

Product datasheet for SC210462

PLEKHM2 (NM_015164) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Symbol: PLEKHM2

Synonyms: SKIP

Mammalian Cell Neomycin

Selection:

Vector: pMirTarget (PS100062)

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

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

TGTTTTTTAAAATAAAATAGACATGTTATATTGCCAA

ACGCGTAAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Safl-Mlul



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



PLEKHM2 (NM_015164) Human 3' UTR Clone | SC210462

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.

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

filter is required.

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