

Product datasheet for SC203467

MSH2 (NM 000251) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: MSH2 (NM_000251) Human 3' UTR Clone

Vector: pMirTarget (PS100062)

Symbol: MSH2

Synonyms: COCA1; FCC1; hMSH2; HNPCC; HNPCC1; LCFS2; MMRCS2

ACCN: NM 000251

Insert Size: 304 bp

>SC203467 3'UTR clone of NM_000251 **Insert Sequence:**

The sequence shown below is from the reference sequence of NM_000251. The complete

sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

ATCATTTCACGAATAAAAGTTACTACGTGAAAAAATCCCAGTAATGGAATGAAGGTAATATTGATAAGCT ATTGTCTGTAATAGTTTTATATTGTTTTATATTAACCCTTTTTCCATAGTGTTAACTGTCAGTGCCCAT GGGCTATCAACTTAATAAGATATTTAGTAATATTTTACTTTGAGGACATTTTCAAAGATTTTTATTTTG AAAAATGAGAGCTGTAACTGAGGACTGTTTGCAATTGACATAGGCAATAATAAGTGATGTGCTGAATTT TATAAATAAAATCATGTAGTTTGTGGAA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul

OTI Disclaimer: Our molecular clone sequence data has been matched to the sequence identifier above as a

point of reference. Note that the complete sequence of this clone is largely the same as the

reference sequence but may contain minor differences, e.g., single nucleotide

polymorphisms (SNPs).

Components: The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The

package also includes 100 pmols of both the corresponding 5' and 3' vector primers in

separate vials.

NM 000251.3 RefSeq:



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MSH2 (NM_000251) Human 3' UTR Clone - SC203467

Summary: This locus is frequently mutated in hereditary nonpolyposis colon cancer (HNPCC). When

cloned, it was discovered to be a human homolog of the E. coli mismatch repair gene mutS, consistent with the characteristic alterations in microsatellite sequences (RER+ phenotype) found in HNPCC. Two transcript variants encoding different isoforms have been found for this

gene. [provided by RefSeq, Apr 2012]

Locus ID: 4436

MW: 11.5