

## **Product datasheet for SC210462**

## PLEKHM2 (NM 015164) Human 3' UTR Clone

## **Product data:**

**Product Type:** 3' UTR Clones

**Product Name:** PLEKHM2 (NM\_015164) Human 3' UTR Clone

**Vector:** pMirTarget (PS100062)

Symbol: PLEKHM2

Synonyms: SKIP

**ACCN:** NM\_015164

**Insert Size:** 865 bp

Insert Sequence: >SC210462 3'UTR clone of NM\_015164

The sequence shown below is from the reference sequence of NM\_015164. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

 ${\sf TAACAATTGGCAGAGCTCAGAATTCAA}{\sf GCGATCGCC}$ 

TGTTTTTAAAATAAAATAGACATGTTATATTGCCAA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

**Restriction Sites:** Sgfl-Mlul

**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).



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

CN: techsupport@origene.cn

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



## PLEKHM2 (NM\_015164) Human 3' UTR Clone - SC210462

**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 015164.4</u>

Summary: This gene encodes a protein that binds the plus-end directed microtubule motor protein

kinesin, together with the lysosomal GTPase Arl8, and is required for lysosomes to distribute

away from the microtubule-organizing center. The encoded protein belongs to the multisubunit BLOC-one-related complex that regulates lysosome positioning. It binds a Salmonella effector protein called Salmonella induced filament A and is a critical host determinant in Salmonella pathogenesis. It has a domain architecture consisting of an N-terminal RPIP8, UNC-14, and NESCA (RUN) domain that binds kinesin-1 as well as the lysosomal GTPase Arl8, and a C-terminal pleckstrin homology domain that binds the Salmonella induced filament A effector protein. Naturally occurring mutations in this gene lead to abnormal localization of lysosomes, impaired autophagy flux and are associated with recessive dilated cardiomyopathy and left ventricular noncompaction. [provided by RefSeq,

Feb 2017]

**Locus ID:** 23207

MW: 30.6