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(RPGR):c.2293_2297del (p.Glu765fs)

Version: 1.0

CA916083905

866191 (ClinVar)

Gene: RPGR (HGNC:6103)
Condition: RPGR-related retinopathy (MONDO:0100437)
Inheritance Mode: X-linked inheritance (primarily recessive with milder female expression)
UUID: 85173f47-8a3c-495d-af5d-4c37133b1f47
Approved on: 2025/9/7
Published on: 2025/9/7

HGVS expressions

NM_001034853.2:c.2293_2297del
NM_001034853.2(RPGR):c.2293_2297del (p.Glu765fs)
NC_000023.11:g.38286703_38286707del
CM000685.2:g.38286703_38286707del
NC_000023.10:g.38145956_38145960del
CM000685.1:g.38145956_38145960del
NC_000023.9:g.38030900_38030904del
NG_009553.1:g.45830_45834del
ENST00000494707.6:c.953+1159_953+1163del
ENST00000642170.1:n.1826+4253_1826+4257del
ENST00000642395.2:c.1905+388_1905+392del
ENST00000642739.1:c.1572+4253_1572+4257del
ENST00000644238.1:c.1386+4253_1386+4257del
ENST00000644337.1:c.1719+388_1719+392del
ENST00000645032.1:c.2293_2297del
ENST00000645124.1:c.*101+388_*101+392del
ENST00000646020.1:c.*594+388_*594+392del
ENST00000318842.11:c.1905+388_1905+392del
ENST00000339363.7:c.2520+388_2520+392del
ENST00000378505.6:c.2293_2297del
ENST00000465127.1:c.172-379418_172-379414del
ENST00000474584.5:c.*37+4253_*37+4257del
ENST00000482855.5:c.1905+388_1905+392del
ENST00000494707.5:c.139+4253_139+4257del
NM_000328.2:c.1905+388_1905+392del
NM_001034853.1:c.2293_2297del
NM_001367245.1:c.1902+388_1902+392del
NM_001367246.1:c.1719+388_1719+392del
NM_001367247.1:c.1572+4253_1572+4257del
NM_001367248.1:c.1602+4253_1602+4257del
NM_001367249.1:c.1569+4253_1569+4257del
NM_001367250.1:c.1569+4253_1569+4257del
NM_001367251.1:c.1386+4253_1386+4257del
NR_159803.1:n.2263+388_2263+392del
NR_159804.1:n.1648+4253_1648+4257del

NR_159805.1:n.1714+4253_1714+4257del
NR_159806.1:n.1866+388_1866+392del
NR_159807.1:n.1622+4253_1622+4257del
NR_159808.1:n.1826+4253_1826+4257del
NM_000328.3:c.1905+388_1905+392del

Likely Pathogenic

Met criteria codes 2

PVS1 PM2_Supporting

Not Met criteria codes 1

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 1.0.0*

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.2293_2297del (p.Glu765ArgfsTer3) is a frameshift variant due to a 5-nucleotide deletion introducing a premature stop codon within exon 15 of 15, which 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). This variant has been reported in at least 2 apparently unrelated probands (PMID: 27620828, PMID: 34985506). However, the number of individuals meeting one of the PS4 requirements of some functional vision impairment in affected males by age 30 years, decreased or absent electroretinogram responses, or a female proband with an affected male family member, was fewer than the requirement of at least 2 unrelated probands, so PS4_Supporting was not met. In summary, this variant is classified as likely 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 and PM2_Supporting.

Met criteria codes

PVS1	✔	This is a frameshift variant that introduces a premature stop codon in exon 15 of 15 that is predicted 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).

Not Met criteria codes

PS4	✖	This variant has been reported in at least 2 apparently unrelated probands (PMID: 27620828, PMID: 34985506). However, the number of individuals meeting one of the PS4 requirements of some functional vision impairment in affected males by age 30, decreased or absent cone and/or rod ERG responses, or a female proband with an affected male family member, was fewer than the requirement of at least 2 unrelated probands, so PS4_Supporting was 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.