

Variant: NM_001130987.2(DYSF):c.441T>C (p.Pro147=)

Version: 1.0

CA426697783 [↗](#)

501050 (ClinVar) [↗](#)

Gene: DYSF ([HGNC:8291](#))

Condition: autosomal recessive limb-girdle muscular dystrophy
([MONDO:0015152](#))

Inheritance Mode: Autosomal recessive inheritance

UUID: 1966b172-cd67-49e8-8831-ce85e822c8a4

Approved on: 2026/4/30

Published on: 2026/5/7

HGVS expressions

NM_001130987.2:c.441T>C

NM_001130987.2(DYSF):c.441T>C (p.Pro147=)

NC_000002.12:g.71511902T>C

CM000664.2:g.71511902T>C

NC_000002.11:g.71739032T>C

CM000664.1:g.71739032T>C

NC_000002.10:g.71592540T>C

NG_008694.1:g.63280T>C

ENST00000258104.8:c.438T>C

ENST00000410020.8:c.441T>C

ENST00000258104.7:c.438T>C

ENST00000394120.6:c.441T>C

ENST00000409366.5:c.441T>C

ENST00000409582.7:c.438T>C

ENST00000409651.5:c.441T>C

ENST00000409744.5:c.441T>C

ENST00000409762.5:c.438T>C

ENST00000410020.7:c.441T>C

ENST00000410041.1:c.441T>C

ENST00000413539.6:c.438T>C

ENST00000429174.6:c.438T>C

NM_001130455.1:c.441T>C

NM_001130976.1:c.438T>C

NM_001130977.1:c.438T>C

NM_001130978.1:c.438T>C

NM_001130979.1:c.438T>C

NM_001130980.1:c.438T>C

NM_001130981.1:c.438T>C

NM_001130982.1:c.441T>C

NM_001130983.1:c.441T>C

NM_001130984.1:c.441T>C

NM_001130985.1:c.441T>C

NM_001130986.1:c.441T>C

NM_001130987.1:c.441T>C

NM_003494.3:c.438T>C

NM_001130455.2:c.441T>C

NM_001130976.2:c.438T>C

NM_001130977.2:c.438T>C
NM_001130978.2:c.438T>C
NM_001130979.2:c.438T>C
NM_001130980.2:c.438T>C
NM_001130981.2:c.438T>C
NM_001130982.2:c.441T>C
NM_001130983.2:c.441T>C
NM_001130984.2:c.441T>C
NM_001130985.2:c.441T>C
NM_001130986.2:c.441T>C
NM_003494.4:c.438T>C

Likely Benign

Met criteria codes 3

BP7 BP4 PM2_Supporting

Not Met criteria codes 4

BP5 BP2 PP4 PM3

Evidence Links 0

Expert Panel

Limb Girdle Muscular Dystrophy VCEP

Criteria Specification Information

Criteria Specification: ClinGen Limb Girdle Muscular Dystrophy Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for DYSF Version 2.0.0

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Limb Girdle Muscular Dystrophy VCEP

The NM_003494.4: c.438T>C p.(Pro146=) variant in DYSF, which is also known as NM_001130987.2: c.441T>C p.(Pro147=), is a synonymous variant that does not affect the protein amino acid sequence. It is not located in a splice region and is not predicted to affect splicing (SpliceAI score 0) (BP4, BP7). This variant has been reported in an individual with disease range dysferlin expression in blood monocytes (Jain Foundation Dysferlin Registry internal data communication), but it was identified in a heterozygous state with two other DYSF variants: one classified as pathogenic by the VCEP and the other a splice region variant predicted to ablate a canonical donor site that has been observed in multiple patients. However, phase was not determined (BP2 not met). This variant fails quality filters in gnomAD v4.1.0 exomes but is absent from genomes (PM2_Supporting). In summary, this variant meets criteria to be classified as Likely Benign for autosomal recessive limb girdle muscular dystrophy. Although there are both pathogenic and benign types of evidence for this variant, the population frequency is not considered inconsistent with the final classification. ACMG/AMP criteria applied, as specified by the ClinGen LGMD VCEP (LGMD VCEP specifications version 2.0.0; 04/30/2026): BP4, BP7, PM2_Supporting.

Met criteria codes

BP7



The NM_003494.4: c.438T>C p.(Pro146=) variant in DYSF, which is also known as NM_001130987.2: c.441T>C p.(Pro147=), is a synonymous variant that is not expected to affect the protein amino acid sequence. It is not located in a splice region and is not predicted to affect splicing (SpliceAI score 0) (BP4, BP7).

BP4



The NM_003494.4: c.438T>C p.(Pro146=) variant in DYSF, which is also known as NM_001130987.2: c.441T>C p.(Pro147=), is a synonymous variant that is not expected to affect the protein amino acid sequence. It is not located in a splice region and is not predicted to affect splicing (SpliceAI score 0) (BP4, BP7).

PM2_Supporting			This variant is absent from gnomAD v4.1.0 genomes but fails quality filters in exomes (PM2_Supporting).
Not Met criteria codes			
BP5			Found in a heterozygous state, phase unknown, with two other DYSF variants, one classified as pathogenic by the VCEP and the other a splice region variant predicted to ablate the canonical donor site (Jain Foundation Dysferlin Registry internal data communication). We do not include this code in our specifications.
BP2			Found in a heterozygous state with two other DYSF variants, one classified as pathogenic by the VCEP and the other a splice region variant predicted to ablate the canonical donor site (Jain Foundation Dysferlin Registry internal data communication), but phase was not confirmed. This variant is not present in gnomAD v2 exomes, and so co-occurrence with the other variants identified in this individual cannot be assessed.
PP4			While this variant was identified in a Jain Foundation Dysferlin Registry participant who had disease range dysferlin in blood monocytes (Jain Foundation Dysferlin Registry internal data communication), the clinical phenotype of this individual was not confirmed, and they were also heterozygous for two other DYSF variants with more evidence for pathogenicity.
PM3			While this variant was identified in a Jain Foundation Dysferlin Registry participant who had disease range dysferlin in blood monocytes (Jain Foundation Dysferlin Registry internal data communication), the clinical phenotype of this individual was not confirmed, and they were also heterozygous for two other DYSF variants with more evidence for pathogenicity: c.937+4A>T, which ablates canonical donor (curation in progress) and c.2779delG p.(Ala927LeufsTer21), classified as Pathogenic. This variant is not present in gnomAD v2 exomes, and so co-occurrence with the other variants identified in this individual cannot be assessed. Emory (Eurofins) is only submitter in ClinVar. Case from Nallamilli 2018 (Emory) is only case in LOVD. No other literature or cases identified.

Curation History 	
    	
Showing 1 to 1 of 1 rows	

