

Product datasheet for **SC215939**

Kir6.2 (KCNJ11) (NM_001166290) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	Kir6.2 (KCNJ11) (NM_001166290) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	KCNJ11
Synonyms:	BIR; HHF2; IKATP; KIR6.2; MODY13; PHHI; PNDM2; TNDM3
ACCN:	NM_001166290
Insert Size:	1701 bp



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Insert Sequence:	<p>>SC215939 3'UTR clone of NM_001166290 The sequence shown below is from the reference sequence of NM_001166290. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site</p> <pre>GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC TTCAGCATCTCTCCAGATTCCCTGTCCTGAGCCATGGTCTCTCGGGCCCCCACACGCGTGTGTACACA CGGACCATGTGGTATGTAGCCCGCCAGGGCCTGGTGTGAGGCTGGGCCAGCCTCAGCTCAGCCTCCCC CTGCTGCTCATCCAGGTGTTACAAGGCACTTGTCACTATGCTATTTCTGGCCTCAGCAGGAACCTGTA CTGGGTTATTTTGTCCCTGCTCCTCCCAACCAATTCAGGACTGGCTCACCCCTCTCCCCGCCCAAG GCTGCAGAGGCTGTGGGAGTACTGGGCCCTAGAGCTGTGCGTCCAGCCAGTCTGGGTCACCGATT GACCAGCCACACTCTGGGCCGTGGCTGGGGAAGAACAATCCCCGAGGGCTGCTGCTTTGCGTCTGTGG CTCCAAGAAGTGCCTGTGGTCAAGCCCCAGCTCTACTTGGTCCCTGAAAAAGCACCTGGCTAAGGGCTG GGCCTGGCCAGCAGGGAGGGCAGTTGATGAGAGAGGGTGTCCCGCTGGAGGGTTGGTGTGTGGAGCC TACACCGGCAGGGACAGCCTGGGGCTGACAGGGCTCCCTCCGAGGGCCAGTTTTCAGGTCTGGAAGGGG AGGAAGCAGGGGAAGGTGACCTGAGGAGCTCGGCTTTGTAGAGCCCCGCTCAGGCACAGGGAGGAGGA GATGCCAGGGCTCCTGCCTTTTGGCCACATCGGCCCTCGTGCAGTGAAGGGCTCTGTGGGCTGGGGCTGCTG CCCCTGCCTACCTCCTGCCTGTCCCCAGAGGCTGAGGAGAGGGGGTACTGTGCCACCACACATGATTA GGCCTCAGACCAACTCTGGTCTGGCTCCACAACAGTGGCTGCCACTCACTTTGTCCAGAAGGTGGCT TGGGGTGGATATCTTTGGGTTGCTGAAAAGGTGTGGAAAGGTTCAAGTGGTGGGAGGGACTGAGGT CCCTGAGGTGAAGAGGCCCTTGGTCTGACGGGTTTGACCCGTGCCTGGACCCTTGAGCAGTGTGTG TGAACTTGCTAGAAGTCTGCCTTCTCCGTTGTCAATAAAGCTCCCCCTCATGACCTAACTTGGGC TTTTCTTGCTGGGAGGCAGCAAGCATGCTGGTGGGAAGGGAGGCAGGGACTGGCAGCTGCCACCCCT TCAAGAGCGCCATAGACCCTAGCGGGAGGGCAGGGGAGGGACGGAAGGCTGGCACCTTTCACCAG TTCAGGGGACTTTCCCTCTCCTGTCTCAGGTGGCCAGCCCTGTCAGCCTGTCTGGCCAACTCAGCC TTTGGGCACTCACCAGGCTTTCAGCCCTGGGCTGTCTCTACTCCAGGGACCTGCTGGAAGGCTGG AGTGCCAGGGAGAGGTATAGAGGTGCATAGGCATTAGTGTAGTAATTGGAGCACTAACTCTCAGGCC AACTGCCTGGGTTCAATCCTGGCTCTAGCTGTATGACTTTTGTCAAGTAACTTAGCCTCTCTGTGTCT CAGTTGCCTTTCTATAACATGGATGCTAATAGTACCTACCTCATAGAATTGTTTTGGAAGTAAATGAA AAATATGTAATAATGCTGAAGTGCCTGGTCTACAGTAAGTGTCAATAAATGTTAACTATTGTGATTGCT GCTGAATCAGCTACATGCTGAGGAAACGCCAAACAAGTGTAAA AGCGGACCGACTTACGCGTAAGCGGCCGCGGCATCTAGATTCAAGAAAATGACCGACCAAGCGACGCC CAACCTGCCATCACGAGATTTTCGATTCCACCGCCG</pre>
Restriction Sites:	Sgfl-RsrII
OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
RefSeq:	<u>NM_001166290.2</u>

Summary:

Potassium channels are present in most mammalian cells, where they participate in a wide range of physiologic responses. The protein encoded by this gene is an integral membrane protein and inward-rectifier type potassium channel. The encoded protein, which has a greater tendency to allow potassium to flow into a cell rather than out of a cell, is controlled by G-proteins and is found associated with the sulfonylurea receptor SUR. Mutations in this gene are a cause of familial persistent hyperinsulinemic hypoglycemia of infancy (PHHI), an autosomal recessive disorder characterized by unregulated insulin secretion. Defects in this gene may also contribute to autosomal dominant non-insulin-dependent diabetes mellitus type II (NIDDM), transient neonatal diabetes mellitus type 3 (TNDM3), and permanent neonatal diabetes mellitus (PNDM). Multiple alternatively spliced transcript variants that encode different protein isoforms have been described for this gene. [provided by RefSeq, Oct 2009]

Locus ID:

3767

MW:

60.1