

Product datasheet for SC332409

Product datasneet for 3C332409

TMEM250 (NM_001256526) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: TMEM250 (NM_001256526) Human Untagged Clone

Tag: Tag Free
Symbol: TMEM250
Synonyms: C9orf69

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC332409 representing NM_001256526.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGTGA

Restriction Sites: Sgfl-Mlul

ACCN: NM_001256526

Insert Size: 420 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a

point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative

RNA splicing form or single nucleotide polymorphism (SNP).

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube

containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).



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Reconstitution Method:

- 1. Centrifuge at 5,000xg for 5min.
- 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
- 3. Close the tube and incubate for 10 minutes at room temperature.
- 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.

5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: NM 001256526.1

 RefSeq Size:
 2804 bp

 RefSeq ORF:
 420 bp

 Locus ID:
 90120

 UniProt ID:
 H0YL14

 Cytogenetics:
 9q34.3

 MW:
 16.1 kDa

Gene Summary: May play a role in cell proliferation by promoting progression into S phase.[UniProtKB/Swiss-

Prot Function]

Transcript Variant: This variant (2) differs in the 5' UTR, compared to variant 1. Variants 1 and 2 encode the same protein. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome

assembly. The genomic coordinates used for the transcript record were based on alignments.