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Variant: NM_001034853.2(RPGR):c.2007G>A (p.Trp669Ter)

Version: 1.0

CA412731784

2138538 (ClinVar)

Gene: RPGR (HGNC:6103)
Condition: RPGR-related retinopathy (MONDO:0100437)
Inheritance Mode: X-linked inheritance
UUID: 422a4b02-d73f-4c91-91d0-1b55d07289fa
Approved on: 2025/7/31
Published on: 2025/7/31

HGVS expressions

NM_001034853.2:c.2007G>A
NM_001034853.2(RPGR):c.2007G>A (p.Trp669Ter)
NC_000023.11:g.38286992C>T
CM000685.2:g.38286992C>T
NC_000023.10:g.38146245C>T
CM000685.1:g.38146245C>T
NC_000023.9:g.38031189C>T
NG_009553.1:g.45544G>A
ENST00000494707.6:c.953+873G>A
ENST00000642170.1:n.1826+3967G>A
ENST00000642395.2:c.1905+102G>A
ENST00000642739.1:c.1572+3967G>A
ENST00000644238.1:c.1386+3967G>A
ENST00000644337.1:c.1719+102G>A
ENST00000645032.1:c.2007G>A
ENST00000645124.1:c.*101+102G>A
ENST00000646020.1:c.*594+102G>A
ENST00000318842.11:c.1905+102G>A
ENST00000339363.7:c.2520+102G>A
ENST00000378505.6:c.2007G>A
ENST00000465127.1:c.172-379129C>T
ENST00000474584.5:c.*37+3967G>A
ENST00000482855.5:c.1905+102G>A
ENST00000494707.5:c.139+3967G>A
NM_000328.2:c.1905+102G>A
NM_001034853.1:c.2007G>A
NM_001367245.1:c.1902+102G>A
NM_001367246.1:c.1719+102G>A
NM_001367247.1:c.1572+3967G>A
NM_001367248.1:c.1602+3967G>A
NM_001367249.1:c.1569+3967G>A
NM_001367250.1:c.1569+3967G>A
NM_001367251.1:c.1386+3967G>A
NR_159803.1:n.2263+102G>A
NR_159804.1:n.1648+3967G>A
NR_159805.1:n.1714+3967G>A
NR_159806.1:n.1866+102G>A

NR_159807.1:n.1622+3967G>A
NR_159808.1:n.1826+3967G>A
NM_000328.3:c.1905+102G>A

Pathogenic

Met criteria codes 3

PM2_Supporting PVS1 PS4_Supporting

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 1.0.0*

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

X-linked Inherited Retinal Disease VCEP

NM_001034853.2(RPGR):c.2007G>A (p.Trp669Ter) is a nonsense variant that introduces a premature stop codon at in amino acid 669 and is predicted to cause a truncated protein and to disrupt a critical C-terminal region required for proper glutamylation of RPGR (PVS1, PMID: 36445968). This variant is absent from gnomAD v4.1.0 (PM2_Supporting). This variant has been reported in at least 2 apparently unrelated probands meeting one of the PS4 requirements of a male with some functional vision impairment by age 30 years and/or decreased or absent electroretinogram responses, or a female with functional visual abnormality and documentation of a male relative affected with retinitis pigmentosa (PMID: 28863407, PMID: 35432464, PS4_Supporting). 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, PM2_Supporting, and PS4_supporting. (date of approval 05/16/2025).

Met criteria codes

PM2_Supporting	✔	This variant is absent from hemizygous individuals in gnomAD v4.1.0 (PM2_Supporting).
PVS1	✔	This is a nonsense variant that introduces a premature stop codon between amino acids 1-1132 that is predicted to either trigger nonsense-mediated decay or to disrupt a critical C-terminal region required for proper glutamylation of RPGR (PVS1, PMID: 36445968).
PS4_Supporting	✔	This variant has been reported in at least 2 apparently unrelated probands meeting one of the PS4 requirements of 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 (PMIDs: 35432464, 28863407, 31054281 PS4_Supporting).

Curation History

Showing 1 to 1 of 1 rows

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