

## Product datasheet for **SC332750**

### **GIRK1 (KCNJ3) (NM\_001260510) Human Untagged Clone**

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** GIRK1 (KCNJ3) (NM\_001260510) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** GIRK1  
**Synonyms:** GIRK1; KGA; KIR3.1  
**Vector:** pCMV6-Entry (PS100001)  
**Fully Sequenced ORF:** >SC332750 representing NM\_001260510.  
Blue=Insert sequence Red=Cloning site Green=Tag(s)

```
ATGTCTGCACTCCGAAGGAAATTTGGGACGATTATCAGGTAGTGACCACATCGTCCAGCGGCTCGGGC
TTGCAGCCCCAGGGGCCAGGCCAGGACCCTCAGCAGCAGCTTGTGCCAAGAAGAAGCGGCAGCGGTTTC
GTGGACAAGAACGGCCGGTGCAATGTACAGCACGGCAACCTGGGCAGCGAGACAAGCCGCTACCTCTCG
GACCTCTTACCACGCTGGTGGACCTCAAGTGGCGCTGGAACCTTTCATCTTCATTCTCACCTACACC
GTGGCCTGGCTTTTCATGGCGTCCATGTGGTGGGTGATCGCCTACACTCGGGGCGACCTGAACAAAGCC
CACGTCGGTAACTACACGCCTTGGTGGCCAATGTCTATAACTTCCCTTCTGCCTTCTCTTCTTTCATC
GAGACGGAGGCCACCATCGGCTATGGCTACCGATACATCACAGACAAGTGCCCGAGGGCATCATCCTC
TTCTCTTCCAGTCCATCCTGGGCTCCATCGTGGACGCCTTCTCATCGGCTGCATGTTCAAGATG
TCCCAGCCCAAGAAGCGCGCCGAGACCCTCATGTTGAGCGAGCACGCGGTGATCTCCATGAGGGACGGGA
AAACTCACGCTTATGTTCCGGGTGGGCAACCTGCGCAACAGCCACATGGTCTCCGCGCAGATTCCGCTGC
AAGCTGCTCAAAGTAAGTGTCCCCGCCCTTCCCCACCGGGAGACCTGCGTCCCCCAAACCCGCGGAG
TAA
```

**Restriction Sites:** SgfI-MluI  
**ACCN:** NM\_001260510  
**Insert Size:** 762 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).



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**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:** [NM\\_001260510.1](#)

**RefSeq Size:** 1011 bp

**RefSeq ORF:** 762 bp

**Locus ID:** 3760

**UniProt ID:** [P48549](#)

**Cytogenetics:** 2q24.1

**Protein Families:** Druggable Genome, Ion Channels: Potassium, Transmembrane

**MW:** 28.7 kDa

**Gene 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 plays an important role in regulating heartbeat. It associates with three other G-protein-activated potassium channels to form a heteromultimeric pore-forming complex that also couples to neurotransmitter receptors in the brain and whereby channel activation can inhibit action potential firing by hyperpolarizing the plasma membrane. These multimeric G-protein-gated inwardly-rectifying potassium (GIRK) channels may play a role in the pathophysiology of epilepsy, addiction, Down's syndrome, ataxia, and Parkinson's disease. Alternative splicing results in multiple transcript variants encoding distinct proteins. [provided by RefSeq, May 2012]

Transcript Variant: This variant (4) lacks multiple 3' terminal exons and contains an additional coding segment, compared to variant 1. These differences result in a protein (isoform 4; also known as GIRK1e) with a truncated and novel C-terminus, 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.