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_000260.4(MYO7A):c.2002C>T (p.Arg668Cys)

Version: 1.0

CA132231

43168 (ClinVar)

Gene: MYO7A (HGNC:4647)
Condition: Usher syndrome (MONDO:0019501)
Inheritance Mode: Autosomal recessive inheritance
UUID: 6a32887c-1612-4a2f-a69d-9c23b9789b97
Approved on: 2026/5/20
Published on: 2026/6/25

HGVS expressions

NM_000260.4(MYO7A):c.2002C>T (p.Arg668Cys)
NM_000260.4:c.2002C>T
NC_000011.10:g.77174822C>T
CM000673.2:g.77174822C>T
NC_000011.9:g.76885868C>T
CM000673.1:g.76885868C>T
NC_000011.8:g.76563516C>T
NG_009086.1:g.51559C>T
NG_009086.2:g.51577C>T
ENST00000409709.9:c.2002C>T
ENST00000409893.6:c.67C>T
ENST00000409619.6:c.1969C>T
ENST00000409709.7:c.2002C>T
ENST00000409893.5:c.2002C>T
ENST00000458637.6:c.2002C>T
ENST00000620575.4:c.2002C>T
NM_000260.3:c.2002C>T
NM_001127179.2:c.2002C>T
NM_001127180.1:c.2002C>T
NM_001127180.2:c.2002C>T
NM_001369365.1:c.1969C>T

Pathogenic

Met criteria codes 3

PP3 PP4 PM3_Very Strong

Not Met criteria codes 1

PM2

Evidence Links 0

Expert Panel

Hearing Loss VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Hearing Loss Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for CDH23, COCH, GJB2, KCNQ4, MYO6, MYO7A, SLC26A4, TECTA and USH2A Version 2*
PDF
Criteria Specification Approval History
Criteria Specifications for this VCEP

Evidence submitted by expert panel

Hearing Loss VCEP

The c.2002C>T variant in MYO7A is a missense variant predicted to cause substitution of arginine by cysteine at amino acid 668. The highest population minor allele frequency in gnomAD v4.1 is 0.00003344 (48/1179790 alleles) in the European non-finnish population, (PM2_Supporting, BS1, and BA1 are not met). The computational predictor REVEL gives a score of 0.794, which is above the threshold of 0.7, evidence that correlates with impact on MYO7A function (PP3 met). This variant has been detected in 3 individuals with usher syndrome and 1 with sensorineural hearing loss. All of those individuals, were compound heterozygous for the variant and a pathogenic variant and 3 of those were confirmed in trans by parental testing (PM3_VeryStrong, PP4; PMID: 20146813, 26969326, SCV001397007.7, Labcorp Genetics internal data). In summary, this variant meets the criteria to be classified as pathogenic for autosomal recessive Usher syndrome based on the ACMG/AMP criteria applied, as specified by the ClinGen Hearing Loss VCEP: PM3_VeryStrong, PP4, PP3. (ClinGen Hearing Loss VCEP specifications version 2; 05/20/2026).

Met criteria codes

PP3	✔	The computational predictor REVEL gives a score of 0.794, which is above the threshold of 0.7, evidence that correlates with impact on MYO7A function
PP4	✔	This variant has been detected in 3 individuals with Usher syndrome. All of those individuals, were compound heterozygous for the variant and a pathogenic variant as confirmed by parental testing
PM3_Very Strong	✔	This variant has been detected in 3 individuals with Usher syndrome and 1 with autosomal recessive nonsyndromic hearing loss. All of those individuals, were compound heterozygous for the variant and a pathogenic variant as confirmed by parental testing

Not Met criteria codes

PM2	✖	The highest population minor allele frequency in gnomAD v4.1 is 0.00003344 (48/1179790 alleles) in the European non-finnish population, (PM2_Supporting not met)

Curation History

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See Report	Preferred Variant Title	Classification	Condition	Published Date	Version	Criteria Specification	Gene
View	NM_000260.4(MYO7A):c.2002C>T (p.Ar...	Pathogenic	Usher Syndrome	2026-06-25	1.0	ClinGen Hearing Loss Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for CDH23, COCH, GJB2, KCNQ4, MYO6, MYO7A, SLC26A4, TECTA and USH2A Version 2	MYO7A

Showing 1 to 1 of 1 rows

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