

## **Product datasheet for MC208975**

## Meis2 (NM\_001159569) Mouse Untagged Clone

## **Product data:**

**Product Type:** Expression Plasmids

**Product Name:** Meis2 (NM\_001159569) Mouse Untagged Clone

Tag: Tag Free Symbol: Meis2

Synonyms: A430109D20Rik; Mei; Mrg; Mrg1; Str; Stra10

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

Cell Selection: Neomycin

Fully Sequenced ORF: >MC208975 representing NM\_001159569

Red=Cloning site Blue=ORF Orange=Stop codon

ATGTTTCTGTACGATGAGCTGCCCCATTACGGCGGGATGGACGGAGTAGGGGTTCCCGCTTCCATGTACG GAGACCCTCACGCGCCGGCCGATCCCCCCGGTTCACCACCTAAACCACGGGCCGCCGCTCCACGCCAC GCCTTGAAAAGAGACAAGGACGCAATCTATGGGCACCCGTTGTTTCCTCTGTTAGCTCTGGTTTTTGAGA AGTGCGAGCTGGCGACCTCCCCGGGAACCCGGAGTGGCCGGCGGAGACGTCTGTTCCTCTGACTC CTTCAACGAGGACATCGCGGTCTTCGCCAAGCAGGTTCGCGCCGAAAAGCCTCTTTTTTCCTCAAACCCA GAGCTGGATAATTTGATGATACAAGCAATTCAAGTACTAAGGTTTCATCTTCTGGAGTTAGAAAAGGTCC ACGAACTATGTGATAACTTCTGCCACCGGTACATTAGCTGTTTGAAGGGAAAAATGCCCATTGACCTCGT GATTGATGAGAGAGATGGAAGCTCCAAGTCAGATCATGAAGAACTTTCAGGCTCCTCCACAAATCTCGCC GACCACAACCCTTCATCCTGGCGAGACCACGATGACGCAACCTCAACGCACTCCGCAGGCACCCCAGGAC CCTCCAGTGGGGGCCATGCTTCCCAGAGTGGAGACAACAGCAGTGAGCAAGGCGATGGGTTAGACAACAG CGTAGCTTCACCTGGCACAGGTGATGACGACGATCCAGACAAGGACAAAAAAACGCCAGAAGAAAAAAGGCC ATATTCCCCAAAGTCGCGACAAATATCATGAGAGCGTGGCTCTTCCAGCATCTCACACACCCCGTACCCTT CAGAAGAACAGAAGAAACAGTTAGCGCAAGACACGGGACTGACAATTCTGCAAGTGAACAACTGGTTTAT CAATGCCAGAAGAAGAATAGTGCAGCCCATGATTGACCAGTCAAATCGAGCAGGTTTTCTTCTTGATCCT TCAGTGAGCCAAGGAGCAGCGTATAGTCCAGAGGGTCAGCCCATGGGGAGCTTTGTGTTTGGATGGTCAGC **GCACTATATGTAA** 

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATTACAAGGATGACGACGATAAGGTTTAA



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## Meis2 (NM\_001159569) Mouse Untagged Clone - MC208975

**Restriction Sites:** Sgfl-Mlul

**ACCN:** NM\_001159569

**Insert Size:** 1203 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:** 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 001159569.1</u>, <u>NP 001153041.1</u>

RefSeq Size:5010 bpRefSeq ORF:1203 bpLocus ID:17536

Cytogenetics: 2 58.28 cM

**Gene Summary:** This gene encodes a homeobox protein belonging to the TALE ('three amino acid loop

extension') family of homeodomain-containing proteins. TALE homeobox proteins are highly conserved transcriptional regulators and several members have been shown to be essential contributors to developmental programs. In mice, a knock-out of this gene leads to lethality at embryonic day 14, accompanied with hemorrhaging. Embryos lacking this gene show defects in tissues derived from the neural crest, suggesting a critical role of this gene during cranial and cardiac neural crest cell development. Alternative splicing results in multiple transcript

variants. [provided by RefSeq, Sep 2016]

Transcript Variant: This variant (5) has multiple differences in the coding region and differs in the 3' UTR, compared to variant 9. The encoded isoform (5) is shorter and has a distinct C-terminus compared to isoform 9. 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.