

Product datasheet for MC227358

Kcnj15 (NM_001039056) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Kcnj15 (NM_001039056) Mouse Untagged Clone
Tag: Tag Free
Symbol: Kcnj15
Synonyms: 4930414N08Rik; AI182284; AI267127; IRKK; Kir4.2
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC227358 representing NM_001039056
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**GCGATCGCC**

ATGGATGCCATTACCTTGGCATGTCCAGTGCCCCACTGGTGAAGCATACCAACGGGGTTGGACTCAAGG
 CCCACAGACCCCGAGTCATGTCAAAGAGTGGGCACAGTAATGTGAGAATCGATAAGGTAGACGGAATCTA
 TTTACTCTACCTCCAGGACTTGTGGACAACCGTCATCGACATGAAGTGGCGATAACAAGCTCACCTATTT
 GCTGCCACCTTTGTGATGACCTGGTTTCTGTTTGGAGTGGTCTACTATGCCATAGCCTTTATTCATGGTG
 ACTTACAACCTGGGGAATCTAATCCAACCACACACCCTGCATTATGAAAGTGGACTCTCTCACAGGAGC
 ATTCCTCTTTTCTTGAATCTCAGACAACATTGGCTACGGGGTCCGTTCCATCACAGAGGAGTGTCCC
 CATGCTATCTTCTCTTAGTCGCCCAACTGGTCATCACCACATTGATTGAGATCTTCATTACGGGGACCT
 TTCTGGCTAAAATTGCAAGACCCAAAAAGCGAGCCGAGACCATTAAGTTCAGCCACTGTGCTGTCATCAG
 CAAGCAGAATGGAAAGCTATGCCTGGTCATCCAGGTGGCCAACATGAGGAAGAGTCTCCTGATTCACTGC
 CAGCTCTCTGGAAACTCCTGCAGACACACGTACCAAAGAGGGAGAACGCATTCTCCTCAACCAGGCCA
 CTGTCAAATCCACGTGGACTCCTTCCGAGAGTCCCTTCTCATCCTGCCATGACCTTCTACCACGT
 GTTGGATGAGACAAGCCCTGCGGGACCTCACACCCAAAAACCTAAAGGAGAAGGAGTTTGAGCTGGTG
 GTACTTCTCAACGCCACGGTGGAGTCTACCAGCGCGTCTGCCAGAGCCGAACGTCTTACATCCCGGAGG
 AGATCTACTGGGCTTTGAGTTTGTGCCTGTGGTTTCTCTCTCCAAAAATGGAAAGTATGTGGTGATTT
 CAGTCAATTTGAGCAGATCAGGAAGAGCCCGATTGTACCTTCTACTGTGCCGATTCTGAGAAGCAGAAG
 CTTGAAGAACAGTACAGGCAAGAGGACCAGAGGGAGCGGGAGCTGAGGAGCCTCTGCTACAGCAGAGCA
 ATGTC**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI



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ACCN:	NM_001039056
Insert Size:	1128 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:	<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_001039056.2 , NP_001034145.1
RefSeq Size:	5046 bp
RefSeq ORF:	1128 bp
Locus ID:	16516
UniProt ID:	O88932
Cytogenetics:	16 55.86 cM
Gene Summary:	<p>Inward rectifier potassium channels are characterized by a greater tendency to allow potassium to flow into the cell rather than out of it. Their voltage dependence is regulated by the concentration of extracellular potassium; as external potassium is raised, the voltage range of the channel opening shifts to more positive voltages. The inward rectification is mainly due to the blockage of outward current by internal magnesium.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (3) differs in the 5' UTR and 5' coding region and uses a downstream start codon, compared to variant 1. The encoded isoform (b) has a shorter N-terminus, compared to isoform a. Variants 2, 3, 5, 7, 9 and 11 encode the same isoform (b). 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.</p>