

Product datasheet for SC200338

OriGene Technologies, Inc.

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MYH (MUTYH) (NM 001048172) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: MYH (MUTYH) (NM 001048172) Human 3' UTR Clone

Symbol: MYH
Synonyms: MYH

Mammalian Cell Neomycin

Selection:

Vector:

pMirTarget (PS100062)

ACCN: NM 001048172

Insert Size: 94 bp

Insert Sequence: >SC200338 3'UTR clone of NM_001048172

The sequence shown below is from the reference sequence of NM_001048172. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

GCACACAGCCTCAACAGTGCAGCCCAGTGACACCTCTGAAAGCCCCCATTCCCTGAGAATCCTGTTGTT

AGTAAAGTGCTTATTTTTGTAGTTA

ACGCGTAAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

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.

RefSeq: <u>NM 001048172.2</u>





MYH (MUTYH) (NM_001048172) Human 3' UTR Clone - SC200338

Summary: This gene encodes a DNA glycosylase involved in oxidative DNA damage repair. The enzyme

excises adenine bases from the DNA backbone at sites where adenine is inappropriately paired with guanine, cytosine, or 8-oxo-7,8-dihydroguanine, a major oxidatively damaged DNA lesion. The protein is localized to the nucleus and mitochondria. This gene product is thought to play a role in signaling apoptosis by the introduction of single-strand breaks following oxidative damage. Mutations in this gene result in heritable predisposition to colorectal cancer, termed MUTYH-associated polyposis (MAP). Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Apr 2017]

Locus ID: 4595

MW: 3.4