

Product datasheet for **MC210049**

Morf4I2 (NM_001168225) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Morf4I2 (NM_001168225) Mouse Untagged Clone
Tag: Tag Free
Symbol: Morf4I2
Synonyms: 2410017O14Rik; mKIAA0026; Mrgx; Sid393p
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC210049 representing NM_001168225
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGAGTCCAGAAAGCAGGCTTCTCAAACCTCGTGGACAACAATCTGCTGAAGAAGACAACTTAAGAAAC
CAACTCGAAGCAATATGCAGAGAAGTAAGATGAGAGGAGCTGCCTCGGAAAGAAGTCAGCTGGTTCGCA
GCCAAAGAATCTCGATCCAGCCCTGCCCGAAGATGGGGAGGTCGCTCTGCTGAGAACCCCTTCCGGT
TCTGTGCGGAAGACCAGGAAGAACAAGCAGAAGGCTCCTGGCAACGGAGACGGAGGCAGTACCAGTGAAG
TCCCCAGCCCCCTCGGAAGAAAAGGGCACGGGCTGACCCCACTGTGGAGAGCGAGGAGGCATTCAGAG
TAGGATGGAGGTGAAGGTGAAGATCCCTGAAGAATTAACCGTGGCTGGTGGAGGACTGGGACTTGGTT
ACGAGGCAGAAGCAGTTGTTCCAGCTCCCTGCTAAAAAGAATGTCGATGCCATTCTTGAGGAGTATGCCA
ATTGTAAGAAGTCGCAGGGAAATGTTGATAATAAGGAGTACGCAGTTAATGAAGTTGTAGGAGGGATAAA
AGAGTATTTCAATGTGATGCTGGCACTCAGCTGCTGTACAAGTTTGAAGGCCTCAGTATGCTGAGATT
CTGCTGGCTCACCTGATGCGCCGATGTCGCAGATCTATGGGGGCCACACCTCCTGAGATTATTCGTGA
GAATTGGGGCAATGTTGGCCTATACGCCCTTGATGAGAAAAGCCTGGCATTATTGCTGGGCTATCTGCA
TGATTTTCCTTAAGTATCTGGCAAAGAATTCTGCCTCTCTGTTTACTGCCAGTGATTACAAAGTGGCTTCT
GCTGACTATCATCGCAAAGCCCTGTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001168225
Insert Size: 867 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).
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_001168225.1, NP_001161697.1</u>
RefSeq Size:	1947 bp
RefSeq ORF:	867 bp
Locus ID:	56397
UniProt ID:	<u>Q9R0Q4</u>
Cytogenetics:	X F1
Gene Summary:	<p>Component of the NuA4 histone acetyltransferase complex which is involved in transcriptional activation of select genes principally by acetylation of nucleosomal histone H4 and H2A. This modification may both alter nucleosome - DNA interactions and promote interaction of the modified histones with other proteins which positively regulate transcription. This complex may be required for the activation of transcriptional programs associated with oncogene and proto-oncogene mediated growth induction, tumor suppressor mediated growth arrest and replicative senescence, apoptosis, and DNA repair. The NuA4 complex ATPase and helicase activities seem to be, at least in part, contributed by the association of RUVBL1 and RUVBL2 with EP400. NuA4 may also play a direct role in DNA repair when directly recruited to sites of DNA damage. Also component of the MSIN3A complex which acts to repress transcription by deacetylation of nucleosomal histones (By similarity).[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) differs in the 5' UTR compared to variant 1. Variants 1 through 7 encode the same protein. 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>