

Variant: NM_000218.3(KCNQ1):c.1343C>A (p.Pro448Gln)

Version: 1.0

CA028774 [↗](#)

219923 (ClinVar) [↗](#)

Gene: KCNQ1 (HGNC:3784)

Condition: long QT syndrome 1 (MONDO:0100316)

Inheritance Mode: Autosomal dominant inheritance

UID: 9b0f0c0e-b44d-44a8-853d-9d14a712aaff

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HGVS expressions

NM_000218.3:c.1343C>A

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NC_000011.10:g.2588804C>A

CM000673.2:g.2588804C>A

NC_000011.9:g.2610034C>A

CM000673.1:g.2610034C>A

NC_000011.8:g.2566610C>A

NG_008935.1:g.148814C>A

ENST00000496887.7:c.986C>A

ENST00000646564.2:c.803C>A

ENST00000155840.12:c.1343C>A

ENST00000335475.6:c.962C>A

ENST00000646564.1:c.449C>A

ENST00000155840.9:c.1343C>A

ENST00000335475.5:c.962C>A

NM_000218.2:c.1343C>A

NM_181798.1:c.962C>A

Uncertain Significance

Not Met criteria codes **6**

PP3 PM1 PM2 BA1 BS1

BP4

Evidence Links **0**

Expert Panel

Potassium Channel Arrhythmia VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** ClinGen Potassium Channel Arrhythmia Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for KCNQ1 Version 1.0.0

[↗](#) **Criteria Specification Approval History**












[↗](#) **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Potassium Channel Arrhythmia VCEP

NM_000218.3(KCNQ1):c.1343C>A is a missense variant predicted to cause substitution of proline by glutamine at amino acid 448 (p.Pro448Gln). To our knowledge, this variant has not been reported in the literature in any individuals with long QT syndrome 1. This variant is present in gnomAD v.4.1.0 at a maximum allele frequency of 0.0001538, with 14 alleles / 91008 total alleles in the South Asian population, which is higher than the ClinGen Potassium Channel Arrhythmia VCEP PM2_Supporting threshold of <0.00001, but lower than the BS1 threshold of >0.0004, so neither criterion is met. To our knowledge, functional assays have not been reported for this variant. The computational predictor REVEL gives a score of 0.512, which is below the ClinGen Potassium Channel Arrhythmia VCEP PP3 threshold of >0.75 but higher than the BP4 threshold of <0.25 and does not strongly predict a damaging effect on KCNQ1 function. The computational splicing predictor SpliceAI gives a score of 0.00 for donor and acceptor gain and loss, which is lower than the ClinGen Potassium Channel Arrhythmia VCEP PP3 threshold of greater than or equal to 0.2 and does not strongly predict a damaging effect on KCNQ1 splicing. In summary, this variant meets the criteria to be classified as a variant of uncertain significance due to insufficient evidence for long QT syndrome 1 based on the ACMG/AMP criteria applied, as specified by the ClinGen Potassium Channel Arrhythmia VCEP. (VCEP specifications version 1.0.0; date of approval 03/04/2025).

Not Met criteria codes

PP3	 	The computational predictor REVEL gives a score of 0.512, which is below the ClinGen Potassium Channel Arrhythmia VCEP PP3 threshold of >0.75 but higher than the BP4 threshold of <0.25 and does not strongly predict a damaging effect on KCNQ1 function. The computational splicing predictor SpliceAI gives a score of 0.00 for donor and acceptor gain and loss, which is lower than the ClinGen Potassium Channel Arrhythmia VCEP PP3 threshold of >0.5 and does not strongly predict a damaging effect on KCNQ1 splicing.
PM1	 	This variant is not a missense substitution within the pore helix consisting of amino acids 300 to 320, which is a well-characterized functional domain required for the channel function and selectivity filter of KCNQ1 (PMID: 15649981), and has been confirmed to show an absence of likely benign or benign variants listed in gnomAD.
PM2		This variant is present in gnomAD v.4.1.0 at a maximum allele frequency of 0.0001538, with 14 alleles / 91008 total alleles in the South Asian population, which is higher than the ClinGen Potassium Channel Arrhythmia VCEP PM2_Supporting threshold of <0.00001, but lower than the BS1 threshold of >0.0004, so neither criterion is met.
BA1	 	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS1	 	This variant is present in gnomAD v.4.0.0 at a maximum allele frequency of 0.0001538, with 14 alleles / 91008 total alleles in the South Asian population, which is higher than the ClinGen Potassium Channel Arrhythmia VCEP PM2_Supporting threshold of <0.00001, but lower than the BS1 threshold of >0.0004, so neither criterion is met.
BP4	 	The computational predictor REVEL gives a score of 0.512, which is below the ClinGen Potassium Channel Arrhythmia VCEP PP3 threshold of >0.75 but higher than the BP4 threshold of <0.25 and does not strongly predict a damaging effect on KCNQ1 function.

Curation History [↗](#)



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