

Variant: *NM_000329.3(RPE65):c.302C>T (p.Thr101Ile)*

Version: 1.0

CA340748300 [↗](#)

865946 (ClinVar) [↗](#)

Gene: RPE65 ([HGNC:6121](#))

Condition: RPE65-related recessive retinopathy ([MONDO:0100368](#))

Inheritance Mode: Autosomal recessive inheritance

UID: e886266e-2f44-4bb3-96a0-eb3bfb13599b

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HGVS expressions

NM_000329.3:c.302C>T

NM_000329.3(RPE65):c.302C>T (p.Thr101Ile)

NC_000001.11:g.68444827G>A

CM000663.2:g.68444827G>A

NC_000001.10:g.68910510G>A

CM000663.1:g.68910510G>A

NC_000001.9:g.68683098G>A

NG_008472.1:g.10133C>T

NG_008472.2:g.10133C>T

ENST00000262340.6:c.302C>T

ENST00000262340.5:c.302C>T

NM_000329.2:c.302C>T

Likely Pathogenic

Met criteria codes **4**

PS3_Supporting

PM3

PM2_Supporting

PP3_Moderate

Evidence Links **0**

Expert Panel

Leber Congenital Amaurosis/early onset Retinal Dystrophy VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** *ClinGen Leber Congenital Amaurosis/early onset Retinal Dystrophy Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for RPE65 Version 1.0.0*

[↗](#) **Criteria Specification Approval History**

[↗](#) **Criteria Specifications for this VCEP**









Evidence submitted by expert panel

Leber Congenital Amaurosis/early onset Retinal Dystrophy VCEP

The NM_000329.3(RPE65):c.302C>T (p.Thr101Ile) variant is a missense variant in RPE65 causing a substitution of threonine with isoleucine at position 101. This variant is present in gnomAD v.4.1.0 at a Grpmax allele frequency of 8.474e-7, with 1 / 1180026 alleles in the European (Non-Finnish) population, which is lower than the ClinGen LCA/eoRD VCEP PM2_Supporting threshold of <0.0002 (PM2_Supporting). The computational predictor REVEL gives a score of 0.88, which is above the ClinGen LCA/eoRD VCEP threshold of ≥ 0.773 and predicts a damaging effect on RPE65 function (PP3_Moderate). The variant exhibited 1.27% enzymatic activity in a retinoid

isomerase assay relative to the wild-type control, which is lower than the ClinGen LCA/eoRD PS3_Supporting threshold of <10% activity, indicating that it triggers a severe defect in protein function (PS3_Supporting, PMID: 19431183). This variant has been reported in at least 1 proband with early-onset severe retinal dystrophy who was compound heterozygous with the c.271C>T p.Arg91Trp variant confirmed in trans by next-generation sequencing data (1 point, VCEP member-provided data), which was previously classified pathogenic by the ClinGen LCA/eoRD VCEP (1 total point, PM3). In summary, this variant meets the criteria to be classified as Likely Pathogenic for RPE65-related recessive retinopathy based on the ACMG/AMP criteria applied, as specified by the ClinGen LCA/eoRD VCEP: PM2_Supporting, PP3_Moderate, PS3_Supporting, PM3 (VCEP specifications version 1.0.0; date of approval 09/21/2023).

Met criteria codes

PS3_Supporting			The variant exhibited 1.27% enzymatic activity in a retinoid isomerase assay relative to the wild-type control, which is lower than the ClinGen LCA / eoRD PS3_Supporting threshold of <10% activity, indicating that it triggers a severe defect in protein function (PS3_Supporting, PMID: 19431183).
PM3			This variant has been reported in at least 1 proband with early-onset severe retinal dystrophy who was compound heterozygous with the c.271C>T p.Arg91Trp variant confirmed in trans by next-generation sequencing data (1 point, VCEP member-provided data), which was previously classified pathogenic by the ClinGen LCA / eoRD VCEP (1 total point, PM3).
PM2_Supporting			This variant is present in gnomAD v.4.1.0 at a Gpmax allele frequency of 8.474e-7, with 1 / 1180026 alleles in the European (Non-Finnish) population, which is lower than the ClinGen LCA / eoRD VCEP PM2_Supporting threshold of <0.0002 (PM2_Supporting).
PP3_Moderate			The computational predictor REVEL gives a score of 0.88, which is above the ClinGen LCA / eoRD VCEP threshold of ≥ 0.773 and predicts a damaging effect on RPE65 function (PP3_Moderate).

Curation History [↗](#)

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