

Product datasheet for SC205339

MUS81 (NM 025128) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: MUS81 (NM 025128) Human 3' UTR Clone

Vector: pMirTarget (PS100062)

Symbol: MUS81
Synonyms: SLX3

ACCN: NM 025128

Insert Size: 417 bp

Insert Sequence: >SC205339 3'UTR clone of NM_025128

The sequence shown below is from the reference sequence of NM_025128. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

CCA

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 025128.5</u>



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ORIGENE

Summary:

This gene encodes a structure-specific endonuclease which belongs to the XPF/MUS81 endonuclease family and plays a critical role in the resolution of recombination intermediates during DNA repair after inter-strand cross-links, replication fork collapse, and DNA double-strand breaks. The encoded protein associates with one of two closely related essential meiotic endonuclease proteins (EME1 or EME2) to form a complex that processes DNA secondary structures. It contains an N-terminal DEAH helicase domain, an excision repair cross complementation group 4 (ERCC4) endonuclease domain, and two tandem C-terminal helix-hairpin-helix domains. Mice with a homozygous knockout of the orthologous gene have significant meiotic defects including the failure to repair a subset of DNA double strand breaks. [provided by RefSeq, Jun 2017]

Locus ID: 80198 **MW:** 15.5