

## Product datasheet for **SC201316**

### **TMEM111 (EMC3) (NM\_018447) Human 3' UTR Clone**

#### **Product data:**

Product Type:	3' UTR Clones
Product Name:	TMEM111 (EMC3) (NM_018447) Human 3' UTR Clone
Symbol:	TMEM111
Synonyms:	POB; TMEM111
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_018447
Insert Size:	1417 bp



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**Insert Sequence:** >SC201316 3'UTR clone of NM\_018447  
The sequence shown below is from the reference sequence of NM\_018447. The complete sequence of this clone may contain minor differences, such as SNPs.  
Blue=Stop Codon Red=Cloning site

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GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
AAAAAGGAATTACAGACCTCTATTTTTTGAAGACCGAGCAGGATTAGCTGTGTCAGGAAGTTGGAGTT
GCCTTAACCTTTGTAACCTTTGTTTGGAGCTGGCACCTCTTGAAATAAAAAGGAGGATGCACGAGCTGGC
AGGCATGCAGCAAGGCTTGTCTGTCTGGGCTGGGTTCCCTTTATGTTTGAACTAGAGGAAATAGG
AGTATGCTGGGCAACTTGTATTTTTAAAATGTTGTAATGTTCCCTTCTGGTGACTCTAGTAATGAAAG
TCAGAGAAAGGGGAAACCTCAGGCTACTGATAATATATAAAAATCTTGGCCAGGCGCAGTGGCTCACGC
CTGTAATCCCAGGATTTGGGAGGCTGAGGCGGGTGGTACAGAGATCAGGAGTTCAAGATCAGCCTGG
CCAAGATGGTGAACCCCATCTCTACTAAAAATACAAAAAAAATAGCCGGGCGTGGTGGTGGGCACC
TGTAATCCAGCTACTTGGGAGGCTGAGGCAGAGAAGTCTTAAACCTAGGAGGCGGAGGATGCAGTGA
GCTGACATCGTGCCACTGCGCTCCAGCCTGGGCGACAGAGCAAACTCCATCTGAAAAAAAAAAAAAAAA
TATATATATATATATATATATATCTATCTTAGCAGAAGCCAGTCTTGAAGGAAGCATTGTTAATTAT
AGCTAATGATTATGTGCAGTCAGCTGACATCTAGCCACAGTAACTCCTGTTTTCTTGGGATCCAAAC
ACCTGTGTTTTACCATTAGTTTTGTTAGTATTGTTAACTTTCTTTACACAAGTAAACCATTTCCACTA
CCAAAGTTTTAGAACTATGGATGAACAAAATGAATCTCCCTGTTCAATTTGAGCCTACATAGACATAG
AGACCAAAATGTCAAAACCTTATTCAAATAAACTCTCTCAGAGTGAATACCCAGGTCAGGACAGAC
TCAGCAAACTTCTATATCACTTAATTTGCCAGTGAATCAGTGACCCTGAGGCACTGCCAGATTC
TAAAGTGCCTTTGGGATCATCAGAGACTGTCTATAAATAATGCAAAATCTTGATCTGGATGTCAGTGT
TCAAATCTTATCAAATCCATTGACAAATCAGTGGTGTATACTGGAAATGGCTACTCTTTGGATGAAG
GACCTCATTTCCAGTTGCTTGGAAACAAAAGAGAATTTACATATTGCTGTAAAGAAGGAGAGACGGCAG
TTGTTGGTAGACACACAGATAAGGGTGCCCAAGAATAATTCTGTCTGGATTAAGGTCCCAGGGAAGTG
ACGGTGCCATTTCTGTACCAAGAGGTGAATATAATTTGCATGTTGAGTGCAGTAATTAAGAACAACGA
CTCGACTCCACAAATTAACCGTCTGTTTTCTCTTC
ACGCGTAAGCGGCCGCGCATCTAGATTCAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTCGATTCCACCGCCCTTCTATGAAAGG
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**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\\_018447.4](#)

**Summary:**

Part of the endoplasmic reticulum membrane protein complex (EMC) that enables the energy-independent insertion into endoplasmic reticulum membranes of newly synthesized membrane proteins (PubMed:30415835, PubMed:29809151, PubMed:29242231, PubMed:32459176, PubMed:32439656). Preferentially accommodates proteins with transmembrane domains that are weakly hydrophobic or contain destabilizing features such as charged and aromatic residues (PubMed:30415835, PubMed:29809151, PubMed:29242231). Involved in the cotranslational insertion of multi-pass membrane proteins in which stop-transfer membrane-anchor sequences become ER membrane spanning helices (PubMed:30415835, PubMed:29809151). It is also required for the post-translational insertion of tail-anchored/TA proteins in endoplasmic reticulum membranes (PubMed:29809151, PubMed:29242231). By mediating the proper cotranslational insertion of N-terminal transmembrane domains in an N-exo topology, with translocated N-terminus in the lumen of the ER, controls the topology of multi-pass membrane proteins like the G protein-coupled receptors (PubMed:30415835). By regulating the insertion of various proteins in membranes, it is indirectly involved in many cellular processes (Probable). [UniProtKB/Swiss-Prot Function]

**Locus ID:**

55831

**MW:**

54.2