

Product datasheet for SC207173

MAL (NM 022440) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: MAL (NM_022440) Human 3' UTR Clone

Symbol: MAL

Synonyms: MVP17; VIP17

Mammalian Cell

Selection:

Neomycin

Vector: pMirTarget (PS100062)

ACCN: NM_022440

Insert Size: 567 bp

Insert Sequence: >SC207173 3'UTR clone of NM_022440

The sequence shown below is from the reference sequence of NM_022440. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

TGTCTTAATGTTCAA

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).



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MAL (NM_022440) Human 3' UTR Clone - SC207173

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 022440.3</u>

Summary: The protein encoded by this gene is a highly hydrophobic integral membrane protein

belonging to the MAL family of proteolipids. The protein has been localized to the

endoplasmic reticulum of T-cells and is a candidate linker protein in T-cell signal transduction. In addition, this proteolipid is localized in compact myelin of cells in the nervous system and has been implicated in myelin biogenesis and/or function. The protein plays a role in the formation, stabilization and maintenance of glycosphingolipid-enriched membrane

microdomains. Down-regulation of this gene has been associated with a variety of human epithelial malignancies. Alternative splicing produces four transcript variants which vary from each other by the presence or absence of alternatively spliced exons 2 and 3. [provided by

RefSeq, May 2012]

Locus ID: 4118

MW: 21.1