

## Product datasheet for **SC329583**

### **Kv beta 2 (KCNAB2) (NM\_001199863) Human Untagged Clone**

#### **Product data:**

**Product Type:** Expression Plasmids  
**Product Name:** Kv beta 2 (KCNAB2) (NM\_001199863) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** KCNAB2  
**Synonyms:** AKR6A5; HKvbeta2; HKvbeta2.1; HKvbeta2.2; KCNA2B; KV-BETA-2  
**Vector:** pCMV6-Entry (PS100001)  
**Fully Sequenced ORF:** >SC329583 representing NM\_001199863.  
Blue=Insert sequence Red=Cloning site Green=Tag(s)

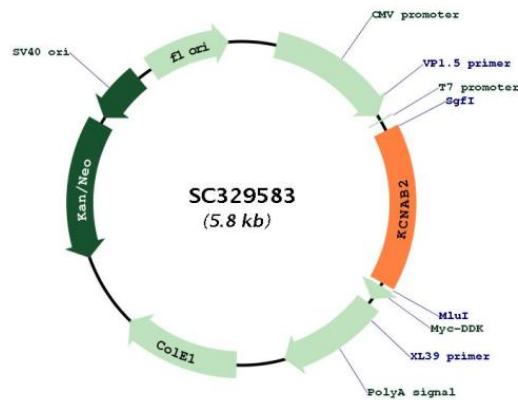
```
ATGGCAGAGCAGCTCATGACCTTGGCCTATGATAATGGCATCAACCTCTTCGATACAGCAGAAGTCTAC
GCAGCCGGCAAGGCTGAAGTGGTACTGGGAAACATCATTAAAGAAGAAAGGATGGAGGCGGTCCAGCCTC
GTCATCACCACCAAGATCTTCTGGGGCGGAAAGGCGGAGACGGAGCGGGCCTGTCCAGGAAGCACATA
ATCGAAGGTCTGAAAGCTTCCCTGGAGCGACTGCAGCTGGAGTACGTGGATGTGGTGTGGTGGTGGTGGT
CCGGACCCCAACACCCCGATGGAAGAGACCGTCCGCGCCATGACCCACGTCATCAACCAGGGGATGGCC
ATGTACTGGGGCACGTACGCTGGAGCTCCATGGAGATCATGGAGGCCTACTCCGTGGCCCGGCAGTTC
AACCTGACCCCGCCCATCTGCGAGCAGGCTGAGTACCACATGTTCCAGCGTGAGAAAAGTGGAGGTGCAG
CTGCCGGAGCTGTTCCACAAGATAGGAGTGGGCGCCATGACCTGGTCCCCTCTGGCCTGTGGCATTGTT
TCTGGCAAGTACGACAGTGGCATCCCACCTACTCAAGAGCCTCCTTGAAGGGCTACCAGTGGCTGAAG
GACAAGATCCTCAGTGAGGAGGGCCGGCGCCAGCAAGCCAAGCTGAAGGAGCTGCAGGCCATCGCCGAG
CGCCTGGGCTGCACCCTGCCCCAGCTGGCCATAGCCTGGTGCCTGAGGAATGAGGGAGTCAGCTCCGTG
CTCCTGGGGCCCTCCAATGCGGACCAGCTCATGGAGAACATTGGGGCAATACAGGTCCTCCGAAACTG
TCATCTTCCATTATCCACGAGATTGATAGTATTTGGGCAATAAACCCCTACAGCAAAAAGGACTACAGA
TCCTAA
```

**Restriction Sites:** Sgfl-Mlul



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## Plasmid Map:



**ACCN:** NM\_001199863

**Insert Size:** 903 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:**

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:	<a href="#">NM_001199863.1</a>
RefSeq Size:	3690 bp
RefSeq ORF:	903 bp
Locus ID:	8514
UniProt ID:	<a href="#">Q13303</a>
Cytogenetics:	1p36.31
Protein Families:	Druggable Genome, Ion Channels: Other
MW:	33.7 kDa

**Gene Summary:** Voltage-gated potassium (Kv) channels represent the most complex class of voltage-gated ion channels from both functional and structural standpoints. Their diverse functions include regulating neurotransmitter release, heart rate, insulin secretion, neuronal excitability, epithelial electrolyte transport, smooth muscle contraction, and cell volume. Four sequence-related potassium channel genes - shaker, shaw, shab, and shal - have been identified in *Drosophila*, and each has been shown to have human homolog(s). This gene encodes a member of the potassium channel, voltage-gated, shaker-related subfamily. This member is one of the beta subunits, which are auxiliary proteins associating with functional Kv-alpha subunits. This member alters functional properties of the KCNA4 gene product. Alternative splicing of this gene results in multiple transcript variants encoding distinct isoforms. [provided by RefSeq, Dec 2010]

Transcript Variant: This variant (6) lacks three exons from the 5' end and contains an alternate 5' exon, resulting in a downstream AUG start codon, as compared to variant 1. The resulting isoform (4) has a shorter N-terminus, as compared to isoform 1. 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.