4	✖	This variant has been reported in at least 2 apparently unrelated probands (PMID: 30105367, 36819107), no detailed individual level data meeting PP4 requirements was provided.
PS4	✖	

This variant has been reported in at least 2 apparently unrelated probands (PMID: 30105367, 36819107). However, the number of individuals meeting the PS4 requirement of being a male with some functional vision impairment by age 30 and/or decreased or absent ERG responses, or a female with functional visual abnormality and documentation of a male relative affected with retinitis pigmentosa was fewer than the requirement of at least 2 unrelated probands, so PS4_Supporting was not met.

Curation History

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