

Variant: *NM_004360.5(CDH1):c.2329G>A (p.Asp777Asn)*

Version: 2.0

[CA157963](#)

[127922 \(ClinVar\)](#)

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

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

Inheritance Mode: Autosomal dominant inheritance

UUID: a72a576c-4686-471f-808d-5e7d66cf6f15

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HGVS expressions

NM_004360.5:c.2329G>A

NM_004360.5(CDH1):c.2329G>A (p.Asp777Asn)

NC_000016.10:g.68829687G>A

CM000678.2:g.68829687G>A

NC_000016.9:g.68863590G>A

CM000678.1:g.68863590G>A

NC_000016.8:g.67421091G>A

NG_008021.1:g.97396G>A

ENST00000261769.10:c.2329G>A

ENST00000261769.9:c.2329G>A

ENST00000422392.6:c.2146G>A

ENST00000562118.1:n.547G>A

ENST00000562836.5:n.2400G>A

ENST00000566510.5:c.*995G>A

ENST00000566612.5:c.*569G>A

ENST00000611625.4:c.2392G>A

ENST00000612417.4:c.1853+3133G>A

ENST00000621016.4:c.1866-4516G>A

NM_004360.3:c.2329G>A

NM_001317184.1:c.2146G>A

NM_001317185.1:c.781G>A

NM_001317186.1:c.364G>A

NM_004360.4:c.2329G>A

NM_001317184.2:c.2146G>A

NM_001317185.2:c.781G>A

NM_001317186.2:c.364G>A

Likely Benign

Met criteria codes **1**

BS2

Not Met criteria codes **25**

BS1 BS4 BS3 BP4 BP3 BP1
BP2 BP5 BP7 BA1 PS1 PS2
PS3 PS4 PP1 PP2 PP3 PP4

Expert Panel

Criteria Specification Information

Criteria Specification: *ClinGen CDH1 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines Version 3.1*



Criteria Specification Approval History

Evidence submitted by expert panel

CDH1 VCEP



The c.2329G>A (p.Asp777Asn) missense variant has a frequency of 0.0001202 (34 of 282,830) in the gnomAD v2.1.1 cohort, with a maximum non-founder allele frequency of 0.0002400 (31 of 129,162) in the non-Finnish European subpopulation (<http://gnomad.broadinstitute.org>). This variant has been observed in >100 individuals without DGC, SRC tumours or LBC and whose families do not suggest HDGC (BS2; SCV000149760.14, SCV000261509.8, PMIDs: 29522266, 26534844, 26976419, 25142776, 24728327). In summary, the clinical significance of this variant is classified as Likely Benign based the ACMG/AMP criteria applied, as specified by the CDH1 Variant Curation Expert Panel (Variant Interpretation Guidelines Version 3.1): BS2.



Met criteria codes



BS2	 	Variant has been observed in >100 individuals without DGC, SRC tumours or LBC and whose families do not suggest HDGC (SCV000149760.14, SCV000261509.8, PMIDs: 29522266, 26534844, 26976419, 25142776, 24728327).
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Not Met criteria codes


BS1	 	Variant present in 34 of 282,830 alleles in gnomAD (0.0001202). Highest subpopulation is non-Finnish European with 31 of 129,162 alleles (0.0002400)
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BS4	 	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
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BS3	 	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
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BP4	 	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
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BP3		No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
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BP1		No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
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BP2	 	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
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BP5		
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			Ambry ClinVar submission (Accession: SCV000186559.5) states co-occurrence with a mutation in another gene that clearly explains a proband's phenotype. However, currently the only gene can apply BP5 is CTNNA1.
BP7			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BA1			Variant present in 34 of 282,830 alleles in gnomAD (0.0001202). Highest subpopulation is non-Finnish European with 31 of 129,162 alleles (0.0002400)
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
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
PM6			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM2			Variant present in 34 of 282,830 alleles in gnomAD (0.0001202). Highest subpopulation is non-Finnish European with 31 of 129,162 alleles (0.0002400)
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 [↗](#)

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