

Product datasheet for MC226182

Cdc42 (NM_001243769) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Cdc42 (NM_001243769) Mouse Untagged Clone
Tag: Tag Free
Symbol: Cdc42
Synonyms: A1747189; AU018915
Mammalian Cell Selection: Neomycin
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Fully Sequenced ORF: >MC226182 representing NM_001243769
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGCC**

ATGCAGACAATTAAGTGTGTTGTTGGTGATGGTGCTGTTGGTAAACATGTCTCCTGATATCTACA
 CAACAAACAAATCCCATCGGAATATGTACCAACTGTTTTGACAACTATGCAGTCACAGTTATGATTGG
 TGGAGAGCCATACACTCTTGACTTTTTGATACTGCAGGGCAAGAGGATTATGACAGACTACGACCGCTA
 AGTTATCCACAGACAGATGTTTTCTAGTATGTTTCTCAGTGGTCTCTCCATCCTCATTTGAAAATGTGA
 AAGAAAAGTGGGTGCCTGAGATAACTCACCAGTGTCCAAAGACTCCTTTCTTGCTTGTGGACCCAAAT
 TGATCTCAGAGATGACCCCTCTACTATTGAGAACTTGCCAAGAACAAACAGAAGCCTATTACTCCAGAG
 ACTGCTGAAAAGCTGGCGCGGGATCTGAAGGCTGTCAAGTATGTGGAGTGCTCTGCCCTCACACAGAGAG
 GTCTGAAGAATGTGTTTGATGAGGCTATCCTAGCTGCCCTCGAGCCTCCGGAACTCAACCCAAAAGGAA
 GTGCTGTATATTC**TAA**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001243769
Insert Size: 576 bp


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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:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<ol style="list-style-type: none"> 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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	<u>NM_001243769.1</u> , <u>NP_001230698.1</u>
RefSeq Size:	1521 bp
RefSeq ORF:	576 bp
Locus ID:	12540
UniProt ID:	<u>P60766</u>
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 actin-rich 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 (2) uses an alternate 3' terminal exon, compared to variant 1. It encodes isoform 2, which is the same length but has a distinct C-terminus, compared to 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.