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Product datasheet for SC200733

TMS1 (PYCARD) (NM_013258) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	TMS1 (PYCARD) (NM_013258) Human 3' UTR Clone
Symbol:	TMS1
Synonyms:	ASC; CARD5; TMS; TMS-1; TMS1
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_013258
Insert Size:	129 bp
Insert Sequence:	>SC200733 3'UTR clone of NM_013258 The sequence shown below is from the reference sequence of NM_013258. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC TACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCCAGCAACACTCCGGTCAGCCCCTGGCAAT CCCACCAAATCATCCTGAATCTGATCTTTTTATACACAATATACGAAAAGCCAGCTTGAA ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG
Restriction Sites:	SgfI-MluI
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:	NM_013258.5

View online »

Summary: This gene encodes an adaptor protein that is composed of two protein-protein interaction domains: a N-terminal PYRIN-PAAD-DAPIN domain (PYD) and a C-terminal caspase-recruitment domain (CARD). The PYD and CARD domains are members of the six-helix bundle death domain-fold superfamily that mediates assembly of large signaling complexes in the inflammatory and apoptotic signaling pathways via the activation of caspase. In normal cells, this protein is localized to the cytoplasm; however, in cells undergoing apoptosis, it forms ball-like aggregates near the nuclear periphery. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]

Locus ID: 29108

MW: 4.8