

Product datasheet for **SC331613**

TMEM16K (ANO10) (NM_001204831) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: TMEM16K (ANO10) (NM_001204831) Human Untagged Clone
Tag: Tag Free
Symbol: TMEM16K
Synonyms: SCAR10; TMEM16K
Vector: pCMV6-Entry (PS100001)
Fully Sequenced ORF: >SC331613 representing NM_001204831.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GTCATAGGTCCTGGGGCTAG
  
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Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001204831
Insert Size:	1884 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:	<ol style="list-style-type: none">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_001204831.1
RefSeq Size:	2746 bp
RefSeq ORF:	1884 bp
Locus ID:	55129
UniProt ID:	Q9NW15
Cytogenetics:	3p22.1-p21.33
Protein Families:	Transmembrane
MW:	72.1 kDa
Gene Summary:	<p>The transmembrane protein encoded by this gene belongs to the anoctamin family of calcium-activated chloride channels, also known as the transmembrane 16 family. The encoded protein contains eight transmembrane domains with cytosolic N- and C-termini. Defects in this gene may cause autosomal recessive spinocerebellar ataxia-10. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2016]</p> <p>Transcript Variant: This variant (2) has multiple differences in the 3' coding region and differs in the 3' UTR, compared to variant 1. The resulting isoform (2) is shorter and has a distinct C-terminus, compared to isoform 1.</p>