

Product datasheet for **MC222856**

Mical2 (NM_177282) Mouse Untagged Clone

Product data:

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|---------------------------|---|
| Product Type: | Expression Plasmids |
| Product Name: | Mical2 (NM_177282) Mouse Untagged Clone |
| Tag: | Tag Free |
| Symbol: | Mical2 |
| Synonyms: | 5330438E18Rik; 9530064J02; MICAL-2; mKIAA0750 |
| Mammalian Cell Selection: | Neomycin |
| Vector: | pCMV6-Entry (PS100001) |
| E. coli Selection: | Kanamycin (25 ug/mL) |



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Fully Sequenced ORF:

>MC222856 representing NM_177282

Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGCATCGCC**

ATGGGAGAGAATGAAGATGAGAAGCAGGCGCAGGCCAGCCAGGTCTTCGAGAACCTTTGTGCAAGCTACCA
CATGCAAAGGGACCCTCCAGGCCTCAACATCCTCACCTGCCTCCTGGACCTAGATCCGCTGGACCATAG
GAACTTCTACTCCCAGCTCAAGTCCAAGGTGAACACCTGGAAGGCCAAAGCCCTGTGGCACAACCTGGAT
AAGCGCGGCTCCCAAGGAGTACAAGCGAGGAAAAGCCTGCTCGAACCTAAGTGTCTCATCGTCGGAG
GAGGACCATGTGGCTTGCCTACTTGAACCTACCTGGGAGCCAAAGTGGTTGTGGTGGAGAA
GAGGGACACCTTCTCCCGAACAATGCTCTGCACCTCTGGCCCTTCACTATCCATGACCTGCGGGCCCTG
GGGGCCAAGAAGTTCTATGGAAATTCGTGCTGGCTCCATCGACCACATCAGTATCCGACAACCTGCAGC
TTATCCTCTTCAAGGTGGCCCTGATGCTGGGAGTGGAGGTCCACGTGAATGTGGAGTTTGTGAGGGTGT
GGAGCCTCCTGAAGACCAAGAGAATCAAAAAGTTGGATGGCGGGCAGAATTCCTTCTGCAGACCACGCC
CTGTCTGACTTTGAGTTTGTATGTCATCATCGGTGCTGACGGTACAGGAACACGCTAGAAGGCTTACGGA
GGAAAGAGTTCAGGAGGAAGCTGGCCATCGCCATCACCGCAACTTCATAAACAGGAACAGCACAGCTGA
GGCCAAGGTGGAGGAGATCAGTGGTGTTCCTTCAACAGAAAGTTTCCAGGACCTGAAGGAA
GAAACAGGGATTGATCTCGAACAATTGTTACTATAAGGACAGTACCCACTACTTTGTCATGACAGCCA
AGAAGCAGAGCCTGCTGGACAAGGGCGTCATCCTTAATGACTACATTGACACAGAGATGCTGCTGTGTTT
GGAGAAATGTGAACCAGGACAACCTGCTCCTACGCCAGAGAAGCCGCTGACTTTGCCACCAACTACCAG
CTGCCATCCTTAGACTTTGCCATCAATCACAACGGGCAGCCTGACGTGGCCATGTTGACTTCCACCTCCA
TGTATGCCTCAGAGAACGCAGCTCTGATGCGTGAGCGCCAGGCACACCAGCTGCTCGTGGCTTTGTGGG
CGACAGCCTGCTTGAGCCATTTTGGCCATGGGCACAGGCTGTGCCCGAGGCTTCCCTGGCAGCCTTTGAC
ACGGCATGGATGGTGAAGAGCTGGGACCAGGGCACCCCTCCCCTGGAGGTATTAGCTGAAAGAGAGAGTC
TTTACAGGCTGTTACCTCAGACAACCCAGAGAACATCAACAAAAATTTTGGAGTACACATTGGACCC
AGCCACGCGGTACCCAAACCTCAACCTGCACTGCGTCAGGCCTCACAGGTGAAGCATTGTACATCACT
AAGGAGATGGACCGCTTCCCTCTCGAGAGATGGGGCTCAGTGAGGAGATCTGTCAGCCTCTCCAGGCGGG
AGTCAGACATCCGGCCTAACAAGCTTTTAACTGGTGCCAGCAGCAGACCAAGGGTTACCAGCACGTGAG
AGTCACTGACCTGACCACATCCTGGCGCAGCGCTTGGCCCTGTGTGCCATCATCCACAGCTTCCGGCCA
GAGCTGATCAACTTTGACTCGTGAATGAAGATGACGCTGTGGAGAACAACCAACTGGCATTGATGTGG
CCAAGCGTGAGTTTGGGATCCTGCTGTGACCACAGGCAAGAGATGGCATCTACCCAGGAGCCAGACAA
GCTCAGCATGGTCATGTACCTCTCCAAGTTCTATGAGCTCTTCCGGGGCACTCCACTGAGACCCATGGAT
TCCTGGCGTAAAACTATGGAGAAAATGCTGACTTTGGCTTGGGCAAAACATTATTTCAGAACTATC
TCAACCTCACATTTGCCAGAAAGAGGACCCACGGGTAGACACCCAGACTGAAGAGAATGACATGAACAA
GAGGCGGCAGACAAGGCTTCAACCACTGGAAGAGCTGCCATCCTTCTCCAGCCGAGCCTGGGCTCCAGT
CAAGAGTATGCTAAAGAAAGTGGCAGTCAAGCAAGGTCAAGCACATGGCCAATCAGTGTAGCCAAGT
TTGAGGAGAACACTCGGAACCTTCACTCGTGAACAGGAATCCCGAGAAAGGCATTCCCCTGAGCCT
GGGCGGCAGAGACACCTGCTACTTTTGAAGAAGCGTGTATACATGATAGAGCGGTGAGTGTGAGGGC
CACTTTTCCACCAAGAGTGCTTCCGTTGCAGCGTCTGCAGTGCCACCCTGCGCCTGGCTGCCTATGCCT
TTGACTGCGATGAAGGCAATTTTACTGAAGCCCATTTTGTACTGCAAAACAGTAGCAAACAGCG
AAAGAGACGGGCAGAGCTGAATCAGCAAAGAGAGGAGGAAGGAACATGGCAGGAGCAGGAAGCACCTCGG
AGGGATGTACCCACAGAAAGCTTGTGTCAGTGGCGGCCATCAGCACGCCAGAAGGCAGCCCCCAGGTA
CCTCCACCTCCTTCTTGAAGGCACTCAGCTGGCCTCTCCGGCTGACAAGAGGCTGCTCAACCTGCC
CCAGAGCCTGCTTAGGTGGATGCAGGGACTCCAGGAGGCTGCTGGCCACCATGTGCGGGACAATGCTCAC
AACTACTGCTTATGTTGAGCTCCTGAGCCTGGGGCTGCTACTGCTCTGGGCTTTCTCCAAGTCTCTGG
CTGCCATGTACAGAGAGTCTGAGGAGTCTTGGAGAACATCCGCAGCTGGCTGCTCAGGTTATCCCACT
GAAGCTGCAGTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

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| Restriction Sites: | Sgfl-Mlul |
| ACCN: | NM_177282 |
| Insert Size: | 2883 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). |
| 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. |
| RefSeq: | <u>NM_177282.5</u> , <u>NP_796256.1</u> |
| RefSeq Size: | 6689 bp |
| RefSeq ORF: | 2883 bp |
| Locus ID: | 320878 |
| UniProt ID: | <u>Q8BML1</u> |
| Cytogenetics: | 7 F1 |
| Gene Summary: | <p>Nuclear 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 (PubMed:23911929, PubMed:23927065). In the absence of actin, it also functions as a NADPH oxidase producing H₂O₂ (By similarity). Acts as a key regulator of the SRF signaling pathway elicited by nerve growth factor and serum: mediates oxidation and subsequent depolymerization of nuclear actin, leading to increase MKL1/MRTF-A presence in the nucleus and promote SRF:MKL1/MRTF-A-dependent gene transcription. Does not activate SRF:MKL1/MRTF-A through RhoA (By similarity).</p> <p>[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (B) lacks 5 alternate exons, resulting in the loss of an in-frame segment in the 3' coding region, and uses an alternate splice site in the 3' coding region, compared to variant 1. The resulting protein (isoform B) is shorter and has a distinct C-terminus, compared to isoform A. 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.</p> |