

## Product datasheet for **SC332744**

### Kv3.2 (KCNC2) (NM\_001260499) Human Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Kv3.2 (KCNC2) (NM\_001260499) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Kv3.2  
**Synonyms:** KV3.2  
**Vector:** pCMV6-Entry (PS100001)  
**Fully Sequenced ORF:** >SC332744 representing NM\_001260499.  
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGGGCAAGATCGAGAACAACGAGAGGGTGATCCTCAATGTCGGGGGCACCCGGCACGAAACCTACCGC
AGCACCCTCAAGACCCTGCCTGGAACACGCCTGGCCCTTCTTGCCTCCTCCGAGCCCCAGGCGACTGC
TTGACCACGGCGGGGACAAAGCTGCAGCCGTGCGCCGCTCCACTGTGCGCCGCGCCGAGAGCGCCCCG
CTGTCCCCCGGGCAGGCGGCTGCTTTCGAGGGCGGCGGGCAACTGCAGTTCGCCGGCGGCGAGGGCC
AGCGACCATCCCGGTGGCGGCCGAGTCTTCTTCGACCGGCACCCGGGCGTCTTCGCCTATGTGCTC
AATTACTACCGCACCGGCAAGCTGCACTGCCCCGAGACGTGTGGGGCCGCTCTTCGAGGAGGAGCTG
GCCTTCTGGGGCATCGACGAGACCGACGTGGAGCCCTGCTGCTGGATGACCTACCGGCAGACCCGGAC
GCCGAGGAGGCGCTGGACATCTTCGAGACCCCCGACCTATTGGCGGCGACCCCGGCGACGACGAGGAC
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TGGAGGAGGCTGCAGCCCCGATGTGGGCCCTCTTCGAAGACCCCTACTCGTCCAGAGCCGCCAGGTTT
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TTCAATATTGTTAAAAACAAGACAGAACCAGTCATCAATGGCACAAGTGTGTTCTACAGTATGAAAT
GAAACGGATCCTGCCTTGACGTATGTAGAAGAGTGTGTGGTGTGTTACTTTTGAATTTTAGTC
CGTATTGTTTTTTCACCCAATAAACTTGAATTCATCAAAAATCTCTTGAATATCATTGACTTTGGGCC
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AGGGTGTCTGGACATACTCTTCGAGCTAGTACTAATGAATTTTTGCTGCTGATAATTTCTGGCTCTA
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GCTAGTGAGCACACAGTTCAAAAACATTTCCATTGGGTTCTGGTGGGCTGTAGTGACCATGACTACC
CTGGTTATGGGGATATGTACCCCAAACATGGTCAGGCATGCTGGTGGGAGCCCTGTGTCTGGCT
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ACTTTTTGCAAGACAGAATTAATATGGCTGCAATAGTACACAGAGTGACACATGTCTGGCAAAGAC
AATCGACTTCTGGAACATAACAGATCAGGATATGAAAAATCCCGAAGCTTAAACAACATAGCGGGCTTG
GCAGGCAATGCTCTGAGGCTCTCTCCAGTAACATCACCTACAACCTCCTTGTCTCTGAGGCGCTCT
CGATCTCCCATCCCATCTATCTGTAA
  
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**Restriction Sites:** SgfI-MluI



<b>ACCN:</b>	NM_001260499
<b>Insert Size:</b>	1752 bp
<b>OTI Disclaimer:</b>	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).
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<a href="#">NM_001260499.1</a>
<b>RefSeq Size:</b>	5347 bp
<b>RefSeq ORF:</b>	1752 bp
<b>Locus ID:</b>	3747
<b>UniProt ID:</b>	<a href="#">Q96PR1</a>
<b>Cytogenetics:</b>	12q21.1
<b>Protein Families:</b>	Druggable Genome, Ion Channels: Potassium, Transmembrane
<b>MW:</b>	64.3 kDa
<b>Gene Summary:</b>	<p>The Shaker gene family of Drosophila encodes components of voltage-gated potassium channels and is comprised of four subfamilies. Based on sequence similarity, this gene is similar to one of these subfamilies, namely the Shaw subfamily. The protein encoded by this gene belongs to the delayed rectifier class of channel proteins and is an integral membrane protein that mediates the voltage-dependent potassium ion permeability of excitable membranes. Several transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, May 2012]</p> <p>Transcript Variant: This variant (6) lacks an alternate in-frame exon compared to variant 2. The resulting isoform (6) has the same N- and C-termini but is shorter compared to isoform KV3.2b. 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>