

Product datasheet for SC332604

OriGene Technologies, Inc.

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TMEM218 (NM_001258246) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: TMEM218 (NM 001258246) Human Untagged Clone

Tag: Tag Free
Symbol: TMEM218

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC332604 representing NM_001258246.

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

CTGGAGCCGATCTATGCCAAACCACTGCACTCCTACTGA

Restriction Sites: Sgfl-Mlul

ACCN: NM_001258246

Insert Size: 453 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).

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.





TMEM218 (NM_001258246) Human Untagged Clone - SC332604

RefSeq: NM 001258246.1

RefSeq Size: 3988 bp
RefSeq ORF: 453 bp
Locus ID: 219854
UniProt ID: A2RU14
Cytogenetics: 11q24.2

Protein Families: Transmembrane

MW: 16.2 kDa

Gene Summary: May be involved in ciliary biogenesis or function.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (4) differs in the 5' UTR, compared to variant 1. Variants 1, 2, 3, and 4 encode the same protein (isoform 1). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were

based on transcript alignments.