

Product datasheet for SC317661

OriGene Technologies, Inc.

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PALM2AKAP2 (NM 053016) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: PALM2AKAP2 (NM 053016) Human Untagged Clone

Tag: Tag Free

PALM2AKAP2 Symbol:

Synonyms: AKAP-2; AKAP-KL; AKAP2; AKAPKL; MISP2; PALM2; PALM2-AKAP2; PRKA2

Mammalian Cell

Selection:

Neomycin

Vector: pCMV6-Entry (PS100001) E. coli Selection: Kanamycin (25 ug/mL)

Fully Sequenced ORF: >SC317661 representing NM_053016.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

ATAGAAGGCAAGCGACAACAGCTTGACGAGCAGATACTTCTGCTGCAGCATTCCAAGTCCAAAGTGCTT CGGGAGAAATGGCTGCTGCAGGGCATACCCGCTGGAACTGCCGAAGAGGAGGAAGCCAGGAGGCGGCAG TCTGAAGAGGATGAGTTCAGAGTCAAGCAACTTGAAGATAACATTCAGAGGCTGGAGCAAGAAATACAA ACGCTAGAAAGTGAAGAGTCCCAGATATCTGCCAAAGAGCAAATCATCCTAGAGAAACTGAAGGAAACA GAAAAATCCTTCAAGGACTTTCAGAAGGGTTTCTCCAGTACGGATGGAGATGCAGTAAATTACATTTCC TCCCAGCTTCCCGACCTGCCAATCCTCTGTTCACGAACAGCAGAACCATCACCTGGGCAGGACGGGACC ATTCTCTCTACATCTACCATTGGCCCAGAGGGGGTCCATCAGAAAGGAGTCAAAGTCTATGATGATGGT ACCAAAGTAGTGTATGAGGTGCGCTCAGGAGGCACCGTAGTAGAAAATGGAGTGCACAAATTAAGCACA AAGGATGTAGAAGAGCTTATTCAGAAGGCTGGACAATCAAGCTTAGGAGGAGGAGGCACGTGTCTGAAAGG ACTGTGATTGCAGATGGGAGCCTCAGCCATCCCAAGGAACACATGCTCTGCAAAGAAGCTAAGTTAGAA ATGGTACATAAGTCTAGGAAAGACCATTCTTCCGGGAACCCAGGGCAGCAGGCCCAAGCCCCCAGCGCT GCAGGGCCGGAGGCAAACTTGGATCAGCCCGTCACCATGATTTTTATGGGCTACCAAAATATCGAGGAT GAAGAGGAGACGAAAAAGGTGCTAGGCTATGATGAAACCATCAAGGCTGAATTGGTCCTCATTGATGAA GCTACAGAGCCAGCCCCAGGTACCCAAAAGAAAAAGCGCTGTCAATGCTGTGTTGTCATGTGA **ACGCGTACGCGCCCCTC**GAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT

TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: Sgfl-Mlul





PALM2AKAP2 (NM_053016) Human Untagged Clone - SC317661

ACCN: NM_053016

Insert Size: 1236 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).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning

into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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).

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: <u>NM 053016.5</u>

 RefSeq Size:
 9500 bp

 RefSeq ORF:
 1236 bp

 Locus ID:
 445815

 UniProt ID:
 Q8IXS6

 Cytogenetics:
 9q31.3

Domains: Paralemmin MW: 45.4 kDa

Gene Summary: This gene belongs to the paralemmin downstream gene (PDG) family defined in

PMID:22855693. Paralemmin downstream genes may have evolved contiguously with the paralemmin genes and are associated with other paralemmin paralogs in humans and several other taxa. The gene encodes three distinct protein isoforms, the PALM2 isoform, the AKAP2 isoform and the PALM2-AKAP2 isoform. The biological significance of the PALM2-AKAP2 isoforms is yet unknown. Earlier, PALM2 and AKAP2 were annotated as separate genes and PALM2-AKAP2 was annotated as a readthrough gene. [provided by RefSeq, May 2019] Transcript Variant: This variant (1) represents the longest transcript and encodes isoform 1 (PALM2). 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.