

Product datasheet for SC210056

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RBED1 (ELMOD3) (NM_001135021) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: RBED1 (ELMOD3) (NM_001135021) Human 3' UTR Clone

Symbol: RBED1

Synonyms: DFNB88; LST3; RBED1; RBM29

Mammalian Cell

Selection:

Neomycin

Vector: pMirTarget (PS100062)

ACCN: NM_001135021

Insert Size: 816 bp

The sequence shown below is from the reference sequence of NM_001135021. The complete

sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

 ${\sf TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC}$

AATTGAGGGAAGGAAATTCATACCAGCAGTTTTCAAATAAAAGAATTGTTCTAA

ACGCGTAAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul





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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 001135021.2</u>

Summary: This gene encodes a member of the engulfment and cell motility family of GTPase-activating

proteins that regulate Arf GTPase proteins. Members of this family are defined by a conserved

engulfment and cell motility domain. In rat cochlea, the encoded protein is found in

stereocilia, kinocilia and cuticular plate of developing hair cells suggesting a function for this protein in cochlear sensory cells. An allelic variant of this family has been associated with autosomal recessive nonsyndromic deafness-88 in humans. Alternative splicing results in

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

Locus ID: 84173

MW: 28.8