

Variant: *NM_000249.4(MLH1):c.2041G>C (p.Ala681Pro)*

Version: 1.0

[CA10578272](#) 

[233523 \(ClinVar\)](#) 

Gene: MLH1 ([HGNC:4292](#))

Condition: Lynch syndrome 1 ([MONDO:0007356](#))

Inheritance Mode: Autosomal dominant inheritance

UID: df18e6c7-94e5-47d6-96b7-87325d098b9d

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HGVS expressions

NM_000249.4:c.2041G>C

NM_000249.4(MLH1):c.2041G>C (p.Ala681Pro)

NC_000003.12:g.37048955G>C

CM000665.2:g.37048955G>C

NC_000003.11:g.37090446G>C

CM000665.1:g.37090446G>C

NC_000003.10:g.37065450G>C

NG_007109.2:g.60606G>C

ENST00000413740.2:c.1668-1531G>C

ENST00000429117.6:c.1747G>C

ENST00000450420.6:c.1559-1531G>C

ENST00000456676.7:c.1896+1272G>C

ENST00000492474.6:c.1318G>C

ENST00000616768.6:c.1948G>C

ENST00000673673.2:c.1876G>C

ENST00000231790.8:c.2041G>C

ENST00000413212.2:c.*959G>C

ENST00000432299.6:c.*1873G>C

ENST00000447829.6:c.*1152G>C

ENST00000539477.6:c.1318G>C

ENST00000616768.5:c.985G>C

ENST00000673673.1:c.1829G>C

ENST00000673741.1:n.1075G>C

ENST00000673889.1:n.1423G>C

ENST00000673897.1:c.*1833G>C

ENST00000673899.1:c.1309G>C

ENST00000673947.1:c.*2181G>C

ENST00000673972.1:c.*1919G>C

ENST00000674019.1:c.1318G>C

ENST00000674111.1:c.*270G>C

ENST00000674125.1:n.752G>C

ENST00000231790.6:c.2041G>C

ENST00000413740.1:c.291-1531G>C

ENST00000435176.5:c.1747G>C

ENST00000450420.5:c.182-1531G>C

ENST00000455445.6:c.1318G>C

ENST00000456676.6:c.1871+1272G>C

ENST00000458205.6:c.1318G>C
ENST00000536378.5:c.1318G>C
ENST00000539477.5:c.1318G>C
NM_000249.3:c.2041G>C
NM_001167617.1:c.1747G>C
NM_001167618.1:c.1318G>C
NM_001167619.1:c.1318G>C
NM_001258271.1:c.1896+1272G>C
NM_001258273.1:c.1318G>C
NM_001258274.1:c.1318G>C
NM_001167617.2:c.1747G>C
NM_001167618.2:c.1318G>C
NM_001167619.2:c.1318G>C
NM_001258274.2:c.1318G>C
NM_001354615.1:c.1318G>C
NM_001354616.1:c.1318G>C
NM_001354617.1:c.1318G>C
NM_001354618.1:c.1318G>C
NM_001354619.1:c.1318G>C
NM_001354620.1:c.1747G>C
NM_001354621.1:c.1018G>C
NM_001354622.1:c.1018G>C
NM_001354623.1:c.1018G>C
NM_001354624.1:c.967G>C
NM_001354625.1:c.967G>C
NM_001354626.1:c.967G>C
NM_001354627.1:c.967G>C
NM_001354628.1:c.1948G>C
NM_001354629.1:c.1942G>C
NM_001354630.1:c.1876G>C
NM_001167617.3:c.1747G>C
NM_001167618.3:c.1318G>C
NM_001167619.3:c.1318G>C
NM_001258271.2:c.1896+1272G>C
NM_001258273.2:c.1318G>C
NM_001258274.3:c.1318G>C
NM_001354615.2:c.1318G>C
NM_001354616.2:c.1318G>C
NM_001354617.2:c.1318G>C
NM_001354618.2:c.1318G>C
NM_001354619.2:c.1318G>C
NM_001354620.2:c.1747G>C
NM_001354621.2:c.1018G>C
NM_001354622.2:c.1018G>C
NM_001354623.2:c.1018G>C
NM_001354624.2:c.967G>C
NM_001354625.2:c.967G>C
NM_001354626.2:c.967G>C
NM_001354627.2:c.967G>C
NM_001354628.2:c.1948G>C
NM_001354629.2:c.1942G>C
NM_001354630.2:c.1876G>C

Uncertain Significance

Met criteria codes **2**

PM2_Supporting PP4

Not Met criteria codes **2**

PP1 PM5

Evidence Links **0**

Expert Panel

[InSiGHT Hereditary Colorectal Cancer/Polyposis VCEP](#)

Criteria Specification Information

[Criteria Specification:](#) *ClinGen InSiGHT Hereditary Colorectal Cancer/Polyposis Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for MLH1 Version 1.0.0*

[Criteria Specification Approval History](#)


[Criteria Specifications for this VCEP](#)



Evidence submitted by expert panel

InSiGHT Hereditary Colorectal Cancer/Polyposis VCEP

The NM_000249.4: c.2041G>C variant in MLH1 is a missense variant predicted to cause substitution of Alanin by Prolin at amino acid 681 (p.Ala681Pro). The variant is not reported in gnomAD (PM2_supporting). The variant was detected in one CRC/Endometrial MSI-H tumour using a standard panel of 5-10 markers and/or loss of MMR protein expression consistent with the variant location (PP4). In summary, this variant meets the criteria to be classified as a variant of uncertain significance (VUS) for Lynch-Syndrome based on the ACMG/AMP criteria applied, as specified by the ClinGen InSiGHT Hereditary Colorectal Cancer/ Polyposis VCEP: PM2_SUP, PP4 (VCEP specifications version 1)



Met criteria codes

PM2_Supporting   The variant is not reported in gnomAD v4.1 (PM2_supporting)

PP4   1 CRC/Endometrial MSI-H tumours using a standard panel of 5-10 markers and/or loss of MMR protein expression consistent with the variant location (PP4)

Not Met criteria codes

PP1   Total segregation odds 2.03, threshold for PP1 is >2.08

PM5   Missense change at an amino acid residue where a different missense change was classified by this VCEP as Pathogenic on the protein level and not due to aberrant splicing; variant p.Ala681Thr is InSiGHT class 5, but PP3_SUP does not apply, therefore PM5 not met

[Curation History](#)



Showing 1 to 1 of 1 rows

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