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_000261.2:c.1130C>A

Version: 2.0

CA343724606

2500837 (ClinVar)

Gene: MYOC (HGNC:4653)
Condition: open-angle glaucoma (MONDO:0005338)
Inheritance Mode: Autosomal dominant inheritance
UUID: 13b7a0ea-fbf4-4ce4-95b6-0cdc104151d8
Approved on: 2026/2/19
Published on: 2026/2/18

HGVS expressions

NM_000261.2:c.1130C>A
NC_000001.11:g.171636310G>T
CM000663.2:g.171636310G>T
NC_000001.10:g.171605450G>T
CM000663.1:g.171605450G>T
NC_000001.9:g.169872073G>T
NG_008859.1:g.21324C>A
ENST00000037502.11:c.1130C>A
ENST00000637303.1:c.235-2320G>T
ENST00000638471.1:c.*468C>A
ENST00000037502.10:c.1130C>A
ENST00000614688.1:c.*94C>A
NM_000261.1:c.1130C>A

Likely Pathogenic

Met criteria codes 4

PP1_Moderate PM2_Supporting PS4_Supporting PP3_Moderate

Not Met criteria codes 10

BS1 BS3 BP7 BP4 PM5 BA1 PM4 PS1 PS2 PS3

Evidence Links 0

Expert Panel

Glaucoma VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Glaucoma Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for MYOC Version 2.0.0*
Criteria Specification Approval History
Criteria Specifications for this VCEP

Evidence submitted by expert panel

Glaucoma VCEP

The c.1130C>A variant in MYOC is a missense variant predicted to cause substitution of Threonine by Lysine at amino acid 377 (p.Thr377Lys). This variant was not found in any genetic ancestry group of gnomAD (v4.1.0), meeting the ≤ 0.0001 threshold set for PM2_Supporting in a genetic ancestry group of at least 10,000 alleles. The REVEL score = 0.908, which was within the 0.773-0.931 range for PP3_Moderate, predicting a damaging effect on MYOC function. There was no functional evidence predicting a damaging or benign impact of this variant on MYOC function. 5 segregations in 1 family, with juvenile open angle glaucoma (JOAG), have been reported (PMID:

11774072), which fulfilled PP1_Moderate (5-6 meioses). 2 probands with JOAG or POAG (primary open angle glaucoma) have been reported carrying this variant (PMIDs: 11774072, 31302906), which met PS4_Supporting (≥ 2 probands). PM5_Supporting could not be applied to this novel missense variant as although it did meet PP3, the Grantham score was lower (=78) than the score for the different missense change at the same amino acid residue determined to be pathogenic by the ClinGen Glaucoma VCEP (c.1130C>T, p.Thr377Met, Grantham score=81). In summary, this variant met the criteria to receive a score of 6 and to be classified as likely pathogenic (likely pathogenic classification range 6 to 9, adapted from PMID: 32720330) for juvenile open angle glaucoma based on the ACMG/AMP criteria met, as specified by the ClinGen Glaucoma VCEP (v2.0.0, 5 Dec 2024): PP1_Moderate, PP3_Moderate, PS4_Supporting, PM2_Supporting

Met criteria codes

PP1_Moderate	✔	5 segregations in 1 family, with juvenile open angle glaucoma (JOAG), have been reported (PMID: 11774072), which fulfilled PP1_Moderate (5-6 meioses).
PM2_Supporting	✔	This variant was not found in any genetic ancestry group of gnomAD (v4.1.0), meeting the ≤ 0.0001 threshold set for PM2_Supporting in a genetic ancestry group of at least 10,000 alleles.
PS4_Supporting	✔	2 probands with JOAG or POAG have been reported carrying this variant (PMIDs: 11774072, 31302906), which met PS4_Supporting (≥ 2 probands).
PP3_Moderate	✔	The REVEL score = 0.908, which was within the 0.773-0.931 range for PP3_Moderate, predicting a damaging effect on MYOC function.

Not Met criteria codes

BS1	✖	This criterion was not met as PM2_Supporting has been met.
BS3	✖	No functional evidence has been found for this variant.
BP7	✖	This is not an intronic, synonymous or non-coding variant.
BP4	✖	This criterion was not met as PP3 has been met.
PM5	✖	PM5_Supporting could not be applied to this novel missense variant as although it did meet PP3, the Grantham score was lower (=78) than the score for the different missense change at the same amino acid residue determined to be pathogenic by the ClinGen Glaucoma VCEP (c.1130C>T, p.Thr377Met, Grantham score=81).
BA1	✖	This criterion was not met as PM2_Supporting has been met.
PM4	✖	This variant does not cause a protein length change.
PS1	✖	An established LP or P variant causing this same amino acid change has not been identified.
PS2	✖	This variant has not been identified de novo.

PS3		✖	No functional evidence has been found for this variant.

Curation History

Showing 1 to 2 of 2 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.