



ACTACCACCCAAAGATCAGGATCATCACTCAGATGCTGCAGTATCACAACAAGGCCCATCTGCTCAACAT  
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 TCCAAGAAGGTACTTTAGGATTTTTTCATCGCAAGTGTGCCAAAGAAGTTAAAAGGGCATTTTTTACTG  
 CAAGGCCTGTCATGATGACGTACAGATCCCAAAAAGAATTAAAAAATGTGGCTGCAGGCGGCTTGAAGAT  
 GAGCAGCCGCCAACCTGTACCAAAAAAAAAAACGTAATGGGGCATGAGGAACTCGCCCAACACCT  
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 CAGCCCTGATTGGCTCCGGAACCTGGTATGCCACTTCGTGCTAGCAACTTTCATCATGAGCTCAA  
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 GTGTCCATATTGCTGTACACCATTAAGTCGGGCTGATTTAAGGGCTGTCAACATCAACCTCTGTGACA  
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 GGCGTCACTCAACATCAATCTATGCAGTTTGTGACAGCATCGGGGTCTTGAGGCTAATTCACAGGA  
 TTCACACCTCCTGGAATGGACAGATCATCACCCGACAACAGCCAGTGCACGGGATGTTACGCCAGCCGT  
 CCATCACAACTGGGGTCAACATTCATCATCAGGAACTCGTAAGCCGGGCAAGTTGCCTTTGGTATC  
 AGTCAATCAGGAAAAAAGAGTGGGACGCACATTTAATGATAACGGAGTTGGTGAATGATACCAATGTT  
 CAGTTTTTGGACCAAGACGATGACGATGACCCTGACACAGAGCTGTACCTCACACAGCCCTTGTGTTG  
 GGACAGCATTTGCCGTACGCTCCTGGACTCACTCATGAGCGGACATACTTCAATGACAATATCCTCAC  
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 CTTTCGAGGAGGCTACAGCACTCCGACAGACATTGGCCAACAGGGACCGTTGCCGAGTGGCCAGTTAGCCC  
 TGTTAGATGGTCCCTTTCGACAGCTTAGGGATGGTGGTTGTTATGGTATCTGTTCTGCAAAGCTCTGAA  
 AACATATAATATGCTTTGTTTGGAAATTAACGGCTGAGAGATGCCACCTCAGCACCCAGCCAGTGT  
 ACAAAAAGGTACGTATACCAATCCTCCCTACGAGTTTGTGCTCGTACCAACAGACCTGATCTTCTGCC  
 TGATGCAGTTTGACCACAACGCTGGCCAATCCCGGGCCAGTCTGTCTATTCTCCACTCCTCACAGTC  
 GTCCAGTAAGAAGAGCTCCTCCGTCCACTCCATCCCGTCCACAGCAAATCGGCCGAACCGGCCAAAGTCC  
 AGGGAGTCCCGGACAAAACAGAATGCAACAAGGATGACTAGAATGGCCAAGAAAAGAAATGGTTTACAG  
 ATGAGCCGGATAATGCCTATCCAGAAACATTCAAATCAAGCCATGAGTACCCACATGGCTAACAGAT  
 CAACCAATATAAATCCACAAGCAGCCTGATCCCTCCAATCAGAGAAGTTGAAGATGAATGTGA

AGCGGACCGACGCGTACGCGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC  
 TGGATTACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:**

SgfI-RsrII

**ACCN:**

NM\_001253360

**Insert Size:**

3774 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).

**OTI Annotation:**

Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.

**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.

**RefSeq:** [NM\\_001253360.1](#), [NP\\_001240289.1](#)

**RefSeq Size:** 5051 bp

**RefSeq ORF:** 3774 bp

**Locus ID:** 16531

**Cytogenetics:** 14 A3

**Gene Summary:** Potassium channel activated by both membrane depolarization or increase in cytosolic Ca(2+) that mediates export of K(+). It is also activated by the concentration of cytosolic Mg(2+). Its activation dampens the excitatory events that elevate the cytosolic Ca(2+) concentration and/or depolarize the cell membrane. It therefore contributes to repolarization of the membrane potential. Plays a key role in controlling excitability in a number of systems, such as regulation of the contraction of smooth muscle, the tuning of hair cells in the cochlea, regulation of transmitter release, and innate immunity. In smooth muscles, its activation by high level of Ca(2+), caused by ryanodine receptors in the sarcoplasmic reticulum, regulates the membrane potential. In cochlea cells, its number and kinetic properties partly determine the characteristic frequency of each hair cell and thereby helps to establish a tonotopic map. Kinetics of KCNMA1 channels are determined by alternative splicing, phosphorylation status and its combination with modulating beta subunits. Highly sensitive to both iberiotoxin (IbTx) and charybdotoxin (CTX).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (3) lacks an in-frame exon and has an alternate splice site in the 3' coding region, which does not affect the reading frame, compared to variant 1. The resulting isoform (3) lacks an internal segment and an internal single aa, compared to isoform 1. 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.