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_001034853.2:c.2800G>T

Version: 1.0

CA412729749

Gene: RPGR (HGNC:6103)
Condition: RPGR-related retinopathy (MONDO:0100437)
Inheritance Mode: X-linked inheritance
UUID: b35950b2-7a07-4bab-9253-6bf0cbc1d8f2
Approved on: 2025/9/5
Published on: 2025/9/5

HGVS expressions

NM_001034853.2:c.2800G>T
NC_000023.11:g.38286199C>A
CM000685.2:g.38286199C>A
NC_000023.10:g.38145452C>A
CM000685.1:g.38145452C>A
NC_000023.9:g.38030396C>A
NG_009553.1:g.46337G>T
ENST00000494707.6:c.953+1666G>T
ENST00000642170.1:n.1826+4760G>T
ENST00000642395.2:c.1905+895G>T
ENST00000642739.1:c.1572+4760G>T
ENST00000644238.1:c.1386+4760G>T
ENST00000644337.1:c.1719+895G>T
ENST00000645032.1:c.2800G>T
ENST00000645124.1:c.*101+895G>T
ENST00000646020.1:c.*594+895G>T
ENST00000318842.11:c.1905+895G>T
ENST00000339363.7:c.2520+895G>T
ENST00000378505.6:c.2800G>T
ENST00000465127.1:c.172-379922C>A
ENST00000474584.5:c.*37+4760G>T
ENST00000482855.5:c.1905+895G>T
ENST00000494707.5:c.139+4760G>T
NM_000328.2:c.1905+895G>T
NM_001034853.1:c.2800G>T
NM_001367245.1:c.1902+895G>T
NM_001367246.1:c.1719+895G>T
NM_001367247.1:c.1572+4760G>T
NM_001367248.1:c.1602+4760G>T
NM_001367249.1:c.1569+4760G>T
NM_001367250.1:c.1569+4760G>T
NM_001367251.1:c.1386+4760G>T
NR_159803.1:n.2263+895G>T
NR_159804.1:n.1648+4760G>T
NR_159805.1:n.1714+4760G>T
NR_159806.1:n.1866+895G>T
NR_159807.1:n.1622+4760G>T

NR_159808.1:n.1826+4760G>T
NM_000328.3:c.1905+895G>T

Pathogenic

Met criteria codes 3

PP4 PVS1 PM2_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.2800G>T (p.Glu934Ter) is a nonsense variant introducing a premature stop in codon 934 within exon 15 of 15 that is predicted 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). At least one proband harboring this variant exhibits a phenotype including presentation with night blindness (0.5 pts) with onset at age 3 years (1 pt), reduced visual acuity (0.5 pts), diminished electroretinogram responses from rods, fundus appearance showing widespread retinal pigment epithelium degeneration with pigment deposits (0.5 pts), optic disc pallor (0.5 pts), cataract, severe macular degeneration, artery attenuation, and genotyping by next-generation sequencing with a 483-gene panel showing no alternative basis for inherited retinal disease (2 pts), which together are specific for RPGR-related retinopathy (5 points, PMID: 36276946, PP4). 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 PP4.

Met criteria codes

PP4	✔	At least one proband harboring this variant exhibits a phenotype including presentation with night blindness (0.5 pts) with onset at age 3 years (1 pt), reduced visual acuity (0.5 pts), diminished electroretinogram responses from rods, fundus appearance showing widespread retinal pigment epithelium degeneration with pigment deposits (0.5 pts), optic disc pallor (0.5 pts), cataract, severe macular degeneration, artery attenuation, and genotyping by next-generation sequencing with a 483-gene panel showing no alternative basis for inherited retinal disease (2 pts), which together are specific for RPGR-related retinopathy (5 points, PMID: 36276946, PP4).
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).
PM2_Supporting	✔	This variant is absent from gnomAD v4.1.0 (PM2_Supporting).

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.