

## **Product datasheet for SC206789**

## ARHGEF10L (NM\_018125) Human 3' UTR Clone

**Product data:** 

Product Type: 3' UTR Clones

Symbol: ARHGEF10L

Synonyms: GrinchGEF

Mammalian Cell Neomycin

Selection:

**Vector:** pMirTarget (PS100062)

**ACCN:** NM\_018125

Insert Size: 519 bp

Insert Sequence: >SC206789 3'UTR clone of NM\_018125

The sequence shown below is from the reference sequence of NM\_018125. The complete sequence of

this clone may contain minor differences, such as  $\ensuremath{\mathsf{SNPs}}\xspace.$ 

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

GAGATGCTGGAATAAAAGACAAGAGTTACATCTGGA

**ACGCGT**AAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul

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).



**OriGene Technologies, Inc.** 9620 Medical Center Drive, Ste 200

Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com

EU: info-de@origene.com CN: techsupport@origene.cn



## ARHGEF10L (NM\_018125) Human 3' UTR Clone | SC206789

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.

Note: Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um

filter is required.

**RefSeq:** <u>NM\_018125.4</u>

Summary: This gene belongs to the RhoGEF subfamily of RhoGTPases. Members of this subfamily are

activated by specific guanine nucleotide exchange factors (GEFs) and are involved in signal transduction. The encoded protein shows cytosolic distribution. Alternative splicing results in

multiple transcript variants. [provided by RefSeq, Jun 2016]

**Locus ID:** 55160

**MW:** 19.9