

Variant: *NM_004360.5(CDH1):c.512T>G (p.Phe171Cys)*

Version: 2.0

CA8129871 [↗](#)

423041 (ClinVar) [↗](#)

Gene: CDH1 ([HGNC:999](#))

Condition: CDH1-related diffuse gastric and lobular breast cancer ([MONDO:0100488](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: 3a340a0d-25b6-41ce-96e4-0b17f8aad1f6

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HGVS expressions

NM_004360.5:c.512T>G

NM_004360.5(CDH1):c.512T>G (p.Phe171Cys)

NC_000016.10:g.68808548T>G

CM000678.2:g.68808548T>G

NC_000016.9:g.68842451T>G

CM000678.1:g.68842451T>G

NC_000016.8:g.67399952T>G

NG_008021.1:g.76257T>G

ENST00000261769.10:c.512T>G

ENST00000261769.9:c.512T>G

ENST00000422392.6:c.512T>G

ENST00000561751.1:c.279T>G

ENST00000562836.5:n.583T>G

ENST00000564676.5:n.794T>G

ENST00000564745.1:n.507T>G

ENST00000566510.5:c.512T>G

ENST00000566612.5:c.512T>G

ENST00000567320.1:n.22T>G

ENST00000611625.4:c.512T>G

ENST00000612417.4:c.512T>G

ENST00000621016.4:c.512T>G

NM_004360.3:c.512T>G

NM_001317184.1:c.512T>G

NM_001317185.1:c.-1104T>G

NM_001317186.1:c.-1308T>G

NM_004360.4:c.512T>G

NM_001317184.2:c.512T>G

NM_001317185.2:c.-1104T>G

NM_001317186.2:c.-1308T>G

Uncertain Significance

Met criteria codes **2**

PM2_Supporting

BS2_Supporting

Not Met criteria codes **24**

Expert Panel

CDH1 VCEP [↗](#)

Criteria Specification Information

BA1BP4BP3BP1BP2BP5BP7BS1BS4BS3PP1PP2PP3PP4PS1PS2PS3PS4PM6PM1PM3PM5PM4PVS1

[Criteria Specification: ClinGen CDH1 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines Version 3.1](#)[Criteria Specification Approval History](#)[Criteria Specifications for this VCEP](#)

Evidence Links 0

Evidence submitted by expert panel

CDH1 VCEP

The c.512T>G (p.Phe171Cys) variant has an allele frequency: 1:251320 (<one out 100.000 alleles) in the gnomAD cohort (PM2_Supporting; http://https://gnomad.broadinstitute.org/). It has been observed in 4 probands w/o DGS, SRC tumor or LBC and whose families do not suggest HDGC (BS2_Supporting; SCV000572669.4, SCV000637836.3). In summary, this variant meets criteria to be classified as VUS based on the ACMG/AMP criteria applied as specified by the CDH1 Variant Curation Expert Panel (Variant Interpretation Guidelines Version 3.1): PM2_Supporting, BS2_Supporting.

Met criteria codes

PM2_Supporting		✓	allele frequency: 1:251320 (<one out 100.000 alleles in gnomAD)
BS2_Supporting		✓	Observed in 4 probands w/o DGS, SRC tumor or LBC and whose families do not suggest HDGC. SCV000637836.3: Proband #1: unaffected male at 40s. Proband #2: female with diffuse gastric cancer at 60s. Proband #3: female with breast cancer (IDC, ER-PR-HER2+) at 50s. Proband #4: female with metastatic diffuse gastric cancer at 40s. Proband #5: female with breast cancer (IDC) at 50s (carries RAD50 pathogenic variant). SCV000572669.4: Proband#1: unaffected male in his 60s

Not Met criteria codes

BA1		✗	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP4		✗	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP3		✗	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP1		✗	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP2		✗	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

BP5			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BP7			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS3			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS4			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM6			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM1			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

PM3		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM5		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM4		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PVS1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

Curation History 		
Showing 1 to 2 of 2 rows		

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