

Variant: NM_000527.5(LDLR):c.731C>G (p.Ser244Cys)

Version: 1.0

CA404079636 [↗](#)

440599 (ClinVar) [↗](#)

Gene: LDLR ([HGNC:3949](#))

Condition: hypercholesterolemia, familial ([MONDO:0007750](#))

Inheritance Mode: Semidominant inheritance

UUID: 149c63e3-72b2-4878-86c5-64c191f9c0e1

Approved on: 2023/4/28

Published on: 2023/4/30

HGVS expressions

NM_000527.5(LDLR):c.731C>G (p.Ser244Cys)

NM_000527.5:c.731C>G

NC_000019.10:g.11106601C>G

CM000681.2:g.11106601C>G

NC_000019.9:g.11217277C>G

CM000681.1:g.11217277C>G

NC_000019.8:g.11078277C>G

NG_009060.1:g.22221C>G

ENST00000252444.10:c.989C>G

ENST00000559340.2:c.731C>G

ENST00000560467.2:c.731C>G

ENST00000558518.6:c.731C>G

ENST00000252444.9:c.985C>G

ENST00000455727.6:c.314-791C>G

ENST00000535915.5:c.608C>G

ENST00000545707.5:c.350C>G

ENST00000557933.5:c.731C>G

ENST00000558013.5:c.731C>G

ENST00000558518.5:c.731C>G

ENST00000558528.1:n.246C>G

ENST00000560467.1:c.331C>G

NM_000527.4:c.731C>G

NM_001195798.1:c.731C>G

NM_001195799.1:c.608C>G

NM_001195800.1:c.314-791C>G

NM_001195803.1:c.350C>G

NM_001195798.2:c.731C>G

NM_001195799.2:c.608C>G

NM_001195800.2:c.314-791C>G

NM_001195803.2:c.350C>G

Uncertain Significance

Met criteria codes1

PM2

Not Met criteria codes20

PS1PS2PS3PS4BP7BP4

BP2PP1PP3PP4PM1

PM3PM4BA1PM6BS1

BS4BS3BS2PVS1

Evidence Links0

Expert Panel

Familial Hypercholesterolemia VCEP

Criteria Specification Information

Criteria Specification: ClinGen Familial Hypercholesterolemia Expert Panel Specifications to the ACMG/AMP Variant Classification Guidelines Version 1.2

PDF

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Familial Hypercholesterolemia VCEP			
The NM_000527.5(LDLR):c.731C>G (p.Ser244Cys) variant is classified as Uncertain significance - insufficient evidence for Familial Hypercholesterolemia by applying evidence code PM2 as defined by the ClinGen Familial Hypercholesterolemia Expert Panel LDLR-specific variant curation guidelines (https://doi.org/10.1016/j.gim.2021.09.012). The supporting evidence is as follows: PM2: No exome data available for this variant in gnomAD v2.1.1. Genome and exome data were available for the neighboring variant, 19-11217264-G-A(GRCh37). The c.731C>G (p.Ser244Cys) variant was present in 1/15432 European (non-Finnish) genomes. The 19-11217264-G-A(GRCh37) variant was tested in 113760 alles from European (non-Finnish) exomes. Final adjusted allele frequency: 1/(15432+ 113760) = 0.0007740417%.			
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PM2			No exome data available for this variant in gnomAD v2.1.1. Genome and exome data were available for the neighboring variant, 19-11217264-G-A(GRCh37). The c.731C>G (p.Ser244Cys) variant was present in 1/15432 European (non-Finnish) genomes. The 19-11217264-G-A(GRCh37) variant was tested in 113760 alleles from European (non-Finnish) exomes. Final adjusted allele frequency: 1/(15432+ 113760) = 0.0007740417%.
Not Met criteria codes			
PS1			Not met.
PS2			Not met.
PS3			Not met.
PS4			Not met.
BP7			Not met.
BP4			Not met.

BP2			Not met.
PP1			Not met.
PP3			Not met.
PP4			Not met.
PM1			Not met.
PM3			Not met.
PM4			Not met.
BA1			Not met.
PM6			Not met.
BS1			Not met.
BS4			Not met.
BS3			Not met.
BS2			Not met.
PVS1			Not met.

Curation History 		
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