Variant: NM_005026.5(PIK3CD):c.112C>T (p.Arg38Cys)

Version: 1.0

CA576774

657939 (ClinVar)

Gene: PIK3CD (HGNC:5293)
Condition: immunodeficiency 14 (MONDO:0014222)
Inheritance Mode: Autosomal dominant inheritance
UUID: f43a574e-777a-40a5-9b8b-4c470e1b761f
Approved on: 2025-12-19
Published on: 2025-12-23

HGVS expressions

NM_005026.5:c.112C>T
NM_005026.5(PIK3CD):c.112C>T (p.Arg38Cys)
NC_000001.11:g.9710567C>T
CM000663.2:g.9710567C>T
NC_000001.10:g.9770625C>T
CM000663.1:g.9770625C>T
NC_000001.9:g.9693212C>T
NG_023434.1:g.63836C>T
ENST00000481137.2:c.112C>T
ENST00000698706.1:n.363C>T
ENST00000698707.1:c.112C>T
ENST00000698708.1:n.320C>T
ENST00000698709.1:c.112C>T
ENST00000698710.1:c.112C>T
ENST00000698711.1:n.465C>T
ENST00000698712.1:c.112C>T
ENST00000698713.1:c.112C>T
ENST00000698714.1:c.112C>T
ENST00000698715.1:c.112C>T
ENST00000698716.1:c.112C>T
ENST00000377346.9:c.112C>T
ENST00000361110.6:c.112C>T
ENST00000377346.8:c.112C>T
ENST00000536656.5:c.112C>T
ENST00000543390.2:c.112C>T
ENST00000628140.2:c.112C>T
NM_005026.3:c.112C>T
NM_001350234.1:c.112C>T
NM_001350235.1:c.112C>T
NM_005026.4:c.112C>T
NM_001350234.2:c.112C>T

Likely Benign

Met criteria codes 1

BP4

Expert Panel

Antibody Deficiencies VCEP

Not Met criteria codes 3

BS1 PM2 PS4

Evidence Links 0

Criteria Specification Information

Criteria Specification: *ClinGen Antibody Deficiencies Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for PIK3CD Version 1.0.0*

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Antibody Deficiencies VCEP

NM_005026.5(PIK3CD):c.112C>T (p.Arg38Cys) is a missense variant causing replacement of arginine with cysteine at amino acid 38. This variant is present in gnomAD v4.1.0 at a total combined allele frequency of 0.00002358, with 37 alleles / 1,613,824 total alleles across all populations of gnomAD, which is higher than the ClinGen Antibody Deficiencies VCEP PM2_Supporting threshold of <0.00000132. The variant is present in gnomAD v.4.1.0 at a GrpMax allele frequency of 0.0002203, with 24 alleles / 74,832 total alleles in the African/African American population, which is lower than the BS1 threshold of >0.000316, so no population code can be applied. The computational predictor REVEL gives a score of 0.238, which is below the ClinGen Antibody Deficiencies VCEP threshold of <0.290 and predicts a non-damaging effect on PIK3CD function. The computational predictor CADD gives a PHRED score of 21.5, which is below the ClinGen Antibody Deficiencies VCEP threshold of <22.7 and predicts a non-deleterious effect on PIK3CD function. The two predictors agree on a non-damaging effect (BP4). In summary, this variant meets the criteria to be classified as likely benign for autosomal dominant immunodeficiency 14 based on the ACMG/AMP criteria applied, as specified by the ClinGen Antibody Deficiencies VCEP: BP4. (VCEP specifications version 1.0.0).

Met criteria codes

BP4	✔	The computational predictor REVEL gives a score of 0.238, which is below the ClinGen Antibody Deficiencies VCEP threshold of <0.290 and predicts a non-damaging effect on PIK3CD function. The computational predictor CADD gives a PHRED score of 21.5, which is below the ClinGen Antibody Deficiencies VCEP threshold of <22.7 and predicts a non-deleterious effect on PIK3CD function. The two predictors agree on a non-damaging effect (BP4).

Not Met criteria codes

BS1	✖	This variant is present in gnomAD v.4.1.0 at a GrpMax allele frequency of 0.0002203, with 24 alleles / 74,832 total alleles in the African/African American population, which is lower than the BS1 threshold of >0.000316, so no population code can be applied.
PM2	✖	This variant is present in gnomAD v4.1.0 at a total combined allele frequency of 0.00002358, with 37 alleles / 1,613,824 total alleles across all populations of gnomAD, which is higher than the ClinGen Antibody Deficiencies VCEP PM2_Supporting threshold of <0.00000132.
PS4	✖	Reported in ClinVar by Ambry

Curation History

Showing 1 to 1 of 1 rows