

## Product datasheet for **RC401648**

### MLH1 (NM\_000249) Human Mutant ORF Clone

#### Product data:

Product Type:	Mutant ORF Clones
Product Name:	MLH1 (NM_000249) Human Mutant ORF Clone
Mutation Description:	K618X
Affected Codon#:	618
Affected NT#:	1852
Nucleotide Mutation:	MLH1 Mutant (K618X), Myc-DDK-tagged ORF clone of Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1), transcript variant 1 as transfection-ready DNA
Effect:	Colorectal cancer, non-polyposis
Symbol:	MLH1
Synonyms:	COCA2; FCC2; hMLH1; HNPCC; HNPCC2; MMRCS1
E. coli Selection:	Kanamycin (25 ug/mL)
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
Tag:	Myc-DDK
ACCN:	NM_000249
ORF Size:	1851 bp
Restriction Sites:	Sgfi-MluI



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**ORF Nucleotide Sequence:**

>RC401648 representing NM\_000249  
 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
 GCC**CGGATCGCC**

ATGTCGTTCTGTCGAGGGGTTATTCGGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGCGGGGGAAG  
 TTATCCAGCGGCCAGCTAATGCTATCAAAGAGATGATTGAGAAGTGTAGATGCAAAATCCACAAGTAT  
 TCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTCAGATCCAAGACAATGGCACCGGATCAGGAAA  
 GAAGATCTGGATATTGTATGTGAAAGGTTCACTACTAGTAAACTGCAGTCCTTTGAGGATTTAGCCAGTA  
 TTTCTACCTATGGCTTTGAGGTGAGGCTTTGGCCAGCATAAGCCATGTGGCTCATGTTACTATTACAAC  
 GAAAACAGCTGATGAAAGTGTGCATACAGAGCAAGTACTCAGATGGAAAAGTAAAGCCCTCTCTAAA  
 CCATGTGCTGGCAATCAAGGGACCCAGATCACGGTGGAGGACCTTTTTTACAACATAGCCACGAGGAGAA  
 AAGCTTTAAAAATCCAAGTGAAGAATATGGGAAAATTTGGAAGTTGTTGGCAGGTATTCAGTACACAA  
 TGCAGGCATTAGTTTCTCAGTTAAAAACAAGGAGAGACAGTAGCTGATGTTAGGACACTACCCAATGCC  
 TCAACCGTGGACAATATTCGCTCCATCTTTGAAAATGCTGTTAGTCGAGAAGTATAGAAATGGATGTG  
 AGGATAAAACCTAGCCTTCAAATGAATGGTTACATATCCAATGCAAACACTCAGTGAAGAAGTGCAT  
 CTTCTTACTCTTCATCAACCATCGTCTGGTAGAATCAACTTCTTGAGAAAAGCCATAGAAAACAGTGTAT  
 GCAGCCTATTTGCCAAAAACACACACCATTCTGTACCTCAGTTTAGAAAATCAGTCCCCAGAATGTGG  
 ATGTTAATGTGCACCCCAAAAGCATGAAGTTCACCTCCTGCACGAGGAGAGCATCCTGGAGCGGGTGCA  
 GCAGCACATCGAGAGCAAGCTCCTGGGCTCCAATTCCTCCAGGATGACTTACCCAGACTTTGCTACCA  
 GGACTTGCTGGCCCTCTGGGGAGATGGTTAAATCCACAACAAGTCTGACCTCGTCTTCTACTTCTGGAA  
 GTAGTGATAAGGTCTATGCCACCAGATGGTTCGTACAGATTTCCGGGAACAGAAGCTGATGCATTTCT  
 GCAGCCTCTGAGCAAACCCCTGTCCAGTCAGCCCAAGGCCATTGTCACAGAGGATAAGACAGATATTTCT  
 AGTGGCAGGGCTAGGCAGCAAGATGAGGAGATGCTTGAACCTCCAGCCCTGCTGAAGTGCTGCCAAAA  
 ATCAGAGCTTGGAGGGGGATACAACAAAGGGGACTTCAGAAAATGTGAGAGAAGAGAGGACCTACTCCAG  
 CAACCCAGAAAAGAGACATCGGGAAGATTCTGATGTGGAATGGTGAAGATGATTTCCGAAAAGGAAATG  
 ACTGCAGCTTGTACCCCGGAGAAGGATCATTAACTCACTAGTGTGTTGAGTCTCCAGGAAGAAATTA  
 ATGAGCAGGGACATGAGGTTCTCGGGAGATGTTGCATAACCCTCCTCGTGGGCTGTGTGAATCCTCA  
 GTGGCCCTTGGCACAGCATCAAACCAAGTTATACCTTCTCAACACCACCAAGCTTAGTGAAGAACTGTT  
 TACCAGATACTATTTATGATTTTGCAATTTTGGTGTCTCAGGTTATCGGAGCCAGCACCGCTCTTTG  
 ACCTTGCCATGCTTGCTTAGATAGTCCAGAGAGTGGCTGGACAGAGGAAGATGGTCCCAAGAAGGACT  
 TGCTGAATACATTGTTGAGTTTCTGAAGAAG

AG**CGGACCG**ACGCGTACGCGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC  
 TGGATTACAAGGATGACGACGA TAAGGTTTAA

**Protein Sequence:**

>RC401648 representing NM\_000249  
 Red=Cloning site Green=Tags(s)

MSFVAGVIRRLDETIVNRIAAGEVIQRPANAIAKEMIENCLDAKSTSIQVIVKEGGLKLIQIQDNGTGIRK  
 EDLDIVCERFTTSKLSQFEDLASISTYGRGEALASISHVAHVITTTKTADGKCAYRASYS DGKLPKPPK  
 PCAGNQGTQITVEDLFYNIATRRKALKNPSEYKILEVVGRYSVHNAGISFSVKKQGETVADVRLPNA  
 STVDNIRSI FGNAVSRELI EIGCEDKTLAFKMNGYISNANYSVKKCIFLLFINHRLVESTSLRKAIVTVY  
 AAYLPKNTHPFLYL SLEISPQNV DVNVHPTKHEVHFLHEESILERVQQHIESKLLGNSSSRMFYQTLLP  
 GLAGPSGEMVKSTTSLTSSSTSGSSDKVYAHQMVRTDSREQKLD AFLQPLSKPLSSQPQAI VTEDEKTDIS  
 SGRARQQDEEMLELPAPAEVAAKNQSLEGDTTKGTSEMSEKRGPTSSNPRKRHRESDVEMVEDDSRKEM  
 TAACTPRRRIINLTSVLSLQEEINEQGHEVLRMLHNHSFVGCVPQWALAQHQTKLYLLNNTKLSEELF  
 YQILIIYDFANFGVLR LSEPAPLFDLAMLALDSPESGWTEEDGPKLEAEYIVEFLKK

SGP**TRRRLEQKLI**SEEDLAANDILDYKDDDDKV



<b>Cytogenetics:</b>	3p22.2
<b>Domains:</b>	DNA_mis_repair, HATPase_c
<b>Protein Families:</b>	Druggable Genome
<b>Protein Pathways:</b>	Colorectal cancer, Endometrial cancer, Mismatch repair, Pathways in cancer
<b>MW:</b>	67.9 kDa
<b>Gene Summary:</b>	<p>The protein encoded by this gene can heterodimerize with mismatch repair endonuclease PMS2 to form MutL alpha, part of the DNA mismatch repair system. When MutL alpha is bound by MutS beta and some accessory proteins, the PMS2 subunit of MutL alpha introduces a single-strand break near DNA mismatches, providing an entry point for exonuclease degradation. The encoded protein is also involved in DNA damage signaling and can heterodimerize with DNA mismatch repair protein MLH3 to form MutL gamma, which is involved in meiosis. This gene was identified as a locus frequently mutated in hereditary nonpolyposis colon cancer (HNPCC). [provided by RefSeq, Aug 2017]</p>