

Variant: NM_025114.4(CEP290):c.3462dup (p.Leu1155fs)

Version: 1.0

CA1139662802 [↗](#)

813157 (ClinVar) [↗](#)

Gene: [CEP290](#)

Condition: CEP290-related ciliopathy ([MONDO:0100451](#))

Inheritance Mode: Autosomal recessive inheritance

UUID: d3659ac7-07bf-44f0-8773-53825ed30815

Approved on: 2026/7/20

Published on: 2026/7/20

HGVS expressions

NM_025114.4(CEP290):c.3462dup (p.Leu1155fs)

NM_025114.4:c.3462dup

NC_000012.12:g.88092683dup

CM000674.2:g.88092683dup

NC_000012.11:g.88486460dup

CM000674.1:g.88486460dup

NC_000012.10:g.87010591dup

NG_008417.1:g.54536dup

NG_008417.2:g.54536dup

ENST00000309041.12:c.3461dup

ENST00000547691.8:c.745dup

ENST00000552810.6:c.3461dup

ENST00000672414.2:c.*1632dup

ENST00000672647.1:n.1821dup

ENST00000673058.2:c.3461dup

ENST00000674971.1:c.3461dup

ENST00000675089.1:c.287-1842dup

ENST00000675230.1:c.3440dup

ENST00000675408.1:c.3461dup

ENST00000675476.1:c.4322dup

ENST00000675628.1:n.3688dup

ENST00000675794.1:c.*1632dup

ENST00000675833.1:c.4229dup

ENST00000676074.1:c.3461dup

ENST00000676181.1:n.1149dup

ENST00000676363.1:n.9187dup

ENST00000676448.1:c.*1374dup

ENST00000309041.11:c.3467dup

ENST00000547691.6:c.641dup

ENST00000552810.5:c.3461dup

NM_025114.3:c.3461dup

NM_025114.4:c.3461dup

Likely Pathogenic

Met criteria codes 2

PVS1PM2_Supporting

Not Met criteria codes 1

PM3

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 CEP290 Version 1.0

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Leber Congenital Amaurosis/early onset Retinal Dystrophy VCEP

NM_025114.4(CEP290):c.3461dup (p.Leu1155ThrfsTer6) is a frameshift variant that introduces a premature stop codon into exon 30 of 54 and is predicted to lead to nonsense-mediated decay in a gene in which loss-of-function is an established mechanism of disease (PVS1). This variant is absent from gnomAD v4.1.0 (PM2_Supporting). This variant has been reported in at least 1 proband with early-onset severe retinal dystrophy who harbored the variant in the compound heterozygous state with the NM_025114.4(CEP290):c.2T>A (p.Met1Lys) variant suspected in trans (PMID: 32531858). However, the proband was not counted for PM3 in order to avoid circularity. There is an additional report of the variant in an inherited retinal disease cohort (PMID: 36460718) but no additional details were available. In summary, this variant meets the criteria to be classified as Likely Pathogenic for CEP290-related ciliopathy based on the ACMG/AMP criteria applied, as specified by the ClinGen LCA/eoRD VCEP: PVS1 and PM2_Supporting. (LCA/eoRD VCEP Specifications for CEP290 Version 1.0.0)

Met criteria codes

PVS1

This is a frameshift variant that introduces a premature stop codon into exon 30 of 54 and is predicted to lead to nonsense-mediated decay in a gene in which loss-of-function is an established mechanism of disease (PVS1).

PM2_Supporting

This variant is absent from gnomAD v4.1.0 (PM2_Supporting).

Not Met criteria codes

PM3

This variant has been reported in at least 1 proband with early-onset severe retinal dystrophy who harbored the variant in the compound heterozygous state with the NM_025114.4(CEP290): p.Met1Lys variant suspected in trans (PMID: 32531858). However, the proband was not counted for PM3 in order to avoid circularity. There is an additional report of the variant in an IRD cohort (PMID: 36460718) but no additional details were available.

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.