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_000257.3(MYH7):c.2360G>A (p.Arg787His)

Version: 2.0

CA012239

42900 (ClinVar)

Gene: MYH7 (HGNC:4625)
Condition: hypertrophic cardiomyopathy (MONDO:0005045)
Inheritance Mode: Autosomal dominant inheritance
UUID: de961e5a-a5f1-47f5-abee-524b09b41cc0
Approved on: 2025-11-14
Published on: 2025-11-14

HGVS expressions

NM_000257.3:c.2360G>A
NM_000257.3(MYH7):c.2360G>A (p.Arg787His)
NC_000014.9:g.23425345C>T
CM000676.2:g.23425345C>T
NC_000014.8:g.23894554C>T
CM000676.1:g.23894554C>T
NC_000014.7:g.22964394C>T
NG_007884.1:g.15317G>A
ENST00000355349.4:c.2360G>A
ENST00000355349.3:c.2360G>A
NM_000257.4:c.2360G>A

Benign

Met criteria codes 4

BS4 BP2 BA1 PM1

Not Met criteria codes 9

BS1 BS3 BP4 PS4 PS3 PP3 PP1 PM2 PM5

Evidence Links 3

Expert Panel

Cardiomyopathy VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Cardiomyopathy Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for MYH7 Version 2.0.0*
Criteria Specification Approval History
Criteria Specifications for this VCEP

Evidence submitted by expert panel

Cardiomyopathy VCEP

NM_000257.4(MYH7):c.2360G>A (p.Arg787His).This variant has been identified in 0.2% (FAF 95% CI; 200/91078) of South Asian chromosomes, including 1 homozygote, in gnomAD v4.1.0 (BA1; https://gnomad.broadinstitute.org). Additionally, this variant has been identified in multiple affected individuals with other pathogenic variants (BP2; summarized in ClinVar ID: 42900) and was shown not to segregate with disease in 2 affected individuals from 2 families (BS4; Oxford Medical Genetics Laboratory (OMGL)). This variant lies in a region of the protein where variants are statistically more likely to be disease-associated (PM1_Strength; Walsh 2019 PMID: 30696458). This is not considered to be in conflict with BA1 since benign variation within this region was considered during that analysis. In summary,

this variant meets criteria to be is classified as benign for hypertrophic cardiomyopathy in an autosomal dominant manner based on BA1, BP2, BS4 and PM1.

Met criteria codes

BS4	✔	Additionally, this variant was shown not to segregate with disease in 2 affected individuals from 2 families (BS4; Oxford Medical Genetics Laboratory (OMGL)). Individual 1: A likely pathogenic variant in MYBPC3 has been identified in this family following non-segregation in some of the affected relatives. MYH7 variant does not segregate. Individual 2. Also Homozygous for the Likely path MYBPC3 variant. Affected brother also has MYBPC3 variant but not MYH7 variant.
BP2	✔	Variant identified in multiple affected individuals with other pathogenic variants (including ClinVar 42900 and SHaRe data) Variant identified in 2 probands with HCM - however both carry pathogenic variants in other genes PubMed:21959974
BA1	✔	This variant has been identified in 0.2% (FAF 95% CI; 200/91078) of South Asian chromosomes, including 1 homozygote, in gnomAD v4.1.0 (BA1; https://gnomad.broadinstitute.org).
PM1	✔	This variant lies in a region of the protein where variants are statistically more likely to be disease-associated (PM1_Strength; Walsh 2019 PMID: 30696458). This is not considered to be in conflict with BA1 since benign variation within this region was considered during that analysis. Variants in head region of the protein (aa 181-937) are statistically more likely to be disease-associated PubMed:27532257 This variant lies in a region of the protein where variants are statistically more likely to be disease-associated (PM1_Strength; Walsh 2019 PMID: 30696458). PubMed:30696458

Not Met criteria codes

BS1	✖	This variant has been identified in 0.2% (FAF 95% CI; 200/91078) of South Asian chromosomes, including 1 homozygote, in gnomAD v4.1.0 (BA1; https://gnomad.broadinstitute.org).
BS3	✖	no studies
BP4	✖	Comp and cons conflicting, revel score not low enough
PS4	✖	PM2 not met
PS3	✖	no studies
PP3	✖	Comp and cons conflicting, revel score not low enough
PP1	✖	

			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM2		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM5		✖	2 VUS, one multiple submitter, 1 single submitter

Curation History

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