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_001042723.2:c.7084G>A

Version: 1.1

CA069115

1214002 (ClinVar)

Gene: RYR1 (HGNC:6261)
Condition: malignant hyperthermia, susceptibility to, 1 (MONDO:0007783)
Inheritance Mode: Autosomal dominant inheritance
UUID: 101e9f25-8179-4cdb-b6f7-31db96672a16
Approved on: 2023/4/6
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HGVS expressions

NM_001042723.2:c.7084G>A
NC_000019.10:g.38499691G>A
CM000681.2:g.38499691G>A
NC_000019.9:g.38990331G>A
CM000681.1:g.38990331G>A
NC_000019.8:g.43682171G>A
NG_008866.1:g.70992G>A
ENST00000599547.6:c.7084G>A
ENST00000359596.8:c.7084G>A
ENST00000355481.8:c.7084G>A
ENST00000359596.7:c.7084G>A
ENST00000360985.7:c.7081G>A
ENST00000594335.5:c.536G>A
NM_000540.2:c.7084G>A
NM_001042723.1:c.7084G>A
NM_000540.3:c.7084G>A

Likely Pathogenic

Met criteria codes 3

PM1 PS4_Moderate PP3_Moderate

Evidence Links 0

Expert Panel

Malignant Hyperthermia Susceptibility VCEP

Criteria Specification Information

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Malignant Hyperthermia Susceptibility VCEP

This pathogenicity assessment is relevant only for malignant hyperthermia susceptibility (MHS) inherited in an autosomal dominant pattern. Variants in RYR1 can also cause other myopathies inherited in an autosomal dominant pattern or in an autosomal recessive pattern. Some of these disorders may predispose individuals to malignant hyperthermia. RYR1 variants may also contribute to a malignant hyperthermia reaction in combination with other genetic and non-genetic factors and the clinician needs to consider such factors in making management decisions. This sequence variant predicts a substitution of glutamic acid with lysine at codon 2362 of the RYR1 protein, p.(Glu2362Lys). This variant was not present in a large population database (gnomAD) at the time this variant was interpreted.

This variant has been reported in two unrelated individuals who have a personal or family history of a malignant hyperthermia reaction, two of these individuals had a positive in vitro contracture test (IVCT) or caffeine halothane contracture test (CHCT) result (if the proband was unavailable for testing, a positive diagnostic test result in a mutation-positive relative was counted), PS4_Moderate (PMID:30236257). No functional studies were identified for this variant. This variant resides in a region of RYR1 considered to be a hotspot for pathogenic variants that contribute to MHS, PM1 (PMID: 21118704). A REVEL score >0.85 (0.885)supports a pathogenic status for this variant, PP3_Moderate. This variant has been classified as Likely Pathogenic. Criteria implemented: PS4_Moderate, PM1, PP3_Moderate.

Met criteria codes

PM1	✔	This variant resides in a region of RYR1 considered to be a hotspot for pathogenic variants that contribute to MHS, PM1 (PMID: 21118704).
PS4_Moderate	✔	This variant has been reported in two unrelated individuals who have a personal or family history of a malignant hyperthermia reaction, two of these individuals had a positive in vitro contracture test (IVCT) or caffeine halothane contracture test (CHCT) result (if the proband was unavailable for testing, a positive diagnostic test result in a mutation-positive relative was counted), PS4_Moderate (PMID:30236257).
PP3_Moderate	✔	A REVEL score >0.85 (0.885)supports a pathogenic status for this variant, PP3_Moderate.

Curation History

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