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Product datasheet for MC226907

Kcnj11 (NM_001204411) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Kcnj11 (NM_001204411) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Kcnj11
Synonyms:	Kir6.2; mBIR
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226907 representing NM_001204411 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGGTCTGGTGGCTCATCGCCTTCGCCCACGGTGACCTGGCCCCCGGAGAGGGCACCAATGTGCCCTGCG TCACAAGCATCCACTCCTTTTCATCTGCCTTCCTTTTCTCCATCGAGGTCCAGGTGACCATTGGTTTCGG CGGGCGCATGGTGACAGAGGAATGTCCCCTGGCCATCCTCATTCTCATTGTGCAGAATATCGTCGGGCTG ATGATCAACGCCATCATGCTGGGCTGCATCTTCATGAAAACGGCCCAGGCCCATCGGCGGGCAGAAACCC TCATCTTCAGCAAGCATGCTGTGATCACCCTGCGCCATGGCCGCCTGTGCTTCATGCTGCGCGTAGGGGA CCTCCGAAAGAGCATGATCATTAGCGCCACCATCCACATGCAGGTGGTGCGCAAGACCACCAGCCCCGAG GGCGAAGTTGTGCCTCTCCACCAGGTAGACATCCCCATGGAGAATGGCGTGGGTGGTAACGGCATCTTCC TGGTGGCCCCACTCATCATCTACCACGTCATCGACTCCAACAGCCCGCTCTACGACCTGGCTCCTAGTGA CCTGCACCACCACCAGGACCTGGAGATCATTGTCATCTTGGAAGGCGTGGTAGAAACCACGGGCATCACC ACCCAGGCCCGCACCTCCTACCTAGCTGACGAGATTCTATGGGGGCAGCGCTTTGTCCCCATTGTGGCCG AGGAGGACGGCCGCTATTCTGTGGACTACTCCAAATTTGGTAACACCATTAAAGTGCCCACACCACTCTG CACAGCCCGCCAGCTTGATGAGGACCGCAGTCTGCTGGATGCCCTGACCCTCGCCTCGTCGCGGGGGCCC CTGCGCAAGCGCAGTGTGGCTGTGGCGAAGGCCAAGCCCAAGTTTAGCATCTCTCCAGATTCCTTGTCCT GA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001204411

Insert Size:	912 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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_001204411.1, NP_001191340.1
RefSeq Size:	2667 bp
RefSeq ORF:	912 bp
Locus ID:	16514
Cytogenetics:	7 29.66 cM
Gene Summary:	This receptor is controlled by G proteins. 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. Can be blocked by extracellular barium. Can form cardiac and smooth muscle-type KATP channels with ABCC9. KCNJ11 forms the channel pore while ABCC9 is required for activation and regulation (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) differs in the 5' UTR, lacks a portion of the 5' coding region and initiates translation at a downstream in-frame start codon, compared to variant 1. The encoded isoform (2) is shorter than 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.