

Variant: NM_000070.3(CAPN3):c.1838del (p.Lys613fs)

Version: 1.0

CA489885447 [↗](#)

554906 (ClinVar) [↗](#)

Gene: CAPN3 ([HGNC:825](#))

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

Inheritance Mode: Autosomal recessive inheritance

UUID: 2e9a54c0-2e50-435c-a657-df050e1fec2b

Approved on: 2025/1/9

Published on: 2025/1/9

HGVS expressions

- NM_000070.3:c.1838del
- NM_000070.3(CAPN3):c.1838del (p.Lys613fs)
- NC_000015.10:g.42408248del
- CM000677.2:g.42408248del
- NC_000015.9:g.42700446del
- CM000677.1:g.42700446del
- NC_000015.8:g.40487738del
- NG_008660.1:g.65146del
- ENST00000337571.9:c.-81-1055del
- ENST00000349748.8:c.1639-1055del
- ENST00000357568.8:c.1820del
- ENST00000397163.8:c.1838del
- ENST00000397204.9:c.-81-1055del
- ENST00000466369.5:n.2329del
- ENST00000495723.1:n.2709del
- ENST00000549793.5:n.2051del
- ENST00000565173.2:n.212del
- ENST00000569136.6:c.-158del
- ENST00000638141.2:n.1654-1055del
- ENST00000673646.1:c.402del
- ENST00000673692.1:c.-3-1539del
- ENST00000673705.1:c.310-1055del
- ENST00000673743.1:c.-179+108del
- ENST00000673750.1:c.-158del
- ENST00000673771.1:c.-158del
- ENST00000673839.1:c.-302del
- ENST00000673851.1:c.-158del
- ENST00000673854.1:n.4282del
- ENST00000673886.1:c.-158del
- ENST00000673890.1:c.-158del
- ENST00000673928.1:c.-82+108del
- ENST00000673936.1:c.-158del
- ENST00000673939.1:c.-81-1055del
- ENST00000673978.1:c.-324del
- ENST00000673987.1:c.-158del
- ENST00000674011.1:c.-158del
- ENST00000674012.1:n.113del

	ENST00000674018.1:c.-158del ENST00000674041.1:c.-81-1055del ENST00000674052.1:c.62del ENST00000674064.1:n.217del ENST00000674093.1:c.-81-1055del ENST00000674119.1:c.-81-1055del ENST00000674135.1:c.-94del ENST00000674139.1:c.-158del ENST00000674140.1:n.989del ENST00000674146.1:c.-158del ENST00000674149.1:c.-158del ENST00000318023.11:c.1694del ENST00000337571.8:c.-81-1055del ENST00000349748.7:c.1639-1055del ENST00000356316.7:c.-90-1046del ENST00000357568.7:c.1820del ENST00000397163.7:c.1838del ENST00000397200.8:c.302del ENST00000397204.8:c.-81-1055del ENST00000561817.5:c.-81-1055del ENST00000565173.1:n.167del ENST00000565274.5:c.50del ENST00000565559.5:c.-94del ENST00000567071.5:c.297del ENST00000569136.5:c.-158del ENST00000569827.5:c.247-1055del NM_000070.2:c.1838del NM_024344.1:c.1820del NM_173087.1:c.1639-1055del NM_173088.1:c.302del NM_173089.1:c.-81-1055del NM_173090.1:c.-81-1055del NM_024344.2:c.1820del NM_173087.2:c.1639-1055del NM_173088.2:c.302del NM_173089.2:c.-81-1055del NM_173090.2:c.-81-1055del
--	--

Pathogenic

Met criteria codes 4

PP4

PM2

PM3

PVS1

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 CAPN3 Version 1.0.0

Criteria Specification Approval History

Criteria Specifications for this VCEP

Limb Girdle Muscular Dystrophy VCEP

The NM_000070.3: c.1838del p.(Lys613ArgfsTer49) variant in CAPN3 is a frameshift variant predicted to cause a premature stop codon in biologically relevant exon 17/24, leading to nonsense mediated decay in a gene in which loss of function is an established disease mechanism (PVS1). This variant has been detected in at least three individuals with features of limb girdle muscular dystrophy (PMID: 16607617, 18055493, ClinVar SCV000953543.3 internal data communication), including confirmed in trans with a pathogenic variant (c.1079G>A p.(Trp360Ter), 1.0 pt, ClinVar SCV000953543.3 internal data communication) (PM3). At least one patient with this variant was clinically suspected to have limb girdle muscular dystrophy or showed progressive limb girdle muscle weakness (PP4). This variant is absent from gnomAD v2.1.1 and v3.1.2 (PM2_Supporting). In summary, this variant meets the criteria to be classified as 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 1.0.0; 01/09/2025): PVS1, PM3, PP4, PM2_Supporting.

Met criteria codes

PP4			At least one patient with this variant was clinically suspected to have limb girdle muscular dystrophy or showed progressive limb girdle muscle weakness (PP4).
PM2			This variant is absent from gnomAD v2.1.1 and v3.1.2 (PM2_Supporting).
PM3			This variant has been detected in at least three individuals with features of calpainopathy (PMID: 16607617, 18055493, SCV000953543.3), including confirmed in trans with a pathogenic variant (c.1079G>A p.(Trp360Ter), 1.0 pt, SCV000953543.3) (PM3).
PVS1			The NM_000070.3: c.1838del p.(Lys613ArgfsTer49) variant in CAPN3 is a frameshift variant predicted to cause a premature stop codon in biologically relevant exon 17/24 leading to nonsense mediated decay in a gene in which loss of function is an established disease mechanism (PVS1).

Curation History



 ▾

 ▾

Showing 1 to 1 of 1 rows

--

