

Product datasheet for **SC328096**

MICAL3 (NM_015241) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	MICAL3 (NM_015241) Human Untagged Clone
Tag:	Tag Free
Symbol:	MICAL3
Synonyms:	MICAL-3
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_015241, the custom clone sequence may differ by one or more nucleotides

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ATGGAGGAGAGGAAGCATGAGACCATGAACCCAGCTCATGTCCTCTTTGACCGGTTTGTC
CAGGCCACCACTGCAAGGGAACCTCAAGGCTTTCCAGGAGCTCTGTGACCACTGGAA
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GGAAAAGCGTGCACTAACACCAAGTGTCTCATCATTGGGGCTGGCCCTGTGGTCTCCGT
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GGTGCCAAAGAAGTTCTATGGCAAGTTCTGTGCTGGAGCCATCGACCATATCAGTATCCGT
CAGCTCCAATAACTTTTGAAGTAGCCTTGATCCTAGGCATTGAAATCCACGTCAT
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GAGAGCCTGGTGAATTCCTCGAACCACCCCAAAATTGACTCGCAATGAGTCTGTAGCTCGT
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 CTGGAGGTGGTGGAGCAGAGAGACTCACTGGTGGCGCTGCTGGAGGAGCAGCGGCTCCGG
 GAGAGAGAGGAGACAAGGACCTGGAGGCTGCCATGCTGTCCAAGGGCTTCAGCCTTAAC
 TGGTCC

Restriction Sites:

Please inquire

ACCN:

NM_015241

OTI Disclaimer:

Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. [More info](#)

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_015241.2, NP_056056.2</u>
RefSeq Size:	9471 bp
RefSeq ORF:	6009 bp
Locus ID:	57553
UniProt ID:	<u>Q7RTP6</u>
Cytogenetics:	22q11.21
Gene Summary:	Monooxygenase that promotes depolymerization of F-actin by mediating oxidation of specific methionine residues on actin to form methionine-sulfoxide, resulting in actin filament disassembly and preventing repolymerization. In the absence of actin, it also functions as a NADPH oxidase producing H₂O₂. Seems to act as Rab effector protein and plays a role in vesicle trafficking. Involved in exocytic vesicles tethering and fusion: the monooxygenase activity is required for this process and implicates RAB8A associated with exocytotic vesicles. Required for cytokinesis. Contributes to stabilization and/or maturation of the intercellular bridge independently of its monooxygenase activity. Promotes recruitment of Rab8 and ERC1 to the intercellular bridge, and together these proteins are proposed to function in timely abscission.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (1) represents the longest transcript and encodes the longest isoform (1). 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.