

## **Product datasheet for MC208002**

## Cdc42 (NM\_009861) Mouse Untagged Clone

**Product data:** 

**Product Type:** Expression Plasmids

Product Name: Cdc42 (NM\_009861) Mouse Untagged Clone

Tag: Tag Free Symbol: Cdc42

**Synonyms:** Al747189; AU018915

Mammalian Cell

Selection:

Neomycin

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

Fully Sequenced ORF: >MC208002 representing NM\_009861

Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC

GCCGCGATCGCC

GTGTGTGCTGCTATGA

**ACGCGT**ACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT

ACAAGGATGACGACGATAAGGTTTAA

Chromatograms: <a href="https://cdn.origene.com/chromatograms/ja2259-a07.zip">https://cdn.origene.com/chromatograms/ja2259-a07.zip</a>

**Restriction Sites:** Sgfl-Mlul ACCN: NM\_009861

**Insert Size:** 576 bp



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## **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 <a href="mailto:customercom">customercom</a> 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. <u>More info</u>

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>BC064792</u>, <u>AAH64792</u>

 RefSeq Size:
 2151 bp

 RefSeq ORF:
 576 bp

 Locus ID:
 12540

 UniProt ID:
 P60766

 Cytogenetics:
 4 69.83 cM



## **Gene Summary:**

Plasma membrane-associated small GTPase which cycles between an active GTP-bound and an inactive GDP-bound state (PubMed:24352656). In its active state binds to a variety of effector proteins to regulate cellular responses. Involved in epithelial cell polarization processes. Regulates the bipolar attachment of spindle microtubules to kinetochores before chromosome congression in metaphase. Regulates cell migration (By similarity). In neurons, plays a role in the extension and maintenance of the formation of filopodia, thin and actinrich surface projections. Required for DOCK10-mediated spine formation in Purkinje cells and hippocampal neurons (PubMed:25851601). Facilitates filopodia formation upon DOCK11-activation (PubMed:22494997). Upon activation by CaMKII, modulates dendritic spine structural plasticity by relaying CaMKII transient activation to synapse-specific, long-term signaling (By similarity). Also plays a role in phagocytosis through organization of the F-actin cytoskeleton associated with forming phagocytic cups (By similarity). [UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (1) represents the longer transcript and encodes 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.