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_001130987.2(DYSF):c.5132C>T (p.Ser1711Phe)

Version: 1.0

CA347220545

3677022 (ClinVar)

Gene: DYSF (HGNC:8291)
Condition: autosomal recessive limb-girdle muscular dystrophy (MONDO:0015152)
Inheritance Mode: Autosomal recessive inheritance
UUID: 5ff7b1e4-45d3-413a-913a-597c64caa713
Approved on: 2026/3/23
Published on: 2026/4/10

HGVS expressions

NM_001130987.2(DYSF):c.5132C>T (p.Ser1711Phe)
NM_001130987.2:c.5132C>T
NC_000002.12:g.71664396C>T
CM000664.2:g.71664396C>T
NC_000002.11:g.71891526C>T
CM000664.1:g.71891526C>T
NC_000002.10:g.71745034C>T
NG_008694.1:g.215774C>T
ENST00000698057.1:c.2546C>T
ENST00000698058.1:c.1763C>T
ENST00000698059.1:c.1871C>T
ENST00000258104.8:c.5015C>T
ENST00000410020.8:c.5132C>T
ENST00000258104.7:c.5015C>T
ENST00000394120.6:c.5018C>T
ENST00000409366.5:c.5081C>T
ENST00000409582.7:c.5129C>T
ENST00000409651.5:c.5111C>T
ENST00000409744.5:c.5039C>T
ENST00000409762.5:c.5066C>T
ENST00000410020.7:c.5132C>T
ENST00000410041.1:c.5069C>T
ENST00000413539.6:c.5108C>T
ENST00000429174.6:c.5078C>T
ENST00000479049.6:n.1900C>T
NM_001130455.1:c.5018C>T
NM_001130976.1:c.4973C>T
NM_001130977.1:c.5036C>T
NM_001130978.1:c.5078C>T
NM_001130979.1:c.5108C>T
NM_001130980.1:c.5066C>T
NM_001130981.1:c.5129C>T
NM_001130982.1:c.5111C>T
NM_001130983.1:c.5081C>T
NM_001130984.1:c.5039C>T
NM_001130985.1:c.5069C>T
NM_001130986.1:c.4976C>T

NM_001130987.1:c.5132C>T
NM_003494.3:c.5015C>T
NM_001130455.2:c.5018C>T
NM_001130976.2:c.4973C>T
NM_001130977.2:c.5036C>T
NM_001130978.2:c.5078C>T
NM_001130979.2:c.5108C>T
NM_001130980.2:c.5066C>T
NM_001130981.2:c.5129C>T
NM_001130982.2:c.5111C>T
NM_001130983.2:c.5081C>T
NM_001130984.2:c.5039C>T
NM_001130985.2:c.5069C>T
NM_001130986.2:c.4976C>T
NM_003494.4:c.5015C>T

Likely Pathogenic

Met criteria codes 3

PM3 PP4_Strong PM2_Supporting

Not Met criteria codes 2

PP3 PM5

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.5015C>T variant in DYSF, which is also known as NM_001130987.2: c.5132C>T p.(Ser1711Phe), is a missense variant predicted to cause substitution of serine to phenylalanine at amino acid 1672, p.(Ser1672Phe). This variant has been reported in at least two patients with features consistent with LGMD (PMID: 33927379, 32528171; LOVD DYSF_001234), where it was identified in unconfirmed phase with a pathogenic variant in both (NM_003494.4: c.797G>A (p.Gly266Glu), 0.5 pts, MYO-SEQ internal data communication, PMID: 32528171; c.799_800del p.(Phe267LeufsTer5), 0.5 pts, PMID: 33927379, LOVD Individuals #00327046 and #0032760) (PM3). At least one of these individuals displayed progressive limb girdle muscle weakness and absent dysferlin on muscle biopsy (PMID: 32528171, MYO-SEQ internal data communication; PP4_Strong). This variant is absent from gnomAD v.4.1.0, meeting the criteria for PM2_Supporting. The computational predictor REVEL gives a score of 0.592, which is below the LGMD VCEP threshold of ≥0.70 (PP3 not met). In summary, this variant meets the criteria to be classified as Likely pathogenic for autosomal recessive limb-girdle muscular dystrophy based on the ACMG/AMP criteria applied, as specified by the ClinGen LGMD VCEP (LGMD VCEP specifications version 2.0.0; 03/23/2026): PM3, PP4_Strong, PM2_Supporting.

Met criteria codes

PM3	✔	This variant has been reported in at least two patients with features consistent with LGMD (PMID: 33927379, 32528171; LOVD DYSF_001234), where it was identified in unconfirmed phase with a pathogenic variant in both (NM_003494.4: c.797G>A (p.Gly266Glu), 0.5 pts, MYO-SEQ internal data communication, PMID: 32528171;

c.799_800del p.(Phe267LeufsTer5), 0.5 pts, PMID: 33927379, LOVD Individuals #00327046 and #0032760) (PM3).
Curated variant is absent from gnomAD, so co-occurrence could not be assessed. no other cases available

PP4_Strong	✔	At least one of these individuals displayed progressive limb girdle muscle weakness and absent dysferlin on muscle biopsy (PMID: 32528171, MYO-SEQ internal data communication; PP4_Strong).
PM2_Supporting	✔	This variant is absent from gnomAD v.4.1.0, meeting the criteria for PM2_Supporting.

Not Met criteria codes

PP3	✖	The computational predictor REVEL gives a score of 0.592, which is below the LGMD VCEP threshold of ≥0.70. SpliceAI Donor Gain 0.04
PM5	✖	no other missense changes at this position seem to have been reported.

Curation History

Showing 1 to 1 of 1 rows

The information on this website is not intended for direct diagnostic use or medical decision-making without review by a genetics professional. Individuals should not change their health behavior solely on the basis of information contained on this website. If you have questions about the information contained on this website, please see a health care professional.

ClinGen Terms of Use.
¤ Powered by BCM's Genboree.