

Product datasheet for SC208990

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S1P (MBTPS1) (NM_003791) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: S1P (MBTPS1) (NM_003791) Human 3' UTR Clone

Symbol: S1P

Synonyms: PCSK8; S1P; SEDKF; SKI-1

Mammalian Cell

Selection:

Neomycin

Vector: pMirTarget (PS100062)

ACCN: NM_003791

Insert Size: 716 bp

Insert Sequence: >SC208990 3'UTR clone of NM_003791

The sequence shown below is from the reference sequence of NM_003791. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

 ${\sf TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC}$

TATGTATTACCCGTCTGAAGCTTAAA

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).



OriGene Technologies, Inc. 9620 Medical Center Drive, Ste 200

CN: techsupport@origene.cn

Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com



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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 003791.4</u>

Summary: This gene encodes a member of the subtilisin-like proprotein convertase family, which

includes proteases that process protein and peptide precursors trafficking through regulated or constitutive branches of the secretory pathway. The encoded protein undergoes an initial autocatalytic processing event in the ER to generate a heterodimer which exits the ER and sorts to the cis/medial-Golgi where a second autocatalytic event takes place and the catalytic activity is acquired. It encodes a type 1 membrane bound protease which is ubiquitously expressed and regulates cholesterol or lipid homeostasis via cleavage of substrates at non-basic residues. Mutations in this gene may be associated with lysosomal dysfunction.

[provided by RefSeq, Feb 2014]

Locus ID: 8720

MW: 27.1